

130312

From: Kaushal, Sumesh  
Sent: Thursday, August 19, 2004 2:14 PM  
To: STIC-Biotech/ChemLib  
Subject: 10787382 : Sequence search

CRIFE

**10/787382 : Sequence search**

Title: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

Inventor: YANG, SHUMIN

Please search

**DNA**

- SEQ ID NO: 4 length 610
- SEQ ID NO: 7 length 402
- SEQ ID NO: 9 length 345
- SEQ ID NO: 18 length 1658
- Oligosearch for SEQ ID NO: 18 -

**PRT**

- SEQ ID NO: 5 length 134
- SEQ ID NO: 10 length 115

*S. Kaushal*

AU1636, REM2.B85

Ph: 571-27-20769

Mail Box: REM2.C70

\*\*\*\*\*

## STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: 8/24/04  
Date Completed: 9/1/04  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search  
NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: 04/02p  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:40:07 ; Search time 96.8675 Seconds  
(without alignments)  
390.857 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLSQLGAAVVSAP.....FLDYQLQVFLGVINTEWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	3	AAV58219 Canine in
2	687	98.7	134	4	AAV72615 Canine in
3	610	87.6	115	3	AAV58220 Canine ma
4	536	77.0	132	2	AAW08479 Ovine IL-
5	430	61.8	134	2	AAW92802 Human int
6	430	61.8	134	4	AAV72617 Human int
7	430	61.8	134	5	ABG94294 Human int
8	430	61.8	134	5	ABG80606 Human pre
9	430	61.8	134	5	AAU10353 Interleuk
10	430	61.8	285	6	AAO30457 hIL5-P30-
11	430	61.8	285	6	AAO30458 hIL5-P2-P
12	429	61.6	84	4	AAV72616 Canine in
13	426	61.2	134	5	AAU10354 Interleuk
14	420	60.3	134	1	AAV81056 Sequence
15	415.5	59.7	287	6	AAO30460 hIL5.37 v
16	413.5	59.4	287	6	AAO30459 hIL5.36 v
17	376	54.0	133	1	AAV71064 Murine eo
18	376	54.0	133	2	AAV96963 T cell re
19	376	54.0	133	2	AAW72949 T cell re
20	376	54.0	133	2	AAW72947 T cell re
21	376	54.0	133	4	AAV72618 Murine in
22	375	53.9	133	1	AAV82969 B cell di
23	359	51.6	136	5	ABG94352 Human C-I
24	359	51.6	136	5	ABG80664 Human ILn
25	357	51.3	113	1	AAV93152 Sequence

26	357	51.3	123	5	ABG94353 Human C-I
27	357	51.3	123	5	ABG80665 Human IL-
28	357	51.3	138	5	ABG94351 Human C-I
29	357	51.3	138	5	ABG80663 Human ILn
30	356	51.1	112	1	AAV80279 Pleiotrop
31	356	51.1	115	1	AAV81038 Sequence
32	356	51.1	115	3	AAV45489 Human int
33	356	51.1	115	5	ABG94295 Human mat
34	356	51.1	115	5	ABG80607 Human mat
35	356	51.1	115	6	AAO30453 Human mat
36	355	51.0	133	1	AAV82800 Murine pl
37	351	50.4	121	2	AAW43436 Human int
38	347	49.9	115	2	AAW05273 N-termina
39	347	49.9	115	2	AAW72948 Truncated
40	347	49.9	134	5	ABG94349 Mouse C-I
41	347	49.9	134	5	ABG80661 Mouse IL-
42	344	49.4	136	5	ABG94348 Mouse C-I
43	344	49.4	136	5	ABG80660 Mouse IL-
44	343	49.3	113	2	AAW05274 N-termina
45	343	49.3	113	5	ABG94296 Mouse int

ALIGNMENTS

RESULT 1  
AAV58219  
ID AAV58219 standard; protein; 134 AA.

AC AAV58219;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-5 (IL-5).  
XX  
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
XX  
OS Canis familiaris.  
XX  
PN WO961618-A2.  
XX  
PD 02-DEC-1999.  
XX  
PF 28-MAY-1999; 99WO-US011942.  
XX  
PR 29-MAY-1998; 98US-0087306P.  
XX  
(HESK-) HESKA CORP.

PA Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI WPI; 2000-072623/06.  
DR N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.  
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease.  
PS Claim 3h; Page 224; 264pp; English.

XX Sequences AAV58219-Y58220 represent encoded and mature canine interleukin  
CC -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3  
CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),  
CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline  
CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides  
CC which encode these immunoregulatory proteins. The proteins, their  
CC associated nucleic acids, specific antibodies and inhibitors may be used  
CC as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX  
 SQ Sequence 134 AA;

Query Match 100.0%; Score 696; DB 3; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-75;  
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKNH 60  
 DB 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKNH 60  
 QY 61 QLCIKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYQ 120  
 DB 61 QLCIKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYQ 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 VFLGVINTEWTPES 134

RESULT 2  
 AAB72615  
 ID AAB72615 standard; protein; 134 AA.

AC AAB72615;  
 DT 04-MAY-2001 (first entry)

DE Canine interleukin-5 protein #1.

KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
 KW inflammatory reaction.

XX Canis sp.

XX WO200111049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021651.

XX 10-AUG-1999; 99US-00371615.

XX (IDEX-) IDEXX LAB INC.

PI Guo H, Lawton R, Mermer B, Aiyappa AP;

XX WPI; 2001-191542/19.

DR N-PSDB; AAF74300.

XX Novel canine interleukin 5 polynucleotide and polypeptides are used for  
 XX generating antibodies which are useful in treating allergies in dogs.

PS Claim 29; Page 46-47; 48pp; English.

XX The present invention provides the protein and coding sequences of the  
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
 CC cancer and inflammatory reactions in dogs. The present sequence is one  
 CC version of the IL-5 protein shown in the specification  
 XX  
 SQ Sequence 134 AA;

Query Match 98.7%; Score 687; DB 4; Length 134;  
 Best Local Similarity 99.3%; Pred. No. 8.2e-74;  
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKNH 60

DB 1 MRMLNLSLLALGAAYVSAPAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKNH 60  
 QY 61 QLCIKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYQ 120  
 DB 61 QLCIKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYQ 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 VFLGVINTEWTPES 134

RESULT 3

AAY58220

ID AAY58220 standard; protein; 115 AA.

XX AAY58220;

AC AAY58220;

XX 14-MAR-2000 (first entry)

DE Canine mature interleukin-5 (IL-5).

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

DR N-PSDB; AAZ55550, AAZ55551.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 XX useful for treating or preventing e.g. tumors or autoimmune disease.

PS Claim 3h; Page 227; 264pp; English.

XX Sequences AAY58219-Y58220 represent encoded and mature canine interleukin  
 CC -5 (IL-5). The invention relates to canine IL-4, canine or feline Flt-3  
 CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),  
 CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline  
 CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides  
 CC which encode these immunoregulatory proteins. The proteins, their  
 CC as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX  
 SQ Sequence 115 AA;

Query Match 87.6%; Score 610; DB 3; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPMNLVAETLLTLLSTHRTWLIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNOTA 79



Db 1 FAVENPMNRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNHQLCIKEVFGIDTLTKNOTA 60  
 Qy 80 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 134  
 Db 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 115

RESULT 4  
 ID AAW08479 standard; protein; 132 AA.  
 XX AAW08479;  
 AC AAW08479;  
 DT 17-OCT-2003 (revised)  
 DT 24-SEP-1997 (first entry)  
 XX XX  
 DE Ovine IL-5.  
 XX Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
 KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
 KW immunosuppression; allergy; reproductive system; growth; early maturity;  
 KW antibody; diagnosis; immunopotentiator;  
 KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
 KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon.  
 XX OS Ovis aries.  
 XX WO9700321-A1.  
 XX 03-JAN-1997.  
 XX 14-JUN-1996; 96WO-AU000360.  
 XX 14-JUN-1995; 95AU-00003502.  
 PR 27-OCT-1995; 95AU-00006244.  
 XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX Seow H, Wood P;  
 PI WPI; 1997-077528/07.  
 DR N-PSDB; AAT50755, AAT50756.  
 XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine  
 PT adjuvants and to treat or prevent microbial infections in livestock.  
 XX Claim 31; Page 39-40; 78pp; English.

CC This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5  
 CC or IL-12 are used to treat and/or prevent infections in livestock (esp.  
 CC cows and sheep), particularly where the animals are stressed, e.g. during  
 CC transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for  
 CC veterinary use (partic. weakly immunogenic subunit or synthetic peptide  
 CC vaccines). They may also be used to treat cancer, immunosuppression and  
 CC allergy, to enhance/suppress the reproductive system and to promote  
 CC growth or early maturity. Optionally interleukin can be delivered from  
 CC constructs or delivery cells and antibodies are useful in enzyme  
 CC immunoassays for rapid diagnosis of infection. The interleukins are  
 CC immunopotentiators, especially IL-5 promotes growth of early  
 CC haematopoietic progenitor cells and generation of cytotoxic cells from  
 CC thymocytes, also it stimulates production and secretion of IgM and IgA  
 CC (in synergism with bacterial endotoxin). IL-12 induces production of  
 CC gamma-interferon by, and proliferation of, T and NK cells and increases  
 CC the (non-)specific cytolytic lymphocyte response. The genetic constructs  
 CC can also be used for in vitro production of IL-5 or -12. (Updated on 17-  
 CC OCT-2003 to standardise OS field)  
 XX Sequence 132 AA;

Query Match 77.0%; Score 536; DB 2; Length 132;  
 Best Local Similarity 78.8%; Pred. No. 9.6e-56;  
 Matches 104; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

Qy 3 MLNLNLSLLAAGAAVVSFAFVENPMNRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNHQL 62  
 Db 1 MHLRUTLVAGAAVVCANAVESTMNLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNHQL 60  
 Qy 63 CIKEVFGIDTLTKNOTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQV 122  
 Db 61 CIEEVFGIDTLTKNOTAOGDAVKKIFRNLSLIKEYIDQKRCGGERWRVQFLDYQLQV 120

Qy 123 LGVINTEWTPES 134  
 Db 121 LGVINTEWTPES 132

RESULT 5  
 ID AAR92802 standard; protein; 134 AA.  
 XX AAR92802;  
 AC AAR92802;  
 DT 24-MAY-1996 (first entry)  
 XX Human interleukin-5.  
 DE DE  
 XX Cytokine; mutein; interleukin-5; agonist; antagonist; diagnosis; therapy;  
 KW cancer; inflammation; degenerative disease.  
 KW Homo sapiens.  
 XX WO9604306-A2.  
 XX 15-FEB-1996.  
 XX 31-JUL-1995; 95WO-US008950.  
 PR 01-AUG-1994; 94US-00284393.  
 XX (SCHE ) SCHERING CORP.  
 XX Zurawski SM, Zurawski G;  
 PI WPI; 1996-129335/13.  
 DR Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and murine  
 PT P600 contg. amino acid substitutions. - useful for the diagnosis and  
 PT treatment of cancer, inflammation, etc.  
 XX Disclosure; Page 43; 52pp; English.

CC Muteins of human interleukin-5 (AAR92802) and other cytokines (see also  
 CC AAR92790-801) are obtd. by site-directed mutagenesis of natural cytokine  
 CC sequences at positions identified as critical for activity. The muteins  
 CC are useful in the screening of cytokine and cytokine receptor levels, and  
 CC in the diagnosis or treatment of e.g. inflammation, cancer, and  
 CC degenerative disorders  
 XX Sequence 134 AA;  
 SQ Query Match 61.8%; Score 430; DB 2; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 4.8e-43;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSLLAAGAAVVSFAFVENPMNRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNH 60  
 Db 1 MRMLNLSLLAAGAAVVSFAFVENPMNRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKNH 60  
 Qy 61 QLCIKEVFGIDTLTKNOTAHGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYQLQ 120  
 Db 61 QLCIEIFQIGTILTSQTVOGTVERLFAVSLINKYIDGQKKCGEERRVNVQFLDYQLQ 120

Qy 121 VFLGVINTEWTPES 134  
 Db 121 EFLGVINTEWTPES 134

```

RESULT 6
AAB72617
ID AAB72617 standard; protein; 134 AA.
AC
XX AAB72617;
XX
DT 04-MAY-2001. (first entry)
XX
DE Human interleukin-5.
XX
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; human.
XX
OS Homo sapiens.
XX
PI WO200111049-A2.
XX
PD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021651.
XX
PR 10-AUG-1999; 99US-00371615.
XX
PA (IDEX-) IDEX LAB INC.
XX
PI Guo H, Lawton R, Mermer B, Aliyappa AP;
XX
DR WPI; 2001-191542/19.
XX
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
XX Disclosure; Fig 2; 48pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is human
CC IL-5
XX
XX Sequence 134 AA;
XX
Query Match 61.8%; Score 430; DB 4; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.8e-43;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLGSLALGAAYVSFAVENPMNRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKXH 60
DB 1 MRMLHLGSLALGAAYVTAIPTETLSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60
QY 61 QLCIKVEFGQIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFLDYLQ 120
DB 61 QLCTEEIFQGIGTLESQTVGGTVERLFKNLSLIKVIYDQKKKGERRRVNQFLDYLQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIIES 134
RESULT 7
ABG94294
ID ABG94294 standard; protein; 134 AA.
XX
AC ABG94294;
XX
XX 10-DEC-2002 (first entry)
XX
DE Human interleukin 5 precursor protein.
XX
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
KW vaccine; infectious disease.
XX
XX
OS Homo sapiens.
XX
PI WO200256905-A2.
XX
PD 25-JUL-2002.
XX
PF 21-JAN-2002; 2002WO-IB000166.
XX
PR 19-JAN-2001; 2001US-0262379P.
XX
PR 04-MAY-2001; 2001US-0288549P.
XX
PR 05-OCT-2001; 2001US-0326998P.
XX
PR 07-NOV-2001; 2001US-0331045P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
PI Piossek C;
XX
XX WPI; 2002-627351/67.
XX
XX Molecular antigen array used in the production of vaccines for infectious
PT diseases.
XX
PS Disclosure; Page 422; 441pp; English.
XX
CC This invention relates to a novel ordered and repetitive antigen array
CC used in the production of vaccines for infectious diseases. The invention
CC also discloses a composition comprising a non-natural molecular scaffold
CC comprising a core particle selected from a core particle of a non-natural
CC origin and a core particle of natural origin and an organiser comprising
CC at least one first attachment site, where the organiser is connected to
CC the core particle by at least one covalent bond. Also disclosed is an
CC antigen or antigenic determinant with at least one second attachment
CC site, where the antigen or antigenic determinant is amyloid beta peptide
CC (Abeta1-42) or its fragment and where the second attachment site is a
CC selected from an attachment site not naturally occurring with the antigen
CC or antigenic determinant and an attachment site naturally occurring with
CC the antigen or antigenic determinant, where the second attachment site is
CC capable of association through at least one non-peptide bond to the first
CC attachment site and where the antigen or antigenic determinant and the
CC scaffold interact through the association to form an ordered and
CC repetitive antigen array. The invention also comprises a coat protein
CC capable of forming a capsid which comprises mutant beta coat proteins
CC having an amino acid sequence selected from five amino acid sequences
CC fully defined in the specification. The compounds of the invention may
CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,
CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in
CC immunisation and as a vaccine. The present sequence represents a protein
CC sequence used to create the compositions of the invention
XX
XX Sequence 134 AA;
XX
Query Match 61.8%; Score 430; DB 5; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.8e-43;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLGSLALGAAYVSFAVENPMNRLVAETLLTLLSTHRTWLIGDGNLMIPTPENKXH 60
DB 1 MRMLHLGSLALGAAYVTAIPTETLSALVKETLALLSTHRTLLIANETLRIPVPVHKNH 60
QY 61 QLCIKVEFGQIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFLDYLQ 120
DB 61 QLCTEEIFQGIGTLESQTVGGTVERLFKNLSLIKVIYDQKKKGERRRVNQFLDYLQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIIES 134
RESULT 8
ABG80606
ID ABG80606 standard; protein; 134 AA.
XX
XX

```

AC ABG80606;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Human precursor Interleukin 5.  
 XX  
 KW Molecular antigen array; vaccine; antigen; antimicrobial;  
 KW molecular scaffold; amyloid beta; Abeta 1-42; influenza;  
 KW graft versus host disease; IGE-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200256907-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PP 21-JAN-2002; 2002WO-IB000168.  
 XX  
 PR 19-JAN-2001; 2001US-0262379P.  
 PR 04-MAY-2001; 2001US-0288549P.  
 PR 05-OCT-2001; 2001US-0326998P.  
 PR 07-NOV-2001; 2001US-0331045P.  
 XX  
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS) NOVARTIS PHARMA AG.  
 PA (MAUR) MAURER P.  
 PA (LECH) LECHNER F.  
 PA (ORTM) ORTMANN R.  
 PA (LUEO) LUECEND R.  
 PA (STAU) STAUFENBIEL M.  
 PA (FREY) FREY P.  
 XX  
 XX Maurer P, Lechner F, Ortmann R, Luecend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
 XX WPI; 2002-636514/68.  
 DR  
 XX  
 PT Molecular antigen array used in the production of vaccines for infectious  
 PT diseases.  
 XX  
 PS Disclosure; Page 399; 418pp; English.  
 XX  
 CC The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a  
 CC core particle of a non-natural origin; and (2) a core particle of natural  
 CC origin; and (ii) an organiser comprising at least one first attachment  
 CC site, where the organiser is connected to the core particle by at least  
 CC one covalent bond; (b) an antigen or antigenic determinant with at least  
 CC one second attachment site, where the antigen or antigenic determinant is  
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
 CC attachment site is selected from: (i) an attachment site not naturally  
 CC occurring with the antigen or antigenic determinant; and (ii) an  
 CC attachment site naturally occurring with the antigen or antigenic  
 CC determinant, where the second attachment site is capable of association  
 CC through at least one non-peptide bond to the first attachment site; and  
 CC where the antigen or antigenic determinant and the scaffold interact  
 CC through the association to form an ordered and repetitive antigen array.  
 CC Also included is a process for producing a non-naturally occurring  
 CC ordered and repetitive antigen array. The composition is used in  
 CC immunisation and as a vaccine for diseases such as influenza, graft  
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult  
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 CC gravis, immunoproliferative disease lymphadenopathy.

CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 CC osteoporosis and infectious diseases. The present sequence is an antigen  
 CC for use in the array of the invention. The antigen is modified to possess  
 CC a cleavage site (enterokinase or factor Xa) and a cysteine- containing N-  
 CC or C-terminal linker peptide which serves as the attachment point to a  
 CC virus like particle or bacterial protein (the scaffold protein)  
 XX  
 SQ Sequence 134 AA;  
 Query Match 61.8%; Score 430; DB 5; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 4.8e-43;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 MEMLNLSLLALGAAYVSAFAVENPMNLVAETLLTSLTRTWLIGDGNLMIPTPENKH 60  
 DB 1 MEMLNLSLLALGAAYVSAFAVENPMNLVAETLLTSLTRTWLIGDGNLMIPTPENKH 60  
 QY 61 QLCIXEVFGIDTTLKNQTAHGEAVDKLPQNLSLKEHIEROKRCAGRWVTKFDLYLQ 120  
 DB 61 QLCITEIFQIGIGTLESQTVGGTVERLPFNLSLIKIDGKKRGGERRVNQFDLYLQ 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 EFLGVNTEWIES 134  
 RESULT 9  
 AAU10353  
 ID AAU10353 standard; protein; 134 AA.  
 AC AAU10353;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE Interleukin 5 (IL5).  
 XX  
 KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;  
 KW haplotyping; inflammatory disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200177132-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 11-APR-2001; 2001WO-US012011.  
 XX  
 PR 11-APR-2000; 2000US-0196250P.  
 XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 XX  
 XX Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;  
 PI Nandabalan K, Parks KE;  
 XX WPI; 2002-041289/05.  
 DR N-PSDB; AAS15002.  
 XX  
 PT New haplotypes of the human interleukin 5 gene, useful to diagnose and  
 PT treat diseases associated with the gene including inflammatory disorders  
 XX such as asthma.  
 PS Claim 27; Fig 3; 65pp; English.  
 XX  
 CC The invention relates to haplotyping the human interleukin 5 (IL5) gene  
 CC of an individual, comprising determining if the individual has one of the  
 CC IL5 haplotypes or haplotype pairs fully defined in the specification.  
 CC Haplotyping the IL5 gene of an individual, comprises determining the  
 CC identity of the nucleotide at two or more polymorphic sites in one copy  
 CC of the gene. The method also involves identifying an association between  
 CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising  
 CC comparing the frequency of the haplotype/pair in a population exhibiting  
 CC the trait with that of a reference population. A higher frequency in the

CC trait population indicates the trait is associated with the haplotype.  
 CC The polynucleotides and screened compounds are useful to develop  
 CC treatment for diseases associated with IL-5 activity including  
 CC inflammatory disorders such as asthma. The present sequence represents  
 CC the amino acid sequence of interleukin 5 (IL5) as described in the method  
 CC of the invention  
 CC  
 CC SQ Sequence 134 AA;  
 Query Match 61.8%; Score 430; DB 5; Length 134;  
 Best Local Similarity 64.9%; Pred. No. 4.8e-43;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 MRMLNLISLLALGAAYVSFAFVNPMLRLVAETLLTSLTHTWLTGDNLMIPTEPNKH 60  
 Db 1 MRMLHLISLLALGAAYVVAIPTPTSAVKETLALLSTHTLLIANETLRIPVVKKH 60  
 QY 61 QLCIKVEFGQIDTLKNTAHEAVDKLPQNLISLKEHIERQKRCAGERRVTKFLDYLQ 120  
 Db 61 QLCTEEIIFQIGTLESQTVQGGTVERLFKNLSLKKYIDGQKKCGERRRVNQFLDYLQ 120  
 QY 121 VFLGVINTEWTPES 134  
 Db 121 EFLGVNTEWIEES 134  
 RESULT 10  
 AA030457  
 ID AA030457 standard; protein; 285 AA.  
 XX  
 AC AA030457;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE hIL5-P30-P2-hIL5 (hIL5.34) fusion construct protein.  
 XX  
 KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 KW IL5; epitope; human; tetanus toxoid; chimeric.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Protein /note= "Human IL5 leader peptide"  
 FT Protein 20..285  
 FT Protein /note= "Mature hIL5.34 protein"  
 XX  
 FN WO2003042244-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 15-NOV-2002; 2002WO-DK000764.  
 XX  
 PR 16-NOV-2001; 2001DK-00001702.  
 XX  
 PR 16-NOV-2001; 2001US-0331575P.  
 XX  
 PA (PHAR-) PHARMEXA AS.  
 PA (KLYS/) KLYSNER S.  
 PA (NIEL/) NIELSEN F S.  
 PA (BRAT/) BRATT T.  
 PA (VOLD/) VOLDBORG B.  
 PA (MOUR/) MOURITSEN S.  
 XX  
 Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;  
 WPI; 2003-449558/42.  
 DR N-PSDB; AAL61293.  
 XX  
 PT New immunogenic analogue of a polymeric protein, useful for preparing a  
 composition for treating inflammatory diseases e.g. arthritis.

XX Claim 20; Page 109-110; 196pp; English.  
 PS  
 CC The invention relates to immunogenic analogues of multimeric proteins  
 CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis  
 CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic  
 CC analogues. The immunogenic analogue is useful for preparing a composition  
 CC for treating inflammatory diseases, e.g., arthritis. It is also used in  
 CC gene therapy. The present sequence is a fusion construct which comprises  
 CC 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes  
 CC P30 and P2. This sequence is used to illustrate the method of the  
 CC invention  
 CC  
 CC SQ Sequence 285 AA;  
 Query Match 61.8%; Score 430; DB 6; Length 285;  
 Best Local Similarity 64.9%; Pred. No. 1.5e-42;  
 Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;  
 QY 1 MRMLNLISLLALGAAYVSFAFVNPMLRLVAETLLTSLTHTWLTGDNLMIPTEPNKH 60  
 Db 1 MRMLHLISLLALGAAYVVAIPTPTSAVKETLALLSTHTLLIANETLRIPVVKKH 60  
 QY 61 QLCIKVEFGQIDTLKNTAHEAVDKLPQNLISLKEHIERQKRCAGERRVTKFLDYLQ 120  
 Db 61 QLCTEEIIFQIGTLESQTVQGGTVERLFKNLSLKKYIDGQKKCGERRRVNQFLDYLQ 120  
 QY 121 VFLGVINTEWTPES 134  
 Db 121 EFLGVNTEWIEES 134  
 RESULT 11  
 AA030458  
 ID AA030458 standard; protein; 285 AA.  
 XX  
 AC AA030458;  
 XX  
 DT 22-SEP-2003 (first entry)  
 XX  
 DE hIL5-P2-P30-hIL5 (hIL5.35) fusion construct protein.  
 XX  
 KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 KW IL5; epitope; human; tetanus toxoid; chimeric.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Protein /note= "Human IL5 leader peptide"  
 FT Protein 20..285  
 FT Protein /note= "Mature hIL5.35 protein"  
 XX  
 FN WO2003042244-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 15-NOV-2002; 2002WO-DK000764.  
 XX  
 PR 16-NOV-2001; 2001DK-00001702.  
 XX  
 PR 16-NOV-2001; 2001US-0331575P.  
 XX  
 PA (PHAR-) PHARMEXA AS.  
 PA (KLYS/) KLYSNER S.  
 PA (NIEL/) NIELSEN F S.  
 PA (BRAT/) BRATT T.  
 PA (VOLD/) VOLDBORG B.  
 PA (MOUR/) MOURITSEN S.  
 XX  
 Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;  
 WPI; 2003-449558/42.  
 DR N-PSDB; AAL61293.  
 XX  
 PT New immunogenic analogue of a polymeric protein, useful for preparing a  
 composition for treating inflammatory diseases e.g. arthritis.

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XX WPI; 2003-449558/42.
DR N-PSDB; AAL61294.
XX
PT New immunogenic analogue of a polymeric protein, useful for preparing a
PT composition for treating inflammatory diseases e.g. arthritis.
XX
PS Claim 20; Page 112-113; 196pp; English.
XX
CC The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC analogues. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is a fusion construct which comprises
CC 2 human interleukin 5 (IL5) monomers joined by tetanus toxoid epitopes
CC p30 and p2. This sequence is used to illustrate the method of the
CC invention
XX
SQ Sequence 285 AA;
Query Match 61.8%; Score 430; DB 6; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTEKNKH 60
DB 1 MRMLNLSSLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTEKNKH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAV 84
DB 61 QLCIKVEFGQIDTLKNQTAHGEAV 84
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVNTEWITIES 134
RESULT 12
AAB72616
ID AAB72616 standard; protein; 84 AA.
XX
AC AAB72616;
XX
DT 04-MAY-2001 (first entry)
XX
DE Canine interleukin-5 protein #2.
XX
KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction.
XX
OS Canis sp.
XX
PN WO200111049-A2.
XX
FD 15-FEB-2001.
XX
PF 09-AUG-2000; 2000WO-US021651.
XX
PR 10-AUG-1999; 99US-00371615.
XX
PA (IDEXX-) IDEXX LAB INC.
XX
PI Guo H, Lawton R, Mermer B, Aiyappa AP;
DR WPI; 2001-191542/19.
DR N-PSDB; AAF74305.
XX
PT Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX
PS Example 1; Fig 1; 48pp; English.
XX

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CC The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is one
CC version of the IL-5 protein shown in the specification
XX
SQ Sequence 84 AA;
Query Match 61.6%; Score 429; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 3.2e-43;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRMLNLSSLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTEKNKH 60
DB 1 MRMLNLSSLALGAAVVSAPAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTEKNKH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAV 84
DB 61 QLCIKVEFGQIDTLKNQTAHGEAV 84
RESULT 13
AAU10354
ID AAU10354 standard; protein; 134 AA.
XX
AC AAU10354;
XX
DT 14-FEB-2002 (first entry)
XX
DE Interleukin 5 (IL5) isoform.
XX
KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;
KW haplotyping; inflammatory disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 93 /note= "wild type Leu substituted by Phe"
XX
PN WO200177132-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US012011.
XX
PR 11-APR-2000; 2000US-0196250P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Benivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;
PI Nandabalan K, Parks KE;
XX
DR WPI; 2002-041289/05.
XX
PT New haplotypes of the human interleukin 5 gene, useful to diagnose and
PT treat diseases associated with the gene including inflammatory disorders
PT such as asthma.
XX
PS Disclosure; Page; 65pp; English.
XX
CC The invention relates to haplotyping the human interleukin 5 (IL5) gene
CC of an individual, comprising determining if the individual has one of the
CC IL5 haplotypes or haplotype pairs fully defined in the specification.
CC Haplotyping the IL5 gene of an individual, comprises determining the
CC identity of the nucleotide at two or more polymorphic sites in one copy
CC of the gene. The method also involves identifying an association between
CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising
CC comparing the frequency of the haplotype/pair in a population exhibiting
CC the trait with that of a reference population. A higher frequency in the
CC trait population indicates the trait is associated with the haplotype.
CC The polynucleotides and screened compounds are useful to develop
CC treatment for diseases associated with IL-5 activity including
CC inflammatory disorders such as asthma. The present sequence represents
XX

```

CC the amino acid sequence of interleukin 5 (IL5) isoform as described in  
 CC the method of the invention. Note: The present sequence is not shown in  
 CC the specification, but is derived from the human IL5 sequence given in  
 CC figure 3 (see AAU10353)  
 XX  
 SQ Sequence 134 AA;

Query Match 61.2%; Score 426; DB 5; Length 134;  
 Best Local Similarity 64.2%; Pred. No. 1.5e-42;  
 Matches 86; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMRLVAETLTLLSTHRTWLGNGLMIPENKNH 60  
 DB 1 MRMLHLSSLALGAAVYVAIPTETPSALVKETLALLSTHRTLLIANETRLILVPVHKH 60  
 QY 61 QLCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYLO 120  
 DB 61 QLCTEEIFQGITLESQTVOGTVVERLFPKLSPIKKYIDGQKKCGEERRVNOFLDYLO 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 EFLGVNTEWIIIES 134

RESULT 14  
 AAP81056  
 ID AAP81056 standard; protein; 134 AA.  
 XX  
 AC AAP81056;  
 DT 25-MAR-2003 (revised)  
 DT 04-DEC-1990 (first entry)  
 XX  
 DE Sequence of human B-cell differentiation factor.  
 XX  
 KW Immunodeficiency disease; cancer therapy; interleukin; lymphocyte.  
 XX  
 OS Homo sapiens.

Key Location/Qualifiers  
 FH Key 1. .48  
 FT Region /note= "Encoded by exon 1"  
 FT Region 49. .59  
 FT Region /note= "Encoded by exon 2"  
 FT Region 60. .102  
 FT Region /note= "Encoded by exon 3"  
 FT Region 103. .134  
 FT Region /note= "Encoded by exon 4"  
 PN EP261625-A.  
 PD 30-MAR-1988.  
 XX  
 PF 21-SEP-1987; 87EP-00113774.  
 XX  
 PR 20-SEP-1986; 86JP-00223284.  
 PR 21-SEP-1987; 87JP-00236842.  
 XX  
 PA (HONJ/) HONJO T.  
 XX  
 PI Honjo T, Takatu K, Severinson E;  
 XX  
 DR WPI; 1988-085927/13.  
 DR N-PSDB; AAN81380, AAN81381.  
 XX  
 PT Recombinant human B-cell differentiation factor - used for diagnosis or  
 treatment of immunodeficiency diseases, various infections and cancers.  
 XX  
 PS Disclosure; Page ?; 5pp; English.

CC Encoded by the human BCDP cDNA sequence which is claimed and by human  
 CC BCDP chromosomal gene (see FT). The BCDP is useful in the diagnosis or  
 CC treatment of e.g. immunodeficiency diseases which occur due to the

CC deficiency of this factor in a living body and also in the treatment of  
 CC various infections and cancers. (Updated on 25-MAR-2003 to correct PR  
 CC field.)  
 XX  
 SQ Sequence 134 AA;

Query Match 60.3%; Score 420; DB 1; Length 134;  
 Best Local Similarity 64.2%; Pred. No. 7.6e-42;  
 Matches 86; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMRLVAETLTLLSTHRTWLGNGLMIPENKNH 60  
 DB 1 MRMLHLSSLALGAAVYVAIPTETPSALVKETLALLSTHRTLLIANETRLILVPVHKH 60  
 QY 61 QLCIKEVFQGITLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYLO 120  
 DB 61 QLCTEEIFQGITLESQTVOGTVVERLFPKLSPIKKYIDGQKKCGEERRVNOFLDYLO 120  
 QY 121 VFLGVINTEWTPES 134  
 DB 121 EFLGVNTEWIIIES 134

RESULT 15  
 AA030460  
 ID AA030460 standard; protein; 287 AA.  
 XX  
 AC AA030460;  
 DT 22-SEP-2003 (first entry)  
 DE hIL5.37 variant protein.  
 XX  
 KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 KW IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Unidentified.  
 OS Chimeric.

Key Location/Qualifiers  
 FH Key 1. .19  
 FT Peptide /note= "Human IL5 leader peptide"  
 FT Protein 20. .287  
 FT Protein /note= "Mature hIL5.37 protein"  
 FT Region 24. .38  
 FT Region /note= "Tetanus toxoid P2 epitope"  
 FT Region 273. .287  
 FT Region /note= "Tetanus toxoid P30 epitope"  
 PN WO2003042244-A2.  
 PD 22-MAY-2003.  
 XX  
 PF 15-NOV-2002; 2002WO-DK000764.  
 XX  
 PR 16-NOV-2001; 2001DK-00001702.  
 PR 16-NOV-2001; 2001US-0331575P.  
 XX  
 PA (PHAR-) PHARMEXA AS.  
 PA (KLYS/) KLYSNER S.  
 PA (NIEL/) NIELSEN P S.  
 PA (BRAT/) BRATT T.  
 PA (VOLD/) VOLDORF B.  
 PA (MOUR/) MOURITSEN S.  
 XX  
 PI Klyener S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;  
 XX  
 DR WPI; 2003-449558/42.  
 DR N-PSDB; AAL61296.  
 XX  
 PT New immunogenic analogue of a polymeric protein, useful for preparing a

PT composition for treating inflammatory diseases e.g. arthritis.  
XX  
PS  
XX Claim 20; Page 117-120; 196pp; English.

CC The invention relates to immunogenic analogues of multimeric proteins  
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis  
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic  
CC analogues. The immunogenic analogue is useful for preparing a composition  
CC for treating inflammatory diseases, e.g., arthritis. It is also used in  
CC gene therapy. The present sequence is a fusion construct variant which  
CC comprises 2 human interleukin 5 (IL5) monomers joined by diglycine linker  
CC and including terminally positioned tetanus toxoid epitopes P30 and P2.  
CC This sequence is used to illustrate the method of the invention

XX SQ Sequence 287 AA;

Query Match	59.7%;	Score 415.5;	DB 6;	Length 287;
Best Local Similarity	58.4%;	Pred. No. 8e-41;		
Matches	87;	Conservative	17;	Mismatches 30; Indels 15; Gaps 1;
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Db	1	MRMLNLSLLALGAAYVSAFVEN-----PMNRLVAETLLSTHRTWLI	60	
QY	46	GDGNLMPTPENKNHOLCIKEVFQIDTLKNQTAHGEAVDKLPONLSLIKEHIEROKKC	105	
Db	61	ANETLRIPVPHKNHQLCTEETFGIGTLESQTVQSGTVERLPKNLSLIKXIDGOKKC	120	
QY	106	AGERWRVKFDYLDYQVFLGVINTEWTPES	134	
Db	121	GEERRRVNQFLDYLDYQVFLGVINTEWTPES	149	

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OM protein - protein search, using sw model

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Listing first 45 summaries

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SUMMARIES

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2	696	100.0	134	4	US-09-451-527-81
3	687	98.7	134	4	US-09-371-615A-2
4	610	87.6	115	4	US-09-322-409-86
5	610	87.6	115	4	US-09-451-527-86
6	430	61.8	134	1	US-08-284-393B-13
7	430	61.8	134	3	US-08-759-628-9
8	430	61.8	134	4	US-09-371-615A-7
9	430	61.8	134	4	US-09-462-941-12
10	430	61.8	134	5	PCT-US95-08950-13
11	430	61.8	134	6	5324640-2
12	376	54.0	133	4	US-09-371-615A-8
13	351	50.4	121	4	US-09-180-864-2
14	74.5	10.7	407	4	US-09-489-847-280
15	74	10.6	323	4	US-09-134-000C-5535
16	72.5	10.4	686	4	US-09-914-259-33
17	72	10.3	15	5	PCT-US94-06555-4
18	71.5	10.3	521	4	US-09-543-681A-6857
19	71.5	10.3	599	4	US-09-543-681A-20368
20	71.5	10.3	673	4	US-09-328-352-5834
21	70.5	10.1	429	4	US-09-328-352-7087
22	69.5	10.0	312	4	US-09-107-532A-6369
23	69.5	10.0	976	3	US-09-560-005-2
24	69.5	10.0	976	3	US-09-195-868-14
25	69.5	10.0	976	3	US-09-418-540-2
26	69.5	10.0	976	4	US-09-969-528-2
27	69.5	10.0	1187	3	US-08-684-362B-8

28 69.5 10.0 1187 3 US-09-311-743-8 Sequence 8, Appli  
29 69.5 10.0 1189 3 US-09-195-868-15 Sequence 15, Appl  
30 69.5 10.0 1229 3 US-09-195-868-28 Sequence 28, Appl  
31 67.5 9.7 364 4 US-09-252-991A-18473 Sequence 18473, A  
32 67.5 9.7 968 1 US-08-434-730-14 Sequence 14, Appl  
33 67.5 9.7 1185 3 US-08-664-962B-2 Sequence 2, Appli  
34 67.5 9.7 1185 3 US-09-311-743-2 Sequence 2, Appli  
35 66.5 9.6 2311 4 US-08-934-386-9 Sequence 9, Appli  
36 66.5 9.6 485 4 US-09-134-001C-4294 Sequence 4294, Ap  
37 66.5 9.6 589 4 US-09-543-681A-4194 Sequence 4194, Ap  
38 66 9.5 465 4 US-09-240-639-8 Sequence 8, Appli  
39 66 9.5 465 4 US-09-557-800C-56 Sequence 56, Appl  
40 66 9.5 465 4 US-09-370-625A-39 Sequence 39, Appl  
41 66 9.5 984 4 US-09-328-352-6926 Sequence 6926, Ap  
42 66 9.5 2325 3 US-08-417-089-6 Sequence 6, Appli  
43 66 9.5 2325 3 US-08-695-651-6 Sequence 6, Appli  
44 66 9.5 2325 3 US-08-930-285-6 Sequence 6, Appli  
45 66 9.5 2325 3 US-08-695-421-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-322-409-81  
; Sequence 81, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-CI  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-322-409-81

Query Match 100.0%; Score 696; DB 4; Length 134;  
Best Local Similarity 100.0%; Pred. No. 3.7e-81;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRMLNLSLLALGAAYVSFAFVENVPMNLVAETLLTSLTHRTWLIGDGNLMIPTENKNH 60  
Db 1 MRMLNLSLLALGAAYVSFAFVENVPMNLVAETLLTSLTHRTWLIGDGNLMIPTENKNH 60  
QY 61 QLCIKEVFQGGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGSRWRVTKFDLYIQ 120  
Db 61 QLCIKEVFQGGIDTLKNQTAHGEAVDKLFQNLSLIKEHIEROKKRCAGSRWRVTKFDLYIQ 120  
QY 121 VFLGVINTEWTPES 134  
Db 121 VFLGVINTEWTPES 134

RESULT 2

US-09-451-527-81  
; Sequence 81, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.

```
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-451-527-81

Query Match      100.0%; Score 696; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.7e-81;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAYSAFAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXH 60
DB 1 MRMLNLSSLALGAAYSAFAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXH 60

QY 61 QLCIKVFQGITLTKNOTAHGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQ 120
DB 61 QLCIKVFQGITLTKNOTAHGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQ 120

QY 121 VFLGVINTEWTPES 134
DB 121 VFLGVINTEWTPES 134

RESULT 3
US-09-371-615A-2
; Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; TITLE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 036040017000US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-371-615A-2

Query Match      98.7%; Score 687; DB 4; Length 134;
Best Local Similarity 92.3%; Pred. No. 5.2e-80;
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAYSAFAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXH 60
DB 1 MRMLNLSSLALGAAYSAFAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXH 60

QY 61 QLCIKVFQGITLTKNOTAHGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQ 120
DB 61 QLCIKVFQGITLTKNOTAHGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQ 120

QY 121 VFLGVINTEWTPES 134
DB 121 VFLGVINTEWTPES 134

RESULT 4
US-09-322-409-86
; Sequence 86, Application US/09322409
```

```
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-322-409-86

Query Match      87.6%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-70;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXHQLCIKVFQGITLKNQTA 79
DB 1 FAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXHQLCIKVFQGITLKNQTA 60

QY 80 HGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQVFLGVINTEWTPES 134
DB 61 HGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQVFLGVINTEWTPES 115

RESULT 5
US-09-451-527-86
; Sequence 86, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-451-527-86

Query Match      87.6%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 3e-70;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXHQLCIKVFQGITLKNQTA 79
DB 1 FAVENPMNRLVAETLTLLSTHRTWLIIGDGNLMIPTPENKXHQLCIKVFQGITLKNQTA 60

QY 80 HGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQVFLGVINTEWTPES 134
DB 61 HGEAVDKLFQNLSLIKHIERQKRCAGRWRTKFLDYLYQVFLGVINTEWTPES 115
```

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RESULT 6
US-08-284-393B-13
; Sequence 13, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-13

Query Match 61.8%; Score 430; DB 1; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAYVSFAFAVENPMNRLVAETLLTLLSTHRTWLTIGDGNLMIPENKNH 60
Db 1 MRMLHLSSLALGAAYVAIPTPTISALVKETALLSTHRTLLIANETLRIPVPVHKH 60
QY 61 QLCIKVEFGIDTLKQNTAHGEAVDKLQNLSLIKEHIERQKRCAGRWRTKFLDYIQ 120
Db 61 QLCTEEIIFQIGTLESQTVGGTVVERLFKNLSLIKVIKIDGKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVNTEWIIIES 134

RESULT 7
US-08-759-628-9
; Sequence 9, Application US/08759628
; Patent No. 6225446
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
```

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; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,628
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,574
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0552Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 20..134
; OTHER INFORMATION: /notes "Peptide of Figure 1"
US-08-759-628-9

Query Match 61.8%; Score 430; DB 3; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAYVSFAFAVENPMNRLVAETLLTLLSTHRTWLTIGDGNLMIPENKNH 60
Db 1 MRMLHLSSLALGAAYVAIPTPTISALVKETALLSTHRTLLIANETLRIPVPVHKH 60
QY 61 QLCIKVEFGIDTLKQNTAHGEAVDKLQNLSLIKEHIERQKRCAGRWRTKFLDYIQ 120
Db 61 QLCTEEIIFQIGTLESQTVGGTVVERLFKNLSLIKVIKIDGKKCGERRRVNQFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVNTEWIIIES 134

RESULT 8
US-09-371-615A-7
; Sequence 7, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Interleukin 5
US-09-371-615A-7
```

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Query Match 61.8%; Score 430; DB 4; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
DB 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
QY 61 QLCIKEVFQGITLTKNOTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQ 120
DB 61 QLCTEEIFQGITLESQTVGGTVERLFLKNLSLIKVIQKKGERRRVNQFLDYQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIES 134

RESULT 9
US-09-462-941-12
; Sequence 12, Application US/09462941
; Patent No. 6608183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/09/462,941
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-462-941-12

Query Match 61.8%; Score 430; DB 4; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
DB 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
QY 61 QLCIKEVFQGITLTKNOTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQ 120
DB 61 QLCTEEIFQGITLESQTVGGTVERLFLKNLSLIKVIQKKGERRRVNQFLDYQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIES 134

RESULT 10
PCT-US95-08950-13
; Sequence 13, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08950
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,393
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08950-13

Query Match 61.8%; Score 430; DB 5; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
DB 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
QY 61 QLCIKEVFQGITLTKNOTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQ 120
DB 61 QLCTEEIFQGITLESQTVGGTVERLFLKNLSLIKVIQKKGERRRVNQFLDYQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIES 134

RESULT 11
5324640-2
; Patent No. 5324640
; APPLICANT: Honjo, Tasuku; Takatsu, Kiyoshi; Severinson, Eva
; TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND
; PROCESS OF PRODUCING SAID FACTOR
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/99,467
; FILING DATE: 21-SEP-1987
; SEQ ID NO: 2
; LENGTH: 134
5324640-2

Query Match 61.8%; Score 430; DB 6; Length 134;
Best Local Similarity 64.9%; Pred. No. 4.2e-47;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
DB 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNH 60
QY 61 QLCIKEVFQGITLTKNOTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYQ 120
DB 61 QLCTEEIFQGITLESQTVGGTVERLFLKNLSLIKVIQKKGERRRVNQFLDYQ 120
QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIES 134
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RESULT 12
US-09-371-615A-8
; Sequence 8, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371.615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: Interleukin 5
US-09-371-615A-8

Query Match      54.0%; Score 376; DB 4; Length 133;
Best Local Similarity 56.8%; Pred. No. 3.4e-40;
Matches 75; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

QY 2 RMLNLSLLALGAAVVSFAVENPMNRLVAETLLTSTHRTWLTGDNLMIPPEKNHQ 61
Db 3 RMLNLSVLTLSGVW--ATAEIPMTSTVVKETLTLSAHLALITSTWPLPPTHKNHQ 60

QY 62 LCIEVFQGGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYLVQ 121
Db 61 LCIEVFQGLDILKNQTVRGTVEMLFQNLSLIKKYIDRQKCKGERRRTRQFLDYLVQ 120

QY 122 FLGVNTWTPPE 133
Db 121 FLGVNTWAWME 132

RESULT 13
US-09-180-864-2
; Sequence 2, Application US/09180864
; Patent No. 6465616
; GENERAL INFORMATION:
; APPLICANT: Lopez, Angel
; APPLICANT: Vadas, Matthew
; APPLICANT: Shannon, Frances
; APPLICANT: Bastiras, Stan
; APPLICANT: Hey, Allan W
; TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
; FILE REFERENCE: 99722
; CURRENT APPLICATION NUMBER: US/09/180,864
; CURRENT FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 08/591,438
; PRIOR FILING DATE: 1994-07-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: modified IL-5
US-09-180-864-2

Query Match      50.4%; Score 351; DB 4; Length 121;
Best Local Similarity 61.6%; Pred. No. 4.7e-37;
Matches 69; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

QY 23 ENPMNRLVAETLLTSTHRTWLTGDNLMIPPEKNHQLCIKEVFGIDTLKNQTAHGE 82
Db 10 EIPTSAVLRKTALLSTHRTLLIANETLRIPVPHKHQLCTEIEFQIGTLESQTQVG 69

QY 83 AVDKLFQNLSLIKEHIERQKRCACGERWRVTKFLDYLVQFLGVNTWTPES 134
Db 70 TVERIFKQLSLIKKYIDQKKCGERRRVNQFLDYLVQFLGVNNTWETIIES 121
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RESULT 14
US-09-489-847-280
; Sequence 280, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-280

Query Match      10.7%; Score 74.5; DB 4; Length 407;
Best Local Similarity 21.4%; Pred. No. 0.73;
Matches 31; Conservative 26; Mismatches 43; Indels 45; Gaps 5;

QY 3 MLNLSLLALGAAVVSFAVENPMNRLVAETLLTSTHRTW-----LIGDGNL 50
Db 70 MLLALLILGIVWVASALIDN-----DAAMESLYDLMEFYLPYLYSCISLMGCLLL 122

QY 51 MIPTPEN-----KNHOLCIKEVFGID-----TLKNQTAHGE-----AV 84
Db 123 LLCTPVGLSRMFTVMGHLVVKPTILEDDEQIVITLSEALQRLNGLSSSVYENIMEL 182

QY 85 DKLFQNLSLIKEHIERQKRCACGER 109
Db 183 EQELENVKTLLTKLERRKKASAWER 207

RESULT 15
US-09-134-000C-5535
; Sequence 5535, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5535
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5535

Query Match      10.6%; Score 74; DB 4; Length 323;
Best Local Similarity 22.5%; Pred. No. 0.6;
Matches 36; Conservative 22; Mismatches 46; Indels 56; Gaps 8;
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QY 9 LIALG-----AAYSAFAVENPMNRLVAETLTLSTHRTWLGDNLMIPTPENKQHLC 63
Db 65 LRAIGPEEWNAYVE--PSRRPADGRYGENPNRLYQHHPQV-----VWKPSPE----- 112
QY 64 IKEVFOGIDTUKNOTAHEAVDKLFQNLSLIKEHIERQKKRCAGERWRV-----TKF- 115
Db 113 IQELY--LESUKLL-----GIDPLEHDIRFVEDNWNENPSMGCAGLWGVWLDGMEITQFT 165
QY 116 -----LDYLQVFLGVINTEWT 131
Db 166 YFQVGGLOCHPVTSEITYGLERLASYIQEVESYDLEWT 205

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Search completed: August 25, 2004, 00:07:15  
Job time : 26.2169 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2004, 00:05:39 ; Search time 90.9478 Seconds  
(without alignments)  
463.015 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLSLLALGAAYVSFA.....FLDYLOVFLGVINTEWTPES 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	9	US-09-755-633-5
2	696	100.0	134	14	US-10-218-654-81
3	696	100.0	134	14	US-10-262-439-81
4	610	87.6	115	9	US-09-755-633-10
5	610	87.6	115	14	US-10-218-654-86
6	610	87.6	115	14	US-10-262-439-86
7	430	61.8	134	14	US-10-289-454-233
8	430	61.8	134	14	US-10-400-377-12
9	430	61.8	134	14	US-10-400-708-12
10	430	61.8	134	14	US-10-298-148-12
11	430	61.8	134	14	US-10-050-902-233
12	430	61.8	134	14	US-10-050-898-233
13	430	61.8	285	14	US-10-295-074-9
14	430	61.8	285	14	US-10-295-074-11
15	415.5	59.7	287	14	US-10-295-074-15

16	413.5	59.4	287	14	US-10-295-074-13	Sequence 13, Appl
17	359	51.6	136	14	US-10-289-454-336	Sequence 316, App
18	359	51.6	136	14	US-10-050-902-336	Sequence 316, App
19	359	51.6	136	14	US-10-050-898-336	Sequence 316, App
20	358	51.4	115	16	US-10-658-834A-588	Sequence 588, App
21	357	51.3	115	16	US-10-658-834A-569	Sequence 569, App
22	357	51.3	123	14	US-10-289-454-337	Sequence 337, App
23	357	51.3	123	14	US-10-050-902-337	Sequence 337, App
24	357	51.3	123	14	US-10-050-898-337	Sequence 337, App
25	357	51.3	138	14	US-10-289-454-335	Sequence 335, App
26	357	51.3	138	14	US-10-050-902-335	Sequence 335, App
27	357	51.3	138	14	US-10-050-898-335	Sequence 335, App
28	356	51.1	115	14	US-10-289-454-234	Sequence 234, App
29	356	51.1	115	14	US-10-050-902-234	Sequence 234, App
30	356	51.1	115	14	US-10-050-898-234	Sequence 234, App
31	356	51.1	115	14	US-10-295-074-1	Sequence 1, Appl
32	356	51.1	115	16	US-10-658-834A-208	Sequence 208, App
33	356	51.1	115	16	US-10-658-834A-574	Sequence 574, App
34	356	51.1	115	16	US-10-658-834A-580	Sequence 580, App
35	356	51.1	115	16	US-10-658-834A-587	Sequence 587, App
36	356	51.1	115	16	US-10-658-834A-589	Sequence 589, App
37	356	51.1	115	16	US-10-658-834A-595	Sequence 595, App
38	355	51.0	115	16	US-10-658-834A-568	Sequence 568, App
39	355	51.0	115	16	US-10-658-834A-575	Sequence 575, App
40	355	51.0	115	16	US-10-658-834A-581	Sequence 581, App
41	355	51.0	115	16	US-10-658-834A-585	Sequence 585, App
42	355	51.0	115	16	US-10-658-834A-596	Sequence 596, App
43	355	51.0	115	16	US-10-658-834A-597	Sequence 597, App
44	354	50.9	115	16	US-10-658-834A-576	Sequence 576, App
45	354	50.9	115	16	US-10-658-834A-582	Sequence 582, App

#### ALIGNMENTS

#### RESULT 1

US-09-755-633-5  
Sequence 5, Application US/09755633  
Patent No. US20020127200A1  
GENERAL INFORMATION:  
APPLICANT: Yang, Shumin  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF  
FILE REFERENCE: IM-2-C1-C1  
CURRENT APPLICATION NUMBER: US/09/755,633  
CURRENT FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: 05/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-755-633-5

Query Match 100.0%; Score 696; DB 9; Length 134;  
Best Local Similarity 100.0%; Pred. No. 4.1e-73;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNLVAETLLSTHRTWLIGDGNLMIPTPENKH 60

Db 1 MRMLNLSLLALGAAYVSFAVENPMNLVAETLLSTHRTWLIGDGNLMIPTPENKH 60

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFQNLISLKEHIEROKKRCAGERNWTKFLDYLO 120

Db 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFQNLISLKEHIEROKKRCAGERNWTKFLDYLO 120

QY 121 VELGVINTEWTPES 134

Db 121 VFLGVINTEWTPES 134  
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RESULT 2  
US-10-262-439-81  
; Sequence 81, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-218-654-81  
Query Match 100.0%; Score 696; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 4.le-73;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLTLLSTHRTWLGDNLMIPPTENKNH 60  
Db 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLTLLSTHRTWLGDNLMIPPTENKNH 60  
QY 61 QLCIKVEFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYIQ 120  
Db 61 QLCIKVEFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYIQ 120  
QY 121 VFLGVINTEWTPES 134  
Db 121 VFLGVINTEWTPES 134  
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RESULT 3  
US-10-262-439-81  
; Sequence 81, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Canis familiaris

US-10-262-439-81  
Query Match 100.0%; Score 696; DB 14; Length 134;  
Best Local Similarity 100.0%; Pred. No. 4.le-73;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEMLINLSLLALGAAYVSFAVENPMNRLVAETLLTLLSTHRTWLGDNLMIPPTENKNH 60  
Db 1 MEMLINLSLLALGAAYVSFAVENPMNRLVAETLLTLLSTHRTWLGDNLMIPPTENKNH 60  
QY 61 QLCIKVEFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYIQ 120  
Db 61 QLCIKVEFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYIQ 120  
QY 121 VFLGVINTEWTPES 134  
Db 121 VFLGVINTEWTPES 134  
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RESULT 4  
US-09-755-633-10  
; Sequence 10, Application US/09755633  
; Patent No. US2002012720CA1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-755-633-10  
Query Match 87.6%; Score 610; DB 9; Length 115;  
Best Local Similarity 100.0%; Pred. No. 3.8e-63;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 20 FAVENPMNRLVAETLLTLLSTHRTWLGDNLMIPPTENKNHQLCKIKVEFGQIDTLKNQTA 79  
Db 1 FAVENPMNRLVAETLLTLLSTHRTWLGDNLMIPPTENKNHQLCKIKVEFGQIDTLKNQTA 60  
QY 80 HGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYIQVFLGVINTEWTPES 134  
Db 61 HGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYIQVFLGVINTEWTPES 115  
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RESULT 5  
US-10-218-654-86  
; Sequence 86, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28



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; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-86

Query Match      87.6%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.8e-63;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPNRLVAETLLTLLSHRTWLTGDNLMPTPENKNHQLCIKEVFGIDTLKNQTA 79
Db 1 FAVENPNRLVAETLLTLLSHRTWLTGDNLMPTPENKNHQLCIKEVFGIDTLKNQTA 60

QY 80 HGEAVDKLFQNLISLKEHIEROKKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 134
Db 61 HGEAVDKLFQNLISLKEHIEROKKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 115

RESULT 6
US-10-262-439-86
; Sequence 86, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Keo
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IN-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-86

Query Match      87.6%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.8e-63;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FAVENPNRLVAETLLTLLSHRTWLTGDNLMPTPENKNHQLCIKEVFGIDTLKNQTA 79
Db 1 FAVENPNRLVAETLLTLLSHRTWLTGDNLMPTPENKNHQLCIKEVFGIDTLKNQTA 60

QY 80 HGEAVDKLFQNLISLKEHIEROKKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 134
Db 61 HGEAVDKLFQNLISLKEHIEROKKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 115

RESULT 7
US-10-289-454-233
; Sequence 233, Application US/10289454
; Publication No. US2003015749A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Jennings, Gary
; APPLICANT: Sonderegger, Ivo
; TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases
; FILE REFERENCE: 1700.0360001
; CURRENT APPLICATION NUMBER: US/10/289,454
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US 60/396,636
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: precursor human IL-5
US-10-289-454-233

Query Match      61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MEMLLNLSLLALGAAYVSFAVENPMNRLVAETLLTLLSHRTWLTGDNLMPTPENKNH 60
Db 1 MEMLLNLSLLALGAAYVVAIPEIPTSALVKETLALLSTHRTLLIANETLAIPVPHKNH 60

QY 61 QLCIKEVFGIDTLKNQTAHGEAVDKLFQNLISLKEHIEROKKRCAGRWRTKFLDYQL 120
Db 61 QLCITEIFGGITLESQTVGGTVERLPKNLSLIKYYIDGQKKCGERRRNQFLDYQL 120

QY 121 VFLGVINTEWTPES 134
Db 121 EFLGVINTEWTPES 134

RESULT 8
US-10-400-377-12
; Sequence 12, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolger Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,377
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-377-12

Query Match      61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MEMLLNLSLLALGAAYVSFAVENPMNRLVAETLLTLLSHRTWLTGDNLMPTPENKNH 60
Db 1 MEMLLNLSLLALGAAYVVAIPEIPTSALVKETLALLSTHRTLLIANETLAIPVPHKNH 60

QY 61 QLCIKEVFGIDTLKNQTAHGEAVDKLFQNLISLKEHIEROKKRCAGRWRTKFLDYQL 120
Db 61 QLCITEIFGGITLESQTVGGTVERLPKNLSLIKYYIDGQKKCGERRRNQFLDYQL 120

QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134
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Db      121 EFLGMVNTWIIIES 134

RESULT 9
US-10-400-708-12
; Sequence 12, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/400,708
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-400-708-12

Query Match      61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY      1 MRMLINSLALGAAYVSFAFVENPMRLVAETLLLSHRTWLICDGNLMIPTENKNH 60
DB      1 MEMULHLSLALGAAYVVAIPTPTISALVKETALLSHRTLLIANETLRIPVPHKNH 60

QY      61 QLCIKVEFGIDTLKNOTANGEAVDKLFQNLISLKEHIERQKRCAGERWRTKFLDY 120
DB      61 QLCIEEIFQGTGTTLESQTQGGTVERLPKNLSLIKXYIDGKKKCGEERRVNOFLDY 120

QY      121 VFLGVINTEWTPES 134
DB      121 EFLGMVNTWIIIES 134

RESULT 10
US-10-298-148-12
; Sequence 12, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/298,148
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; PRIOR FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-298-148-12

Query Match      61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY      1 MRMLINSLALGAAYVSFAFVENPMRLVAETLLLSHRTWLICDGNLMIPTENKNH 60
DB      1 MEMULHLSLALGAAYVVAIPTPTISALVKETALLSHRTLLIANETLRIPVPHKNH 60

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QY 61 QLCICEVFGQIDTLKNOTAHEAVDKLFQNLISLIKEHIEQKRCAGERRWRTKFLDYQ 120
DB 61 QLCIEEFQIGTLESQVGGTVERLFLKNLISLIKKYIDQKKKGERRRNVQFLDYQ 120

QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIES 134

RESULT 11
US-10-050-902-233
; Sequence 233, Application US/10050902
; Publication No. US20030175290A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190004
; CURRENT APPLICATION NUMBER: US/10/050,902
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-902-233

Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-42;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSLIALGAAVYSAFVNPVNRVAETLTLLSTHRTWLIGDGNLMPTPENKNH 60
DB 1 MRMLHLISLIALGAANYVYALPTTIPISALVKETALLSTHRTLLANETLRIPEVPHKNH 60

QY 61 QLCICEVFGQIDTLKNOTAHEAVDKLFQNLISLIKEHIEQKRCAGERRWRTKFLDYQ 120
DB 61 QLCIEEFQIGTLESQVGGTVERLFLKNLISLIKKYIDQKKKGERRRNVQFLDYQ 120

QY 121 VFLGVINTEWTPES 134
DB 121 EFLGVMNTEWIES 134

RESULT 12
US-10-050-898-233
; Sequence 233, Application US/10050898
; Publication No. US20030175711A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Maurer, Patrick
; APPLICANT: Lechner, Franziska
; APPLICANT: Sebbel, Peter
; APPLICANT: Piossek, Christine
; APPLICANT: Ortmann, Rainer
; APPLICANT: Luond, Rainer

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; APPLICANT: Staufenbiel, Matthias
; APPLICANT: Frey, Peter
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0190005
; CURRENT APPLICATION NUMBER: US/10/050,898
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/262,379
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/288,549
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/326,998
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 233
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-050-898-233

Query Match 61.8%; Score 430; DB 14; Length 134;
Best Local Similarity 64.9%; Pred. No. 5.3e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
DQ 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLKSLIKHEIERQKRCAGRWRTKFLDYLO 120
DQ 61 QLCITEEFQIGTLESQTVGGTVRFLFKNLKSLIKKYIDGQKKCGEERRVNOFLDYLO 120
QY 121 VFLGVINTEWTPES 134
DQ 121 EFLGVNTEWIEIS 134

RESULT 13
US-10-295-074-9
; Sequence 9, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2 human IL5 monomers joined by P30 and P2 epitopes
US-10-295-074-9

Query Match 61.8%; Score 430; DB 14; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
DQ 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLKSLIKHEIERQKRCAGRWRTKFLDYLO 120
DQ 61 QLCITEEFQIGTLESQTVGGTVRFLFKNLKSLIKKYIDGQKKCGEERRVNOFLDYLO 120
QY 121 VFLGVINTEWTPES 134
DQ 121 EFLGVNTEWIEIS 134

RESULT 15
US-10-295-074-15
; Sequence 15, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human IL5 monomers joined by a di-glycine linker and including
; OTHER INFORMATION: g terminally positioned tetanus toxoid P2 and P30 epitopes
US-10-295-074-15

Query Match 59.7%; Score 415.5; DB 14; Length 287;
Best Local Similarity 58.4%; Pred. No. 7.4e-40;
Matches 87; Conservative 17; Mismatches 30; Indels 15; Gaps 1;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
DQ 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
QY 46 GGNLMIPENKXHQLCIKVEFGQIDTLKNQTAHGEAVDKLQNLKSLIKHEIERQKRC 105
DQ 61 ANETLRIPVPVKNHQLCTEETIFQIGTLESQTVGGTVRFLFKNLKSLIKKYIDGQKK 120
QY 121 VFLGVINTEWTPES 134
DQ 121 EFLGVNTEWIEIS 134
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Db 121 EFLGVNTEWIEIS 134

RESULT 14
US-10-295-074-11
; Sequence 11, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2 human IL5 monomers joined by P2 and P30 epitopes
US-10-295-074-11

Query Match 61.8%; Score 430; DB 14; Length 285;
Best Local Similarity 64.9%; Pred. No. 1.5e-41;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
DQ 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLQNLKSLIKHEIERQKRCAGRWRTKFLDYLO 120
DQ 61 QLCITEEFQIGTLESQTVGGTVRFLFKNLKSLIKKYIDGQKKCGEERRVNOFLDYLO 120
QY 121 VFLGVINTEWTPES 134
DQ 121 EFLGVNTEWIEIS 134

RESULT 15
US-10-295-074-15
; Sequence 15, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Two human IL5 monomers joined by a di-glycine linker and including
; OTHER INFORMATION: g terminally positioned tetanus toxoid P2 and P30 epitopes
US-10-295-074-15

Query Match 59.7%; Score 415.5; DB 14; Length 287;
Best Local Similarity 58.4%; Pred. No. 7.4e-40;
Matches 87; Conservative 17; Mismatches 30; Indels 15; Gaps 1;

QY 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
DQ 1 MRMLNLSSLALGAAVYSAFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPENKXH 60
QY 46 GGNLMIPENKXHQLCIKVEFGQIDTLKNQTAHGEAVDKLQNLKSLIKHEIERQKRC 105
DQ 61 ANETLRIPVPVKNHQLCTEETIFQIGTLESQTVGGTVRFLFKNLKSLIKKYIDGQKK 120
QY 121 VFLGVINTEWTPES 134
DQ 121 EFLGVNTEWIEIS 134
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Oy 106 AGERRVTKELDYLOVFLGVINTENTPES 134  
Db 121 GEERRVNQFLDYLOVFLGVNTENTWIES 149

Search completed: August 25, 2004, 00:21:34  
Job time : 91.9478 secs

OM protein - protein search, using sw model  
Run on: August 24, 2004, 23:55:53 ; Search time 26.3695 Seconds  
(without alignments)  
488.810 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLSLLALGAAYVSFA.....FLDYLVQLVGLVNTWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	79.2	134	JCS116	interleukin-5 precursor - bovine
2	430	61.8	134	A28477	interleukin-5 precursor - bovine
3	376	54.0	133	ICM85	interleukin-5 precursor - bovine
4	361	51.9	132	A48418	interleukin-5 precursor - bovine
5	83.5	12.0	1199	G59698	RNA polymerase (beta)
6	78.5	11.3	258	T47758	hypothetical protein
7	77.5	11.1	331	G83878	hypothetical protein
8	77	11.1	478	T33735	ATP-dependent deox
9	74.5	10.7	1232	B39432	hypothetical protein
10	73.5	10.6	253	T47757	hypothetical protein
11	72.5	10.4	207	C71914	phosphoserine phosphatase
12	72.5	10.4	451	S33816	kinase light chain
13	72.5	10.4	649	S33813	kinase light chain
14	72.5	10.4	677	S33814	kinase light chain
15	72.5	10.4	686	S33815	kinase light chain
16	72	10.3	253	C97331	arac-type DNA-binding protein
17	72	10.3	401	S28653	hypothetical protein
18	71	10.2	216	B69498	hypothetical protein
19	71	10.2	300	F84594	hypothetical protein
20	71	10.2	328	F64187	p-aminobenzoate synthase
21	71	10.2	446	S76228	hypothetical protein
22	71	10.2	461	T38698	nucleic acid binding protein - fis
23	71	10.2	544	T42932	virion tegument protein
24	70.5	10.1	1055	T10432	DNA-directed RNA polymerase
25	70	10.1	215	F45355	ORF2 protein - Aut
26	70	10.1	933	A59250	myosin - Acetabula
27	70	10.1	1871	D96898	probable DNA polymerase
28	70	10.1	1894	T21555	DNA-directed DNA polymerase
29	69.5	10.0	1188	JC4889	phosphatidylinositol 3-kinase

30 69 9.9 215 2 B72854  
31 69 9.9 346 2 S6958  
32 69 9.9 437 2 S50006  
33 69 9.9 759 2 F46662  
34 68.5 9.8 189 2 D89966  
35 68.5 9.8 190 2 S23712  
36 68.5 9.8 638 2 A21115  
37 68.5 9.8 709 2 T32089  
38 68.5 9.8 756 2 T12697  
39 68.5 9.8 1102 2 S65235  
40 68 9.8 215 2 T41780  
41 68 9.8 304 2 B23431  
42 68 9.8 414 2 G84311  
43 68 9.8 416 2 T35282  
44 68 9.8 529 2 S35306  
45 68 9.8 767 1 COZPCD

ALIGNMENTS

RESULT 1

JCS116  
interleukin-5 precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 02-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 20-Jun-2000  
C:Accession: JCS116  
R:Mertens, B.; Gobright, E.; Seow, H.F.  
Gene 176, 273-274, 1996  
A:Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.  
A:Reference number: JCS116; MUID:97075944; PMID:8918267  
A:Accession: JCS116  
A:Molecule type: mRNA  
A:Residues: 1-134 <MER>  
A:Cross-references: EMBL:267872; NID:g1113120; PIDN:CAA91779.1; PID:g1113121  
A:Experimental source: lymphocytes  
C:Comment: this protein plays a role in the eosinophilia associated with parasitic disease  
C:Genetics:  
A:Gene: IL-5  
C:Superfamily: interleukin-5  
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:20-134/Product: interleukin-5 #status predicted <MAT>  
F:63/Disulfide bonds: interchain (to 105) #status predicted  
F:76/Binding site: carbonyl (Asn) (covalent) #status predicted  
F:105/Disulfide bonds: interchain (to 63) #status predicted

Query Match 79.2%; Score 551; DB 2; Length 134;  
Best Local Similarity 79.9%; Pred. No. 2,2e-46;  
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNLVAETLTLLSTHTWIGDNLMIPTENKH 60

Db 1 MRMLNLSLLALGAAYVSFAVENPMNLVAETLTLLSTHTWIGDNLMIPTENKH 60

QY 61 QLCIEVFOGIDTLKNQTAHGEAVDKLPONLSLKEHIEROKKRCAGEWVTKFLDYLO 120

Db 61 QLCIEVFOGIDTLKNQTAHGEAVDKLPONLSLKEHIEROKKRCAGEWVTKFLDYLO 120

QY 121 VFLGVINTEWTPES 134

Db 121 VFLGVINTEWTPES 134

RESULT 2

A28477  
interleukin-5 precursor - human  
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil  
C:Species: Homo sapiens (man)  
C:Date: 01-Dec-1989 #sequence\_revision 07-Jul-1995 #text\_change 22-Jun-1999  
C:Accession: A28477; A33883; A26112; A39881; JX0106; S15775  
R:Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.  
J. Biol. Chem. 262, 16580-16584, 1987

ICM55  
interleukin-5 precursor - mouse  
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 22-Jun-1999  
C:Accession: S00807; A38758; A24898; JS0077; PH0102; B39881  
R:Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Mayo, G.; Clutterbuck, E.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6629-6633, 1987  
A:Title: Molecular cloning, nucleotide sequence, and expression of the gene encoding hum  
n-5.  
A:Reference number: A33883; MUID:88016145; PMID:3498940  
A:Accession: A33883  
A:Molecule type: DNA  
A:Residues: 1-134 <CAM>  
A:Cross-references: GB:J02971; NID:G186340; PIDN:AAA98620.1; PID:G386823  
R:Azuma, C.; Tanabe, T.; Konishi, M.; Kinashi, T.; Noma, T.; Matsuda, F.; Yacita, Y.; Ta  
Nucleic Acids Res. 14, 9149-9158, 1986  
A:Title: Cloning of cDNA for human T-cell replacing factor (interleukin-5) and compariso  
n-5.  
A:Reference number: A26112; MUID:87065782; PMID:3024129  
A:Accession: A26112  
A:Molecule type: mRNA  
A:Residues: 1-134 <AZU>  
A:Cross-references: GB:X04688; NID:G33835; PIDN:CAA28390.1; PID:G33836  
R:Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel  
de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987  
A:Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum  
an interleukin-5.  
A:Reference number: A39881; MUID:88041112; PMID:2823259  
A:Accession: A39881  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-134 <YOK>  
R:Proudfoot, A.E.I.; Davies, J.G.; Turcatti, G.; Wingfield, P.T.  
FEBS Lett. 283, 61-64, 1991  
A:Title: Human interleukin-5 expressed in Escherichia coli: assignment of the disulfide  
A:Reference number: S15775; MUID:91243878; PMID:2037074  
A:Contents: annotation; disulfide bonds  
R:Minamide, Y.; Kodama, S.; Katayama, T.; Adachi, H.; Tanaka, S.; Tsujimoto, M.  
J. Biochem. 107, 292-297, 1990  
A:Title: Structure of recombinant human interleukin 5 produced by chinese hamster ovary  
A:Reference number: JX0106; MUID:90299868; PMID:2361960  
A:Contents: annotation; disulfide bonds; glycosylation sites  
C:Genetics:  
A:Gene: GDB:115  
A:Cross-references: GDB:120097; OMIM:147850  
A:Map position: 5q31.1-5q31.1  
A:Introns: 48/3; 59/3; 102/3  
C:Superfamily: interleukin-5  
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-134/Product: interleukin-5 #status predicted <MAT>  
F:22/Binding site: carbohydrate (thr) (covalent) #status experimental  
F:47,90/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:63/Disulfide bonds: interchain (to 105) #status experimental  
F:105/Disulfide bonds: interchain (to 63) #status experimental

Query Match 61.8%; Score 430; DB 1; Length 134;  
Best Local Similarity 64.9%; Pred. No. 1.3e-34;  
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLTSLTHTWLGDNLMITPENKNH 60  
Db 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLTSLTHTWLGDNLMITPENKNH 60

Qy 61 QLCIKVEFGQIDTLKNTAAGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 120  
Db 61 QLCIKVEFGQIDTLKNTAAGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 120

Qy 121 VFLGVNTEWTPES 134  
Db 121 EFLGVNTEWTPES 134

ICM55  
interleukin-5 precursor - mouse  
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil d  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 22-Jun-1999  
C:Accession: S00807; A38758; A24898; JS0077; PH0102; B39881  
R:Campbell, H.D.; Tucker, W.Q.J.; Hort, Y.; Martinson, M.E.; Mayo, G.; Clutterbuck, E.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6629-6633, 1987  
A:Title: Molecular cloning, nucleotide sequence, and expression of the gene encoding hum  
n-5.  
A:Reference number: S00807; MUID:88254802; PMID:3133208  
A:Accession: S00807  
A:Molecule type: DNA  
A:Residues: 1-133 <CAM>  
A:Cross-references: EMBL:X06271; NID:G52685; PIDN:CAA29607.1; PID:G52686  
R:Azuma, C.; Tanabe, T.; Konishi, M.; Kinashi, T.; Noma, T.; Matsuda, F.; Yacita, Y.; Ta  
Nucleic Acids Res. 14, 9149-9158, 1986  
A:Title: Cloning of cDNA for human T-cell replacing factor (interleukin-5) and compariso  
n-5.  
A:Reference number: A26112; MUID:87065782; PMID:3024129  
A:Accession: A26112  
A:Molecule type: mRNA  
A:Residues: 1-134 <AZU>  
A:Cross-references: GB:X04688; NID:G33835; PIDN:CAA28390.1; PID:G33836  
R:Yokota, T.; Coffman, R.L.; Hagiwara, H.; Rennick, D.M.; Takebe, Y.; Yokota, K.; Gemmel  
de Vries, J.; Lee, F.D.; Arai, N.; Arai, K.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7388-7392, 1987  
A:Title: Isolation and characterization of lymphokine cDNA clones encoding mouse and hum  
an interleukin-5.  
A:Reference number: JX0106; MUID:90299868; PMID:2361960  
A:Contents: annotation; disulfide bonds; glycosylation sites  
C:Genetics:  
A:Gene: GDB:115  
A:Cross-references: GDB:120097; OMIM:147850  
A:Map position: 5q31.1-5q31.1  
A:Introns: 48/3; 59/3; 102/3  
C:Superfamily: interleukin-5  
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-134/Product: interleukin-5 #status predicted <MAT>  
F:22/Binding site: carbohydrate (thr) (covalent) #status experimental  
F:47,90/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:63/Disulfide bonds: interchain (to 105) #status experimental  
F:105/Disulfide bonds: interchain (to 63) #status experimental

Query Match 54.0%; Score 376; DB 1; Length 133;  
Best Local Similarity 56.8%; Pred. No. 2.2e-29;  
Matches 75; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

Qy 2 RMLNLSLLALGAAYVSFAVENPMNRLVAETLLTSLTHTWLGDNLMITPENKNH 61  
Db 3 RMLNLSLLALGAAYVSFAVENPMNRLVAETLLTSLTHTWLGDNLMITPENKNH 60

Qy 62 LCICEVFGQIDTLKNTAAGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 121  
Db 61 LCICEVFGQIDTLKNTAAGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLO 120

QY 122 FLGVINTEWTE 133  
Db 121 FLGVINTEWAME 132

RESULT 4  
A48418  
interleukin-5 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A48418; S37641  
R:Ueberli, K.; Li, W.Q.; Qin, Z.H.; Richter, G.; Raabe, T.; Diamantstein, T.; Blankenstein  
Cytokine 3, 72-81, 1991  
A:Title: The rat interleukin-5 gene: characterization and expression by retroviral gene  
A:Reference number: A48418; MUID:91355638; PMID:1653053  
A:Accession: A48418  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-132 <UBE>  
A:Cross-references: EMBL:X54419; NID:G313254; PIDN:CAA38283.1; PID:G313255  
A:Experimental source: cell line TR5-1  
A:Note: sequence extracted from NCBI backbone (NCBI:63651, NCBI:63652)  
C:Superfamily: interleukin-5  
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-132/Product: interleukin-5 #status predicted <MAT>  
F:45,74,88/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:61/Disulfide bonds: interchain (to 103) #status predicted  
F:103/Disulfide bonds: interchain (to 61) #status predicted

Query Match 51.9%; Score 361; DB 1; Length 132;  
Best Local Similarity 54.9%; Pred. No. 6.3e-28;  
Matches 73; Conservative 21; Mismatches 37; Indels 2; Gaps 1;

QY 1 MRMLNLISLLALGAAVVSFAVENPMNLVAETLLSHRTWLTGDNLMIPTEPNKNH 60  
Db 1 MRMLNLCLNLTSCVW--ATAMIPMGTVVKEITQLSHRTALLTNETWRLPVPFKNH 58

QY 61 QLCIKVFQGITLKNQTAHGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFLDYIQ 120  
Db 59 QLCIGETFGDLIKNQTGRTGVTVEILFQNLISLKYIDQCKEGERKTRHFLDYIQ 118

QY 121 VELGVINTEWTE 133  
Db 119 EFLGVINTEWAME 131

RESULT 5  
G69698  
RNA polymerase (beta' subunit) rpoC - Bacillus subtilis  
C:Species: Bacillus subtilis  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 02-Sep-2000  
C:Accession: G69698  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Estian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koeter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sako, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scofone, P.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: G69698  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1199 <KUN>

A:Cross-references: GB:Z99104; GB:AL009136; NID:G2632267; PIDN:CAB11884.1; PID:e1182041;  
A:Experimental source: strain 168  
C:Genetics: rpoC  
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 12.0%; Score 83.5; DB 2; Length 1199;  
Best Local Similarity 27.1%; Pred. No. 8;  
Matches 35; Conservative 20; Mismatches 41; Indels 33; Gaps 6;

QY 1 MRMLNLISLLALGAAVVSFAVENPMNLVAETLLSHRTWLTGDNLMIPTEPNKN 59  
Db 114 MGLVLDMSPRALEEVIYFASVYVTDPAN-----TPLEKK 147

QY 60 HOLCIKEVFGIDITLKN--QTAHG-EAVDKLFQNLISLKE--HIERQKRCAGE-RWRVT 113  
Db 148 QLLSEKEVAYLDKYGNKFOASMGAEALHKLQIDLDVKEVDMLKEELKTSQGGRRTEAI 207

QY 114 KFLDYLOVF 122  
Db 208 KRLEVLEAF 216

RESULT 6  
T47758  
hypothetical protein F2413.60 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 28-Jul-2000  
C:Accession: T47758  
R:Nyakatura, G.; Rartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, February 2000  
A:Reference number: Z24475  
A:Accession: T47758  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-258 <NVA>  
A:Cross-references: EMBL:AL138655  
A:Experimental source: cultivar Columbia; BAC clone F2413  
C:Genetics:  
A:Map position: 3  
A:Introns: 109/3  
A:Note: F2413.60  
C:Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 11.3%; Score 78.5; DB 2; Length 258;  
Best Local Similarity 26.8%; Pred. No. 4;  
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 28 RLVAETLLSHRTWLTGDNLMIPTEPNKNHQLCIKEVFGID---TLKNQTAHGEA 83  
Db 161 KAVANYIVTSVATR---LGDNEVMVQISSKIHNFISNVLSGLEEDRFVLVDMSSSRSQ 217

QY 84 VDKLFQNLISLKEHIERQKRC 105  
Db 218 GERLFYTLHLQVEKIENYKLC 239

RESULT 7  
G83876  
hypothetical protein BH1815 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C:Accession: G83876  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: AB3650; MUID:20512582; PMID:11058132  
A:Accession: G83876  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <STO>  
A:Cross-references: GB:AP001513; GB:BA000004; NID:G10174345; PIDN:BA055534.1; GSPDB:GN01  
A:Experimental source: strain C-125





C71914  
phosphoserine phosphatase - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 22-Jun-1999  
C:Accession: C71914  
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A:Reference number: A71800; MUID:99120557; PMID:9923682  
A:Accession: C71914  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-207 <ARN>  
A:Cross-references: GB:AE001491; GB:AE001439; NID:g4155127; PIDN:AAD06170.1; PID:g415514  
A:Experimental source: strain J99  
C:Genetics:  
A:Gene: serB  
C:Superfamily: phosphoserine phosphatase

Query Match 10.4%; Score 72.5; DB 2; Length 207;  
Best Local Similarity 29.8%; Pred. No. 12;  
Matches 31; Conservative 14; Mismatches 34; Indels 25; Gaps 5;

QY 9 LLALGRAVVSAPAVE-NPMRLVA-----ETLTLSSTHRTWLGIGNLM 51  
Db 109 LLNDLAAFSNLIVNNALNGLVTCWMFYSKGEMLLALQRLINLSKORTLVVGGAND 168

QY 52 ITPENKNHOLCIKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIK 95  
Db 169 LSMFKHAH---IKIAPNAKEILKQATH--CIDK--PNLALIK 204

RESULT 12  
S33816  
kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-Sep-1997  
C:Accession: S33816  
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
J. Mol. Biol. 231, 155-158, 1993  
A:Title: Sequences of sea urchin kinesin light chain isoforms.  
A:Reference number: S33813; MUID:93267648; PMID:8496962  
A:Accession: S33816  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-451 <WED>  
A:Cross-references: EMBL:L08258; NID:g161531; PID:g161532

Query Match 10.4%; Score 72.5; DB 2; Length 451;  
Best Local Similarity 25.9%; Pred. No. 30;  
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103  
Db 15 GQGNL-----SQEQIITGTREVIKGLEQKNE--HNDILNSLYQSLKMLKDDTPGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124  
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 13  
S33813  
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Sep-1997  
C:Accession: S33813  
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
J. Mol. Biol. 231, 155-158, 1993  
A:Title: Sequences of sea urchin kinesin light chain isoforms.  
A:Reference number: S33813; MUID:93267648; PMID:8496962

Query Match 10.4%; Score 72.5; DB 2; Length 451;  
Best Local Similarity 25.9%; Pred. No. 30;  
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103  
Db 15 GQGNL-----SQEQIITGTREVIKGLEQKNE--HNDILNSLYQSLKMLKDDTPGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124  
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 14  
S33814  
kinesin light chain - sea urchin (Strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Sep-1997  
C:Accession: S33814  
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
J. Mol. Biol. 231, 155-158, 1993  
A:Title: Sequences of sea urchin kinesin light chain isoforms.  
A:Reference number: S33813; MUID:93267648; PMID:8496962  
A:Accession: S33814  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-677 <WED>  
A:Cross-references: EMBL:L10234; NID:g161527; PID:g161528

Query Match 10.4%; Score 72.5; DB 2; Length 677;  
Best Local Similarity 25.9%; Pred. No. 48;  
Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMIPTPENKNHQLC--IKEVFGQIDTLKNQTAHGEAVDKLFQNLSLIKHEIERQKK 103  
Db 15 GQGNL-----SQEQIITGTREVIKGLEQKNE--HNDILNSLYQSLKMLKDDTPGDSN 65

QY 104 RCAGERNVTKFLDYLOVFLG 124  
Db 66 LVEKTDIIKSLSLSLGLG 86

RESULT 15  
S33815  
kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 01-Dec-2000  
C:Accession: S33815; S36727  
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
J. Mol. Biol. 231, 155-158, 1993  
A:Title: Sequences of sea urchin kinesin light chain isoforms.  
A:Reference number: S33813; MUID:93267648; PMID:8496962  
A:Accession: S33815  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-686 <WED>  
A:Cross-references: EMBL:L10235  
R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S36727  
A:Accession: S36727  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-569, A', 570-686 <WE2>  
A:Cross-references: EMBL:L10235; NID:g161529; PID:g161530

Query Match 10.4%; Score 72.5; DB 2; Length 686;



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QM protein - protein search, using sw model

Run on: August 24, 2004, 23:41:12 ; Search time 15.0683 Seconds  
(without alignments)  
463.052 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRLMLNLSLALCAAYVSAP.....FLDYQLVFLGVINTEWTPES 134

Scoring table: BLOSUM62

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	100.0	134	1 IL5_CANFA	Q95J76 felis famil
2	591	84.9	134	1 IL5_FELCA	O77515 felis silve
3	567	81.5	134	1 IL5_HORSE	O02699 equus cabal
4	551	79.2	134	1 IL5_BOVIN	P52173 bos taurus
5	536	77.0	132	1 IL5_SHEEP	Q28586 ovis aries
6	430	61.8	134	1 IL5_HUMAN	P05113 homo sapien
7	429	61.6	134	1 IL5_CERTO	P46685 cercocobus
8	426	61.2	134	1 IL5_MACMU	P48093 macaca mula
9	414.5	59.6	135	1 IL5_CAVPO	O08987 cavia porce
10	388	55.7	132	1 IL5_MERUN	Q62575 meriones un
11	388	55.7	132	1 IL5_SIGHI	Q9es19 sigmodon hi
12	376	54.0	133	1 IL5_MOUSE	P04401 mus musculu
13	372	53.4	139	1 IL5_MACEU	Q9xt91 macropus eu
14	361	51.9	132	1 IL5_RAT	O08125 rattus norv
15	98.5	14.2	590	1 MP44_MYXVL	Q9q8q1 myxoma viru
16	83.5	12.0	1199	1 RPOC_BACSU	P37871 bacillus su
17	77	11.1	437	1 SECV_STRGB	O59912 streptomyc
18	74.5	10.7	1232	1 ADDA_BACSU	P23478 bacillus su
19	72.5	10.4	686	1 KLC_STRPU	Q05090 strongyloce
20	72	10.3	401	1 Y148_METSM	P22344 methanobrev
21	71	10.2	216	1 Y387_ARCFU	O28292 archaeoglob
22	71	10.2	328	1 YB70_HARIN	O57537 haemophilus
23	71	10.2	461	1 TIPI1_SCHPO	P79055 schizosacch
24	70.5	10.1	1055	1 RPOC_PEDAC	P77917 pediococcus
25	69	9.9	215	1 Y034_NPVAC	P21287 autographa
26	69	9.9	346	1 UFEL1_YEAST	P41834 saccharomyc
27	68.5	9.8	349	1 EGC2_VIBVU	O8d400 vibrio vuln
28	68.5	9.8	439	1 ARLY1_THETN	Q8r7c3 thermoaer
29	68	9.8	169	1 HSCB1_BUCBP	O9a17 buchnera ap
30	68	9.8	529	1 CRT1_MYXPA	O02861 myxococcus
31	68	9.8	767	1 CC10_SCHPO	P01129 schizosacch
32	67.5	9.7	247	1 Y179_ARCFU	Q30058 archaeoglob
33	67	9.6	189	1 INAC_BOVIN	P05009 bos taurus

34	67	9.6	317	1 SVGA_LACLA	Q9cgl1 lactococcus
35	67	9.6	437	1 SECV_STRCO	P46785 streptomyc
36	67	9.6	437	1 SECV_STELI	P49977 streptomyc
37	66.5	9.6	767	1 CUL1_SCHPO	O13790 schizosacch
38	66	9.5	119	1 RPOZ_CAUCR	P58066 caulobacter
39	66	9.5	360	1 HIS8_LACLA	Q02135 lactococcus
40	66	9.5	864	1 SYL_WIGBR	Q8d333 wiggleswort
41	66	9.5	1197	1 EVGS_ECO57	P58402 escherichia
42	65.5	9.4	248	1 NAG1_CANAL	Q04802 candida alb
43	65.5	9.4	756	1 CYTM_SOLTU	P37842 solanum tub
44	65.5	9.4	889	1 SECV_DROME	Q3vq4 drosophila
45	65.5	9.4	3859	1 TRAP_HUMAN	Q3y4a5 homo sapien

ALIGNMENTS

RESULT 1  
IL5\_CANFA STANDARD; PRT; 134 AA.  
AC Q95J76;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN IL5.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21334408; PubMed=1140633;  
RA Yang S., Sellins K.S., Weber E., McCall C.;  
RT "Canine interleukin-5: molecular characterization of the gene and  
expression of biologically active recombinant protein.";  
RL J. Interferon Cytokine Res. 21:361-367 (2001).  
CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
developing B-cells to immunoglobulin secreting cells (By  
similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-5 family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC  
CC EMBL; AF331920; AAL10716.1; -;  
CC DR EMBL; AF331919; AAL10715.1; -;  
CC DR InterPro; IPR009079; 4\_helix\_cytokine.  
CC DR InterPro; IPR000186; Interleukin\_5.  
CC DR Pfam; PF02025; IL5; 1.  
CC DR PRINTS; PR004432; INTERLEUKIN5.  
CC DR ProDom; PD006721; Interleukin\_5; 1.  
CC DR Cytokine; Growth factor; Glycoprotein; Signal.  
CC SIGNAL 1 21  
CC CHAIN 22 134 INTERLEUKIN-5.  
CC FT DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).  
CC FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).  
CC FT CARBOHYD 76 76 N-LINKED (GLCNAC...) (POTENTIAL).  
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).  
CC SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;  
Query Match 100.0%; Score 696; DB 1; Length 134;  
Best Local Similarity 100.0%; Pred.No. 5.3e-62;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRMLLSLLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
Db 1 MRMLLSLLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
QY 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDYIQ 120
Db 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134
RESULT 2
IL5_FELCA
ID IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; 062740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452715; PubMed=9781459;
RA Padraig P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RT "Sequence and structural analysis of feline interleukin-5 cDNA.";
RL Am. J. Vet. Res. 59:1263-1269(1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbours D.A., Helps C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; AF025436; AAC64505.1; -.
CC EMBL; AF051372; AAC05752.1; -.
CC HSSP; P05113; 1HUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 134
CC INTERLEUKIN-5.
CC BY SIMILARITY.
CC FT DISULFID 63 63
CC FT DISULFID 105 105
CC FT CARBOHYD 76 76
CC FT CARBOHYD 90 90
CC FT CONFLICT 104 105
CC FT CONFLICT 108 111
CC FT CONFLICT 114 114
CC FT CONFLICT 117 117
CC FT CONFLICT 121 121
CC FT CONFLICT 125 126
CC VI -> LL (IN REF. 2).
CC SEQUENCE 134 AA; 15224 MW; 87D18DB8F8CAC820 CRC64;
QY 1 MRMLLSLLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
Db 1 MRMLLSLLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
QY 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDYIQ 120
Db 61 QLCIKEVFGQIDTLKNTQTAHGEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134
RESULT 3
IL5_HORSE
ID IL5_HORSE STANDARD; PRT; 134 AA.
AC 003699;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandergriff E.V., Horchov D.W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U91947; AAB51382.1; -.
CC HSSP; P05113; 1HUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19
CC CHAIN 20 134
CC INTERLEUKIN-5.
CC BY SIMILARITY.
CC FT DISULFID 63 63
CC FT DISULFID 105 105
CC FT CARBOHYD 76 76
CC FT CARBOHYD 90 90
CC FT CONFLICT 104 105
CC FT CONFLICT 108 111
CC FT CONFLICT 114 114
CC FT CONFLICT 117 117
CC FT CONFLICT 121 121
CC FT CONFLICT 125 126
CC VI -> LL (IN REF. 2).
CC SEQUENCE 134 AA; 15081 MW; 2914840E3E7A006D CRC64;
QY 1 MRMLLSLLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60
Db 1 MRMLLSLLALGAAYSAFAVENPMRLVAETLLTLLSTHRTWLIGDGNLMIPPTENKH 60

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QY 61 QLCICEVFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120  
DB 61 QLCICEVFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120  
QY 121 VFLGVINTEWTPES 133  
DB 121 EFLGVINTEWTPES 133  
RESULT 4  
IL5\_BOVIN  
ID IL5\_BOVIN STANDARD; PRT; 134 AA.  
AC P2173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN IL5.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=97075944; PubMed=8918267;  
RA Mertens B., Gibrig E., Seow H.F.;  
RT "The nucleotide sequence of the bovine interleukin-5 encoding cDNA.";  
RL Gene 176:273-274 (1996).  
CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
CC developing B-cells to immunoglobulin secreting cells (By  
CC similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-5 family.  
CC  
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CC  
CC EMBL; Z67872; CAA91779.1; -.  
CC PIR; JCS116; JCS116.  
CC HSP; P05113; IHUL.  
CC InterPro; IPR000186; Interleukin\_5.  
CC Pfam; PF02025; IL5; 1.  
CC PRINTS; PR00432; INTERLEUKINS.  
CC ProDom; PD006721; Interleukin\_5; 1.  
CC Cytokine; Growth factor; Glycoprotein; Signal.  
CC SIGNAL 1 21 BY SIMILARITY.  
CC CHAIN 22 134 INTERLEUKIN-5.  
CC DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).  
CC FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).  
CC FT CARBOHYD 76 76 N-LINKED (GLCNAC...) (POTENTIAL).  
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).  
CC SEQUENCE 134 AA; 15229 MW; 0B3A2328EE7431F4 CRC64;  
Query Match 79.2%; Score 551; DB 1; Length 134;  
Best Local Similarity 79.8%; Pred. No. 1.2e-47;  
Matches 107; Conservative 15; Mismatches 12; Indels 0; Gaps 0;  
QY 1 MRMLNLSLALGAAYSAFAVENPMLVAETLLSTHRTWLIGDGNMIPTEPKH 60  
DB 1 MRMLNLSLALGAAYSAFAVENPMLVAETLLSTHRTWLIGDGNMIPTEPKH 60  
QY 61 QLCICEVFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120

DB 61 QLCICEVFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 120  
QY 121 VFLGVINTEWTPES 134  
DB 121 VFLGVINTEWTPES 134  
RESULT 5  
IL5\_SHEEP  
ID IL5\_SHEEP STANDARD; PRT; 132 AA.  
AC Q28586;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN IL5.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Seow H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;  
RT "Cloning of ovine interleukin-5 cDNA";  
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
CC developing B-cells to immunoglobulin secreting cells (By  
CC similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-5 family.  
CC  
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CC  
CC EMBL; U17053; AAS60629.1; -.  
CC EMBL; U17052; AAS60629.1; JOINED.  
CC EMBL; U35038; AAC9991.1; -.  
CC HSP; P05113; IHUL.  
CC InterPro; IPR000186; Interleukin\_5.  
CC Pfam; PF02025; IL5; 1.  
CC PRINTS; PR00432; INTERLEUKINS.  
CC ProDom; PD006721; Interleukin\_5; 1.  
CC Cytokine; Growth factor; Glycoprotein; Signal.  
CC SIGNAL 1 19 BY SIMILARITY.  
CC CHAIN 20 132 INTERLEUKIN-5.  
CC DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).  
CC FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).  
CC FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).  
CC FT CARBOHYD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).  
CC SEQUENCE 132 AA; 14974 MW; D783F2B720E249D9 CRC64;  
Query Match 77.0%; Score 536; DB 1; Length 132;  
Best Local Similarity 78.8%; Pred. No. 3.6e-46;  
Matches 104; Conservative 15; Mismatches 13; Indels 0; Gaps 0;  
QY 3 MLNLSLALGAAYSAFAVENPMLVAETLLSTHRTWLIGDGNMIPTEPKH 62  
DB 1 MELRLTVALGAAYCANAVESTMNLVAETLLSTHRTWLIGDGNMIPTEPKH 60  
QY 63 CIKEVFGQIDTLKNOTAHEAVDKLFQNLISLKEHIERQKRCACGERWRVTKFDLYLQ 122

Db 61 CIEVFQIDTLKQTAQDAVKKIPRNLSIKYIDLOKRCGGGRWRVKQFDLYQVF 120  
QY 123 LGVINTWTPES 134  
121 LGVINTWTPES 132  
Db 121 LGVINTWTPES 132

RESULT 6  
ID IL5 HUMAN STANDARD; PRT; 134 AA.  
AC P05113; Q13840;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
GN (Eosinophil differentiation factor) (B cell differentiation factor I).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=87066782; PubMed=3024129;  
RA Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuda F.,  
RA Yaota Y., Takatsu K., Hammarstrom L., Smith C.I.E., Severinson E.,  
RA Honjo T.;  
RT "Cloning of cDNA for human T-cell replacing factor (interleukin-5)  
RT and comparison with the murine homologue";  
RL Nucleic Acids Res. 14:9149-9158(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;  
RT "Molecular cloning and structure of the human interleukin-5 gene";  
RL J. Biol. Chem. 262:16580-16594(1987).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Campbell H.D., Tucker W.Q.J., Hott Y., Martinson M.E., Mayo G.,  
RA Clutterbuck E.J., Sanderson C.J., Young I.G.;  
RT "Molecular cloning, nucleotide sequence, and expression of the gene  
RT encoding human eosinophil differentiation factor (interleukin 5)";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Yokota T., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,  
RA Yokota K., Gemmell L., Shrader B., Yang G., Meyerson P., Luh J.,  
RA Hoy P., Pene J., Briere F., Spits H., Banchereau J., de Vries J.,  
RA Lee F.D., Araki N., Araki K.;  
RT "Isolation and characterization of lymphokine cDNA clones encoding  
RT mouse and human IgA-enhancing factor and eosinophil  
RT colony-stimulating factor activities: relationship to interleukin  
RT 5";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Honjo T., Takatsu K., Severinson E.;  
RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE OF 20-134, AND DISULFIDE BONDS.  
RA Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,  
RA Tsujimoto M.;  
RT "Structure of recombinant human interleukin 5 produced by Chinese  
RT hamster ovary cells";  
RL J. Biochem. 107:292-297(1990).

RN [8]  
RP DISULFIDE BONDS.  
RX MEDLINE=91243878; PubMed=2037074;  
RA Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;  
RT "Human interleukin-5 expressed in Escherichia coli: assignment of the  
RT disulfide bridges of the purified unglycosylated protein";  
RL FEBS Lett. 283:61-64(1991).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE=93247642; PubMed=8483502;  
RA Milburn M.V., Hassell A.M., Lambert M.H., Jordan S.R.,  
RA Proudfoot A.E.I., Graber P., Welis T.N.C.;  
RT "A novel dimer configuration revealed by the crystal structure at  
RT 2.4-A resolution of human interleukin-5";  
RL Nature 363:172-176(1993).  
CC !- FUNCTION: Factor that induces terminal differentiation of late-  
CC developing B-cells that immunoglobulin secreting cells.  
CC !- SUBUNIT: Homodimer; disulfide-linked.  
CC !- SUBCELLULAR LOCATION: Secreted.  
CC !- SIMILARITY: Belongs to the IL-5 family.  
CC !- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL5;  
CC WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyid=207".  
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CC  
CC EMBL; X04688; CAA28390.1; -  
CC EMBL; J03478; AAN74469.1; -  
CC EMBL; J02971; AAN98620.1; -  
CC EMBL; X12705; CAA31210.1; -  
CC EMBL; X12706; CAA31211.1; -  
CC EMBL; AF353265; AAK19759.1; -  
CC PIR; A28477; A28477.  
CC PDB; 1HUL; 07-DEC-95.  
CC Genew; HGNC:6016; IL5.  
CC MIM; 147850; -  
CC GO; GO:0005576; C:extracellular; TAS.  
CC GO; GO:0005137; F:interleukin-5 receptor binding; TAS.  
CC GO; GO:0009626; P:hypersensitive response; TAS.  
CC GO; GO:0006954; P:inflammatory response; TAS.  
CC InterPro; IPR000186; Interleukin\_5.  
CC Pfam; PF02025; IL5; 1.  
CC PRINTS; PR00432; INTERLEUKINS.  
CC ProDom; PD00672; Interleukin\_5; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.  
FT SIGNAL 1 19  
FT CHAIN 20 134 INTERLEUKIN-5.  
FT DISULFID 63 63 INTERCHAIN (WITH C-105).  
FT DISULFID 105 105 INTERCHAIN (WITH C-63).  
FT CARBOHYD 22 22 O-LINKED.  
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .).  
FT CONFLICT 88 88 F -> L (IN REF. 5; CAA31210).  
FT HELIX 26 38  
FT TURN 39 40  
FT TURN 41 45  
FT TURN 46 46  
FT STRAND 51 54  
FT HELIX 60 62  
FT HELIX 64 77  
FT TURN 82 82  
FT HELIX 83 103  
FT TURN 104 105  
FT STRAND 108 111  
FT HELIX 112 128  
FT TURN 129 129  
SQ SEQUENCE 134 AA; 15238 MW; DC984467179556A3 CRC64;  
Query Match 61.8%; Score 430; DB 1; Length 134;

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Best Local Similarity 64.9%; Pred. No. 1.2e-35;
Matches 87; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLSSLLAAGAAVSAFAVENPMRLVAETLTLLSTHRTWLIGDGNLMIPENKNH 60
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Db 1 MRMLNLSSLLAAGAAVSAFAVENPMRLVAETLTLLSTHRTWLIGDGNLMIPENKNH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 VFLGVINTEWTPES 134
    |||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EFLGVNTEWTEIES 134
    |||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
IL5_CERTO
ID IL5_CERTO STANDARD; PRT; 134 AA.
AC P46685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecidae;
OC NCBI_TaxID=9544;
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=75611102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; L26033; AAA99971.1; -.
CC HSSP; P05113; IHUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin 5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT DISULFID 63 63
FT INTERCHAIN (WITH C-105) (BY SIMILARITY).
FT DISULFID 105 105
FT INTERCHAIN (WITH C-63) (BY SIMILARITY).
FT CARBOHYD 22 22
FT O-LINKED (BY SIMILARITY).
FT CARBOHYD 47 47
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 90 90
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 134 AA; 15339 MW; 7BDD491C437981ED CRC64;

Query Match 61.6%; Score 429; DB 1; Length 134;
Best Local Similarity 64.2%; Pred. No. 1.5e-35;
Matches 86; Conservative 20; Mismatches 28; Indels 0; Gaps 0;
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QY 1 MRMLNLSSLLAAGAAVSAFAVENPMRLVAETLTLLSTHRTWLIGDGNLMIPENKNH 60
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Db 1 MRMLNLSSLLAAGAAVSAFAVENPMRLVAETLTLLSTHRTWLIGDGNLMIPENKNH 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLPQNLISLKEHIEROKKRCAGERNVTKFLDYIQ 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 VFLGVINTEWTPES 134
    |||||:|||||:|||||:|||||:|||||:|||||:
Db 121 EFLGVNTEWTEIES 134
    |||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
IL5_MACMU
ID IL5_MACMU STANDARD; PRT; 134 AA.
AC P48093;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecidae;
OC NCBI_TaxID=9544;
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=75611102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; U19848; AAA86710.1; -.
CC HSSP; P05113; IHUL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKINS.
CC ProDom; PD006721; Interleukin 5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 134
FT DISULFID 63 63
FT INTERCHAIN (WITH C-105) (BY SIMILARITY).
FT DISULFID 105 105
FT INTERCHAIN (WITH C-63) (BY SIMILARITY).
FT CARBOHYD 22 22
FT O-LINKED (BY SIMILARITY).
FT CARBOHYD 47 47
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 90 90
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 134 AA; 15150 MW; DC985ECF4B86A3 CRC64;

Query Match 61.2%; Score 426; DB 1; Length 134;
Best Local Similarity 64.9%; Pred. No. 2.9e-35;
Matches 87; Conservative 16; Mismatches 31; Indels 0; Gaps 0;
```

Db 1 MRMLSLALGAAVYIAPTIPASALVKETALLSTHRTLLIANETLRIPVPHKNH 60  
 QY 61 QLCICEVFOGIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQ 120  
 Db 61 QLCIEHIFQIGTLESQTVGGTVERLKNLSLKKYIGGKKCKGEEERRRVNQFLDYQ 120  
 QY 121 VFLGVINTEWTPES 134  
 Db 121 EFLGVNTEWIES 134

RESULT 9  
 ID IL5\_CAVPO STANDARD; PRT; 135 AA.  
 AC O08987;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 GN IL5.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96289181; PubMed=8764226;  
 RA Mansour M., Kamilowicz M., Hawrylik S.J., Nalcerio B., Angilly J.,  
 RA Conklyn M.J., Lilly C.M., Drazan J.M., Lee S.E., Auperin D.D.,  
 RA de Wet J.R., Cohan V.L., Showell H.J., Danley D.E.;  
 RT "Production and characterization of guinea pig IL-5 in baculovirus-  
 infected insect cells";  
 RL Am. J. Physiol. 270:L1002-L1007(1996).  
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
 developing B-cells to immunoglobulin secreting cells (By  
 similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -!- SIMILARITY: Belongs to the IL-5 family.  
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 DR EMBL; U34588; AAB61357.1; -.  
 DR HSSP; P05113; 1HUL.  
 DR InterPro: IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1  
 DR PRINTS; PR00432; INTERLEUKIN\_5.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Growth factor; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 135  
 FT INTERLEUKIN-5.  
 FT DISULFID 64 64  
 FT INTERCHAIN (WITH C-64) (BY SIMILARITY).  
 FT DISULFID 106 106  
 FT INTERCHAIN (WITH C-64) (BY SIMILARITY).  
 FT CARBOHYD 48 48  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 77 77  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 91 91  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 135 AA; 15291 MW; EB85252132F52731 CRC64;

Query Match 59.6%; Score 414.5; DB 1; Length 135;  
 Best Local Similarity 64.9%; Pred. No. 4e-34;  
 Matches 8; Conservative 14; Mismatches 32; Indels 1; Gaps 1;  
 QY 1 MRMLSLALGAAVYIAFAVEN-PNRLVAETLLSTHRTWLLIGDGNLMPTPENKN 59  
 Db 1 MRVLLQLGLGALGAVCVCAIPKQSATLRALVRETLTLLSTHRTLLKGNETLRISVPAHN 60

QY 60 HQLCICEVFOGIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQ 119  
 Db 61 HQLCIEHIFQIGIDTLKNOTAHGEALATFQNLISLKKHIDLQKCKGEEERRRVKQFLDYQ 120  
 QY 120 QVFLGVINTEWTPES 133  
 Db 121 QEFLAVINTEWIE 134

RESULT 10  
 ID IL5\_MERUN STANDARD; PRT; 132 AA.  
 AC O62575;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 GN IL5.  
 OS Meriones unguiculatus (Mongolian jird) (Mongolian Gerbil).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 OX NCBI\_TaxID=10047;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-Spleen;  
 RA Mai Z., Klei T.R.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
 developing B-cells to immunoglobulin secreting cells (By  
 similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-5 family.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; L37780; AAA65675.1; -.  
 DR HSSP; P05113; 1HUL.  
 DR InterPro: IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1  
 DR PRINTS; PR00432; INTERLEUKIN\_5.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Growth factor; Glycoprotein; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 132  
 FT INTERLEUKIN-5.  
 FT DISULFID 61 61  
 FT INTERCHAIN (WITH C-61) (BY SIMILARITY).  
 FT DISULFID 103 103  
 FT INTERCHAIN (WITH C-61) (BY SIMILARITY).  
 FT CARBOHYD 45 45  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 74 74  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 88 88  
 FT N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 132 AA; 15164 MW; 60CE3852F9F84261 CRC64;

Query Match 55.7%; Score 388; DB 1; Length 132;  
 Best Local Similarity 59.4%; Pred. No. 1.7e-31;  
 Matches 79; Conservative 21; Mismatches 31; Indels 2; Gaps 1;

QY 1 MRMLSLALGAAVYIAFAVEN-PNRLVAETLLSTHRTWLLIGDGNLMPTPENKN 60  
 Db 1 MRLPLQLSILT--AWWVAVALETPMSAVVKTLLQIQLSTHRTLLTSNETVRLPVPVTHKN 58  
 QY 61 QLCICEVFOGIDTLKNOTAHGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQ 120  
 Db 59 QLCICEVFOGIDTLKNOTAHGEAVDKLFQNLISLKKYIDRQKCKGEEERRRVKQFLDYQ 118



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QY 121 VFLGVINTEWTP 133
||||:|||||
Db 119 EFLGVSTWTEWME 131

RESULT 11
IL5_SIGHI
ID IL5_SIGHI STANDARD; PRT; 132 AA.
AC Q9ES19;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor)
DE (Eosinophil differentiation factor)
GN IL5
OS Sigmogon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmogon.
OX NCBI_TaxID=42415;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20510033; PubMed=11054577;
RA Howard S., Jacquet A., Haumont M., Daminet V., Milican F., Glineur F.,
RA Bollen A.;
RT "Cloning, expression and purification of recombinant cotton rat
RT interleukin-5.";
RL Gene 257:149-135(2000).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
EMBL: AF148211; AGL6722.1; -.
DR HSP; P05113; IHUL.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 132 INTERLEUKIN-5.
FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 132 AA; 15434 MW; B328B81B2371F3E9 CRC64;

Query Match 55.7%; Score 388; DB 1; Length 132;
Best Local Similarity 59.4%; Pred. No. 1.7e-31;
Matches 79; Conservative 19; Mismatches 33; Indels 2; Gaps 1;

QY 1 MRMLNLSLALGAAYVSAFVAPENMNLVAETLLTSHRTWLIGDNLMIPTPENKX 60
||||:|||||
Db 1 MRMLNLSLITL--ACVWTFVPIPTVVKETLIQLSHRALLTSNETVRLPVPVTHKH 58
||||:|||||

QY 61 QLCIKYFQGIIDTKNTAHGEAVDKLFQNLSLIKHEIERQKRCRAGERWRVTKFDYILQ 120
||||:|||||
Db 59 QLCIGEIFRGLDKNTVGGTGVETLQNLSLIKKYIDRQKCKGERRRTRQFLDYILQ 118
||||:|||||

QY 121 VFLGVINTEWTP 133
||||:|||||
```

```
Db 119 EFLGVSTWTEWME 131

RESULT 12
IL5_MOUSE
ID IL5_MOUSE STANDARD; PRT; 133 AA.
AC P04401;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell
DE growth factor II) (BCGF-II) (Eosinophil differentiation factor)
DE (Cytotoxic T lymphocyte inducer).
GN IL5 OR IL-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88254802; PubMed=3133208;
RA Campbell H.D., Sanderson C.J., Wang Y., Hori Y., Martinson M.E.,
RA Tucker W.O.J., Stellwagen A., Strath M., Young I.G.;
RT "Isolation, structure and expression of cDNA and genomic clones for
RT murine eosinophil differentiation factor. Comparison with other
RT eosinophilopoietic lymphokines and identity with interleukin-5.";
RL Eur. J. Biochem. 174:345-352(1988).
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
CC MEDLINE=87065032; PubMed=3024009;
RA Kinashi T., Harada N., Severinson E., Tanabe T., Sideras P.,
RA Konishi M., Azuma C., Tomimaga A., Bergstedt-Lindqvist S.,
RA Takahashi M., Matsuda F., Yacita Y., Takatsu K., Honjo T.;
RT "Cloning of complementary DNA encoding T-cell replacing factor and
RT identity with B-cell growth factor II.";
RL Nature 324:70-73(1986).
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=90180853; PubMed=3078564;
RA Mizuta T.R., Tanabe T., Nakakubo H., Noma T., Honjo T.;
RT "Molecular cloning and structure of the mouse interleukin-5 gene.";
CC Growth Factors 1:51-57(1988).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
EMBL: X06270; CAA29606.1; -.
DR EMBL; X06271; CAA29607.1; -.
DR EMBL; X04601; CAA28266.1; -.
DR FIR; S00807; ICM55.
DR HSP; P05113; IHUL.
DR MGD; MGI:96557; IL5.
DR InterPro; IPR00186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 INTERLEUKIN-5.
FT DISULFID 62 62 INTERCHAIN (WITH C-104) (BY SIMILARITY).
FT DISULFID 104 104 INTERCHAIN (WITH C-62) (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC...) (POTENTIAL).
```

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 133 AA; 15410 MW; C6DC091682452AF4 CRC64;

Query Match 54.0%; Score 376; DB 1; Length 133;  
 Best Local Similarity 56.8%; Pred. No. 2.6e-30;  
 Matches 75; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

QY 2 RMLINSLALGAAAYVSAFAVENPMRLVAETLLSTHRTWLIGNLMIPENKNH 61  
 DB 3 RMLHLVLTSCVW--ATAMEIPMTVVKRTLTLSAHRALTSNETMRLFPVPTKHNH 60  
 QY 62 LCICEVFGQIDTLKNQTAHGEAVDKLFONLSLKEHIERQKKKACAGERWRVTKFDYLOV 121  
 DB 61 LCICEVFGQIDTLKNQTVRGTVEMLFONLSLKKYIDRQKCKGERRRTRQFDYLOE 120  
 QY 122 FLGVINTEWTPPE 133  
 DB 121 FLGVINTEWTPPE 132

RESULT 13  
 ID IL5\_MACEU STANDARD; PRT; 139 AA.  
 AC Q9XT91;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (Eosinophil differentiation factor).  
 GN IL5.  
 OS Macropus eugenii (Tamar wallaby).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OX NCBI\_TaxID=9315;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9432005; PubMed=10501836;  
 RA Hawken R.J., Maccarone P., Toder R., Marshall Graves J.A.,  
 RA Macdoux J.F.;  
 RT "Isolation and characterization of marsupial IL5 genes."  
 RL Immunogenetics 49:942-948(1999).  
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells (By  
 CC similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -!- SIMILARITY: Belongs to the IL-5 family.  
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DR EMBL; AF064209; AAD37462.1; -.  
 DR HSP; P05113; IHUL.  
 DR InterPro; IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Growth factor; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 139  
 FT INTERLEUKIN-5.  
 FT DISULFID 64 64  
 FT INTERCHAIN (WITH C-106) (BY SIMILARITY).  
 FT DISULFID 106 106  
 FT INTERCHAIN (WITH C-64) (BY SIMILARITY).  
 FT CARBOHYD 48 48  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 77 77  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 91 91  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 139 AA; 15784 MW; CE16342A68F10622 CRC64;

Query Match 53.4%; Score 372; DB 1; Length 139;  
 Best Local Similarity 55.1%; Pred. No. 6.8e-30;  
 Matches 76; Conservative 23; Mismatches 35; Indels 4; Gaps 1;

QY 1 MEMLINLSLALGAAAYVSAFAVENPMRLVAETLLSTHRTWLIGNLMIPENKNH 60  
 DB 2 MKILVCLPLTLTYAGCVGIATGNPVSRLVTETLSLTAHRTLLIGNGTLRISIPDPQH 61  
 QY 61 QLCICEVFGQIDTLKNQTAHGEAVDKLFONLSLKEHIERQKKKACAGERWRVTKFDYLO 120  
 DB 62 PLCICEVFGQIDTLKNQTAHGEAVDKLFONLSLKEHIERQKKKACAGERWRVTKFDYLO 121  
 QY 121 VFLGVI---NTEWTPES 134  
 DB 122 EFLRTINIEWTEWTVES 139

RESULT 14  
 ID IL5\_RAT STANDARD; PRT; 132 AA.  
 AC Q08I25;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell  
 DE growth factor II) (BCGF-II) (Eosinophil differentiation factor)  
 DE (Cytotoxic T lymphocyte inducer).  
 GN IL5 OR IL-5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Lewis.  
 RX MEDLINE=91355638; PubMed=1653053;  
 RA Ueberia K.T., Li W., Guin Z., Richter G., Raabe T.,  
 RA Diamantstein T., Blanckenstein T.;  
 RT "The rat interleukin-5 gene: characterization and expression by  
 RT retroviral gene transfer and polymerase chain reaction."  
 RL Cytokine 3:72-81(1991).  
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells.  
 CC -!- SUBUNIT: Homodimer; disulfide-linked.  
 CC -!- SIMILARITY: Belongs to the IL-5 family.  
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DR EMBL; X54419; CAA38283.1; -.  
 DR PIR; A48418; A48418.  
 DR HSP; P05113; IHUL.  
 DR InterPro; IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR ProDom; PD006721; Interleukin\_5; 1.  
 KW Cytokine; Growth factor; Glycoprotein; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 132  
 FT INTERLEUKIN-5.  
 FT DISULFID 61 61  
 FT INTERCHAIN (WITH C-103) (BY SIMILARITY).  
 FT DISULFID 103 103  
 FT INTERCHAIN (WITH C-61) (BY SIMILARITY).  
 FT CARBOHYD 45 45  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 74 74  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 88 88  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 132 AA; 15207 MW; 214A928B4C047031 CRC64;

Query Match 51.9%; Score 361; DB 1; Length 132;

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Db          279 YKKIRLCYGDDFLMNVVLSFFCIRHDFDLYTIVNTD 315

Search completed: August 25, 2004, 00:02:57
Job time : 17.0683 secs

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[illegible]

Qy	121	VEFGVINTWTYPE	133
		:	
		:	
Db	119	EFLGMSTEWAME	131

```

RESULT 15
MP44 MIXVL STANDARD; PRT; 590 AA.
ID MP44 MIXVL
AC Q908Q1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable metalloendopeptidase Gl-type (EC 3.4.24.-).
GN M045L.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20032073; PubMed=10562494;
RA Cameron C., Horta-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus.";
RL Virology 264:298-318(1999).
CC -1- FUNCTION: Seems to be involved in viral proteins maturation by
CC cleavage at Ala-Gly-I-Xaa motifs [By similarity].
CC -1- COFACTOR: Binds 1 zinc ion (Potential).
CC -1- SIMILARITY: Belongs to peptidase family M44.
CC -----
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CC	----
DR	EMBL; AF170726; AAF14933.1; -
DR	MEROSES; M44.001; --
DR	IatePro; IPR005073; Peptidase_M44.
DR	Pfam; PF03410; Peptidase_M44; 1.
KW	Hydrolase; Metalloprotease; Zinc.
FT	METAL 41 41 ZINC (CATALYTIC) (POTENTIAL).
FT	ACT_SITE 44 44 ZINC (CATALYTIC) (POTENTIAL).
FT	METAL 45 45 ZINC (CATALYTIC) (POTENTIAL).
SQ	SEQUENCE 590 AA; 68324 MW; IDEEL78930G75884 CRC64;

Query Match	14.2%	Score 98.5;	DB 1;	Length 590;
Best Local Similarity	26.1%;	Pred. No. 0.045;		
Matches	41: Conservative	23: Mismatches	38: Indels	55: Gaps
				8:

```

Qy      7  LSLALGAAYVSAFAVENPMRLVAETLLSLSTHRTWLIGDGNLMITPT-----ENK 58
      |||||
Db     180  LSLLA-----NTFGRLPACPLTIPCTVRT-IIIGKTIIMPSPFYTMVRVPS 226
      |||||
Qy     59  NHC---LCIKVFQGITLKNQTAHGEAVD-KLFQNLSLIKSH-----I 98
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    227  LHNLSILCLYFIYHLVDY-----ETVDNKLYVTFSFIHSDYVERFLQSGRLNLT 278
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Qy     99  EROKKECAGERWRTKFDYLQV-----FLGVINTE 129
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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Blank sheet

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:54:03 ; Search time 78.0321 Seconds  
(without alignments)  
541.821 Million cell updates/sec

Title: US-10-787-382-5  
Perfect score: 696  
Sequence: 1 MRMLNLSLLALGAAYVSAP.....FLDYLVQLGVINTWTPES 134

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriap:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	100.0	134	6 Q95J76	Q95J76 canis famil
2	586	84.2	134	6 Q9TSD7	Q9TSD7 felis silve
3	578	83.0	134	6 Q9MYM5	Q9MYM5 sus scrofa
4	571	82.0	118	6 Q9TV10	Q9TV10 canis famil
5	448	64.4	134	6 Q9MKH1	Q9MKH1 saimiri sci
6	354	50.9	132	11 Q9R2C9	Q9R2C9 rattus norv
7	109.5	15.7	40	6 Q9XT92	Q9XT92 smnthopsis
8	81.5	11.7	488	13 Q7ZUA6	Q7ZUA6 gallus gall
9	80.5	11.6	485	13 Q7ZZ21	Q7ZZ21 gallus gall
10	79.5	11.4	610	5 Q9NA53	Q9NA53 caenorhabdi
11	79	11.4	676	8 Q7YK5	Q7YK5 mapania par
12	78.5	11.3	258	10 Q9M1K0	Q9M1K0 arabidopsis
13	78.5	11.3	463	11 Q91WC6	Q91WC6 mus musculu
14	78.5	11.3	490	11 Q9JIT0	Q9JIT0 mus musculu
15	77.5	11.1	331	16 Q9KBV9	Q9KBV9 bacillus ha
16	77	11.1	478	5 Q9PYV7	Q9PYV7 caenorhabdi

17	76.5	11.0	158	5 O96575	O96575 leucophaea
18	75.5	10.8	284	4 Q8NDP7	Q8NDP7 homo sapien
19	75.5	10.8	490	4 Q8WVF7	Q8WVF7 homo sapien
20	75.5	10.8	490	4 Q96QZ5	Q96QZ5 homo sapien
21	75	10.8	292	17 Q8PUD3	Q8PUD3 methanosarc
22	74.5	10.7	313	16 Q8PNY3	Q8PNY3 xanthomonas
23	74	10.6	241	8 Q8SKZ3	Q8SKZ3 myosotis ra
24	74	10.6	241	8 Q8SKY6	Q8SKY6 myosotis di
25	74	10.6	302	16 Q83IU2	Q83IU2 enterococcu
26	74	10.6	395	5 Q9VKL1	Q9VKL1 arabidopsis
27	73.5	10.6	253	10 Q9MIK1	Q9MIK1 shewanella
28	73.5	10.6	1293	16 Q8EY1	Q8EY1 myosotis ma
29	73	10.5	241	8 Q8SKY3	Q8SKY3 helianthus
30	73	10.5	248	10 Q8RVK0	Q8RVK0 xanthomonas
31	73	10.5	313	16 Q8PCA2	Q8PCA2 xanthomonas
32	73	10.5	623	10 Q7XSA0	Q7XSA0 cryza sativ
33	73	10.5	661	11 Q921P5	Q921P5 mus musculu
34	73	10.5	664	11 Q8K2B3	Q8K2B3 mus musculu
35	73	10.5	827	10 Q8W3A1	Q8W3A1 cryza sativ
36	72.5	10.4	207	16 Q9ZLI2	Q9ZLI2 helicobacte
37	72.5	10.4	229	16 Q9CLP5	Q9CLP5 pasteurella
38	72.5	10.4	310	17 Q8ZS2	Q8ZS2 pyrobaculum
39	72.5	10.4	313	2 O6466	O6466 xanthomonas
40	72.5	10.4	418	10 Q8S1N1	Q8S1N1 cryza sativ
41	72.5	10.4	510	10 Q8GW74	Q8GW74 arabidopsis
42	72.5	10.4	645	5 Q8IHQ8	Q8IHQ8 plasmodium
43	72	10.3	253	16 Q97DG5	Q97DG5 clostridium
44	72	10.3	296	17 Q8TQV4	Q8TQV4 methanosarc
45	72	10.3	562	12 Q7TH69	Q7TH69 lycoris pot

ALIGNMENTS

RESULT 1

Q95J76 PRELIMINARY; PRT; 134 AA.  
ID Q95J76  
AC Q95J76;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Interleukin-5.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21334408; PubMed-11440633;  
RA Yang S., Sellins K.S., Weber E., McCall C.;  
RT "Canine interleukin-5: molecular characterization of the gene and  
expression of biologically active recombinant protein.";  
J. Interferon Cytokine Res. 21:361-367(2001).  
RL EMBL; AF331920; AAL10716.1; -  
DR EMBL; AF331919; AAL10715.1; -  
DR GO; GO:0005576; Extracellular; IEA.  
DR GO; GO:0005373; Fintreleukin-5 receptor binding; IEA.  
DR GO; GO:0005955; Pimmune response; IEA.  
DR InterPro; IPR000186; Interleukin\_5.  
DR PRINTS; PR00432; INTERLEUKIN5.  
DR ProDom; PD006721; Interleukin\_5; 1.  
SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;

Query Match 100.0%; Score 696; DB 6; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.5e-63;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRMLNLSLLALGAAYVSAPFNPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKNH	60
Db	1	MRMLNLSLLALGAAYVSAPFNPNRLVAETLTLLSTHRTWLIGDGNLMPTPENKNH	60
Qy	61	QLCICEVFOGIDTLKNQTAHGEAVDKLFQNLSLIKEHIERQKRCAGERWRTKFLDYQLQ	120

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Db 61 QLCIKVEFGQIDTLKNTAGHGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 2
Q9TSD7
ID Q9TSD7 PRELIMINARY; PRT; 134 AA.
AC Q9TSD7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin_5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandegrift E., Hughes K.J., O'Reilly K.L.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068770; AAC27616.1; -.
DR HSSP; POS113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8C820 CRC64;

Query Match 84.2%; Score 586; DB 6; Length 134;
Best Local Similarity 85.0%; Pred. No. 3e-52;
Matches 113; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKH 60
Db 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKH 60
QY 61 QLCIKVEFGQIDTLKNTAGHGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYIQ 120
Db 61 QLCIKVEFGQIDTLKNTAGHGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYIQ 120
QY 121 VFLGVINTEWTPES 133
Db 121 VFLGVINTEWTPES 133

RESULT 3
Q9TSD7
ID Q9TSD7 PRELIMINARY; PRT; 134 AA.
AC Q9TSD7;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin_5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20130134; PubMed=10663563;
RA Sylvan H., Matvienko O., Leonchiks A., Alving K., van der Ploeg I.;
RT "Molecular cloning, expression, and purification of pig interleukin-5."
RL Immunogenetics 51:59-64 (2000).
RN [2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,
RA Heegaard P.M.H.;
RT "Sus scrofa mRNA for interleukin-5."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010088; CAB70611.2; -.
DR EMBL; AJ133452; CAB36328.1; -.
DR HSSP; POS113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15191 MW; B485D562A028A899 CRC64;

Query Match 83.0%; Score 578; DB 6; Length 134;
Best Local Similarity 85.1%; Pred. No. 2e-51;
Matches 114; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKH 60
Db 1 MRMLNLSLLALGAAYVSFAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKH 60
QY 61 QLCIKVEFGQIDTLKNTAGHGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYIQ 120
Db 61 QLCIKVEFGQIDTLKNTAGHGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYIQ 120
QY 121 VFLGVINTEWTPES 134
Db 121 VFLGVINTEWTPES 134

RESULT 4
Q9TSD7
ID Q9TSD7 PRELIMINARY; PRT; 118 AA.
AC Q9TSD7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine interleukin-5."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091133; AAD46991.1; -.
DR HSSP; POS113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON TER 1
FT NON TER 118
SQ SEQUENCE 118 AA; 13507 MW; 36A5563DD67C968C CRC64;

Query Match 82.0%; Score 571; DB 6; Length 118;
Best Local Similarity 93.8%; Pred. No. 8.9e-51;
Matches 106; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 18 SAFAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKHOLCIKEVFGQIDTLKNO 77
Db 6 SAFAVENPMNRLVAETLLSTHRTWLIGDGNLMIPTPENKHOLCIKEVFGQIDTLKNO 65

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QY 78 TAHEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQVFLGVNTIEW 130
DB 66 TAHEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQVFLGVNTIEW 118

RESULT 5
Q8MKH1
ID Q8MKH1 PRELIMINARY; PRT; 134 AA.
AC Q8MKH1; 2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Interleukin-5.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21972723; PubMed=11976788;
RA Harad J.M., Laverne A., Kazanji M.;
RT "Molecular cloning, characterization, and quantification of squirrel
RL monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL Immunogenetics 54:20-29(2002).
DR EMBL; AF294756; AAK92043.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15210 MW; EAFACASDB48767C CRC64;

Query Match 64.48; Score 448; DB 6; Length 134;
Best Local Similarity 67.98; Pred. No. 4.3e-38;
Matches 91; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

QY 1 MRMLNLALLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60
DB 1 MRMLNLALLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQ 120
DB 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQ 120

QY 121 VFLGVNTIEWTPES 134
DB 121 VFLGVNTIEWTPES 134

RESULT 6
Q9R2C9
ID Q9R2C9 PRELIMINARY; PRT; 132 AA.
AC Q9R2C9;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Interleukin-5 precursor.
GN IL-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Lou M;
RA Pierrot C.;
RT "Cloning, expression of rat IL-5 and production of neutralizing
RT antiserum: comparative study of IL-5 activity expressed in E.coli and
RT baculovirus system.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011299; CAA09587.1; -.

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DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
KW Signal.
FT CHAIN 1 17 POTENTIAL.
FT CHAIN 18 132 INTERLEUKIN-5.
SQ SEQUENCE 132 AA; 15191 MW; 814A87CBAC04702B CRC64;

Query Match 50.9%; Score 354; DB 11; Length 132;
Best Local Similarity 54.1%; Pred. No. 1.9e-28;
Matches 72; Conservative 21; Mismatches 38; Indels 2; Gaps 1;

QY 1 MRMLNLALLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 60
DB 1 MRMLNLALLALGAAYVSFAVENPMNRLVAETLTLLSTHRTWLTGDNLMIPTPENKNH 58

QY 61 QLCIKVEFGQIDTLKNQTAHGEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQ 120
DB 59 QLCIKVEFGQIDTLKNQTAHGEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQ 118

QY 121 VFLGVNTIEWTPES 133
DB 119 EFLGVNTIEWTAWME 131

RESULT 7
Q9XT92
ID Q9XT92 PRELIMINARY; PRT; 40 AA.
AC Q9XT92;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
GN IL5.
OS Smnithopsis macroura (Stripe-faced dunnart).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Smnithopsis.
OX NCBI_TaxID=9302;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99432005; PubMed=10501836;
RA Hawken R.J., Maccarone P., Todter R., Marshall Graves J.A.,
RA Maddox J.F.;
RT "Isolation and characterization of marsupial IL5 genes.";
RL Immunogenetics 49:942-948(1999).
DR EMBL; AF064208; AAD37461.1; -.
DR HSSP; P05113; 1HUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4695 MW; 54B93064203EA70B CRC64;

Query Match 15.7%; Score 109.5; DB 6; Length 40;
Best Local Similarity 53.8%; Pred. No. 0.00056;
Matches 21; Conservative 9; Mismatches 8; Indels 1; Gaps 1;

QY 71 IDTLKNQTAHGEAVDKLFONLSLTIKEHIEROKKRCACGERWRVTKEFDLYLQ 109
DB 1 IETLKQTAEDNVVERIFQNFSLKEHITTKKQC-GEK 38

RESULT 8

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RN
RP SEQUENCE FROM N.A.
RA Givnish T.J., Pires J.C., Graham S.W., McPherson M., Prince L.M.,
RA Patterson T.B., Rai H., Roalson E.H., Evans T.M., Hahn W.J.,
RA Millam K.C., Molvray M., Kores P.J., O'Brien H., Hall J.C.,
RA Kress W.J., Sytoma K.J.;
RT "A monocoat-wide phylogeny based on the highly informative cpDNA gene
RT ndhF: evidence for widespread concerted convergence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129256; AAN05045.1; -
KW Chloroplast.
FT NON TER 1 676
FT NON TER 676
FT NON TER 676
SQ SEQUENCE 676 AA; 7B225B10D13A3C39 CRC64;

Query Match 11.4%; Score 79; DB 8; Length 676;
Best Local Similarity 25.4%; Pred. No. 23;
Matches 35; Conservative 13; Mismatches 40; Indels 50; Gaps 6;

QY 3 MLNLSLALGAAVYSAFAVENPMNLVAETLLSTHRTWLIGDGNLMIPENKNH-- 60
Db 519 MLFPLLLLVFTVFGISGIGHFERGI---DLILS---KWLISSTNLF--ESSNYCV 569

QY 61 -----QICKEVFQGDITLKNQTAHGEAVDKLFQNLSLIKEHIEROK 102
Db 570 NSVEFLKNTIFSVSATFGLCIAYFYG-----SVYSFFQNLVFINSPFKRGV 617

QY 103 KRCAGERWRYTKFLDYIQ 120
Db 618 KR-----SFLDQIQ 626

RESULT 12
Q9MIKO PRELIMINARY; PRT; 258 AA.
ID Q9MIKO
AC Q9MIKO
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Putative bHLH transcription factor).
GN F24I3.60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Nyakatura G., Fartmann B., Dauner D., Steir W., Holland R.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,
RA Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Jacoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
RA "Basic-helix-loop-helix (bHLH) transcription factors in Arabidopsis
RT thaliana.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BEJONGS TO THE BASIC HELIX-LOOP-HELIX (bHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
DR EMBL; AL138655; CAB72168.1; -
DR EMBL; AF488577; AAM10941.1; -
DR PIR; T47758; T47758.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00888; HLH_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 258 AA; 29004 MW; 2AE6CBF05422D3E0 CRC64;
```

```
RN
RP SEQUENCE FROM N.A.
RA Givnish T.J., Pires J.C., Graham S.W., McPherson M., Prince L.M.,
RA Patterson T.B., Rai H., Roalson E.H., Evans T.M., Hahn W.J.,
RA Millam K.C., Molvray M., Kores P.J., O'Brien H., Hall J.C.,
RA Kress W.J., Sytoma K.J.;
RT "A monocoat-wide phylogeny based on the highly informative cpDNA gene
RT ndhF: evidence for widespread concerted convergence.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129256; AAN05045.1; -
KW Chloroplast.
FT NON TER 1 676
FT NON TER 676
FT NON TER 676
SQ SEQUENCE 676 AA; 7B225B10D13A3C39 CRC64;

Query Match 11.3%; Score 78.5; DB 10; Length 258;
Best Local Similarity 26.8%; Pred. No. 8;
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 28 RLVAETLLSTHRTWLIGDGNLMIPENKNHQLCIKEVFQGDID---TLKNQTAHGEA 83
Db 161 KAVANYISTVSATR---LGDNEVAVQISSSKIHNFISNVLSGLEEDRFVLVDMSSSRSQ 217

QY 84 VDKLFQNLSLIKEHIEROKKRC 105
Db 218 GERLFYTLHLQVKIENYKLCN 239

RESULT 13
Q91WC6 PRELIMINARY; PRT; 463 AA.
ID Q91WC6
AC Q91WC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to limb region 1.
GN LMBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RC TISSUE=Eye, and Retina;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016110; AAH16110.1; -
DR MGI; 1861746; Lmbri.
DR InterPro; IPR008075; Lipocalin1_recep.
DR InterPro; IPR006876; LMBR1.
DR Pfam; PF04791; LMBR1; 1.
DR PRINTS; PR01692; LIPOCALIN1MR.
SQ SEQUENCE 463 AA; 52005 MW; 8A115C85384A0C6 CRC64;

Query Match 11.3%; Score 78.5; DB 11; Length 463;
Best Local Similarity 22.8%; Pred. No. 16;
Matches 33; Conservative 31; Mismatches 36; Indels 45; Gaps 7;

QY 3 MLNLSLALGAAVYSAFAVENPMNLVAETLLSTHRTWLIGDGNL 50
Db 126 MLLLLALLILGVVWVASALID-----SDAASMESLYDLWEFYLPLYSCILMGCLLL 178

QY 51 MIPTPENKNH-----QICIK-EVFGID-----TLKNQ-----AHGEA-----V 84
Db 179 LLCTPVGLSRMFTVMGQLLVKPAILEDDEQIYMITLEEEALQRLHGLSSSVYNNMEL 238

QY 85 DKLFQNLSLIKEHIEROKKRC 109
Db 239 EQELENVKILTKLERKKASAWER 263

RESULT 14
Q9JITO PRELIMINARY; PRT; 490 AA.
ID Q9JITO
AC Q9JITO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE LMBR1 long form.
GN LMBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.D2/nsn.
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:40:07 ; Search time 83.1325 Seconds  
(without alignments)  
390.857 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 PAVENPMRLVAETLLTLLST.....FLDYQLQVFLGVINTEWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	610	100.0	115	3 AAY58220	Canine ma
2	610	100.0	134	3 AAY58219	Canine in
3	601	98.5	134	4 AAB72615	Canine in
4	487	79.8	132	2 AAW08479	Ovine IL-
5	357	58.5	113	1 AAP93152	Sequence
6	357	58.5	287	6 AAO30459	hIL5.36 v
7	356	58.4	112	1 AAP80279	Pleiotrop
8	356	58.4	115	1 AAP81038	Sequence
9	356	58.4	115	3 AAB45489	Human int
10	356	58.4	115	5 ABG94295	Human mat
11	356	58.4	115	5 ABG80607	Human mat
12	356	58.4	115	6 AAO30453	Human C-I
13	356	58.4	123	5 ABG94353	Human IL-
14	356	58.4	123	5 ABG80665	Human IL-
15	356	58.4	134	2 AAB92802	Human int
16	356	58.4	134	4 AAB72617	Human int
17	356	58.4	134	5 ABG94294	Human pre
18	356	58.4	134	5 ABG80606	Human pre
19	356	58.4	134	5 AAU10353	Interleuk
20	356	58.4	136	5 ABG94352	Human C-I
21	356	58.4	136	5 ABG80664	Human ILn
22	356	58.4	138	5 ABG94351	Human C-I
23	356	58.4	138	5 ABG80663	Human ILn
24	356	58.4	285	6 AAO30457	hIL5-P30-
25	356	58.4	285	6 AAO30458	hIL5-P2-P

26	356	58.4	287	6 AAO30460	hIL5.37 v
27	352	57.7	134	5 AAU10354	Interleuk
28	351	57.5	121	2 AAW43436	Human int
29	347	56.9	115	2 AAW05273	N-termina
30	347	56.9	115	2 AAW72948	Truncated
31	347	56.9	133	1 AAP71064	Murine eo
32	347	56.9	133	1 AAP82969	B cell di
33	347	56.9	133	1 AAP82969	B cell di
34	347	56.9	133	2 AAR96963	T cell re
35	347	56.9	133	2 AAW72949	T cell re
36	347	56.9	133	2 AAW72947	T cell re
37	347	56.9	133	4 AAB72618	Murine in
38	347	56.9	134	5 ABG94349	Mouse C-I
39	346	56.7	134	1 AAP81056	Sequence
40	344	56.4	136	5 ABG94348	Mouse C-I
41	344	56.4	136	5 ABG80660	Mouse IL-
42	343	56.2	84	4 AAB72616	Canine in
43	343	56.2	113	2 AAW05274	N-termina
44	343	56.2	113	5 ABG94296	Mouse int
45	343	56.2	113	5 ABG80608	Mouse mat

ALIGNMENTS

RESULT 1

AAY58220  
ID AAY58220 standard; protein; 115 AA.

AC AAY58220;

XX 14-MAR-2000 (first entry)

DT Canine mature interleukin-5 (IL-5).

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine.

OS Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

XX N-PSDB; AAZ55550, AAZ55551.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease.

XX Claim 3h; Page 227; 264pp; English.

Sequences AAY58219-Y58220 represent encoded and mature canine interleukin-5 (IL-5). The invention relates to canine IL-4, canine or feline ILT-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha), and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while

CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX SQ Sequence 115 AA;

Query Match 100.0%; Score 610; DB 3; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-64;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60  
 DB 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60  
 QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115  
 DB 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115

RESULT 2  
 AAY58219  
 ID AAY58219 standard; protein; 134 AA.  
 XX AC AAY58219;  
 XX DT 14-MAR-2000 (first entry)  
 XX DE Canine interleukin-5 (IL-5).  
 XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.  
 XX OS Canis familiaris.  
 XX PN W09961618-A2.  
 XX PD 02-DEC-1999.  
 XX PF 28-MAY-1999; 99WO-US011942.  
 XX PR 29-MAY-1998; 98US-0087306P.  
 XX PA (HESK-) HESKA CORP.  
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX WPI: 2000-072623/06  
 XX N-PSDB; AAZ55546, AAZ55547, AAZ55548, AAZ55549.  
 XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 XX useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX PS Claim 3h; Page 224; 264pp; English.

CC Sequences AAY58219-Y58220 represent encoded and mature canine interleukin  
 CC -5 (IL-5). The invention relates to canine IL-4, canine or feline ILT-3  
 CC ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand),  
 CC canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline  
 CC granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides  
 CC which encode these immunoregulatory proteins. The proteins, and their  
 CC associated nucleic acids, specific antibodies and inhibitors may be used  
 CC as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response for a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug

CC targeting  
 XX SQ Sequence 134 AA;  
 Query Match 100.0%; Score 610; DB 3; Length 134;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-64;  
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60  
 DB 20 FAVENPNRLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 79  
 QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115  
 DB 80 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 134

RESULT 3  
 AAB72615  
 ID AAB72615 standard; protein; 134 AA.  
 XX AC AAB72615;  
 XX DT 04-MAY-2001 (first entry)  
 XX DE Canine interleukin-5 protein #1.  
 XX KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
 XX KW inflammatory reaction.  
 XX OS Canis sp.  
 XX PN W0200111049-A2.  
 XX PD 15-FEB-2001.  
 XX PF 09-AUG-2000; 2000WO-US021651.  
 XX PR 10-AUG-1999; 99US-00371615.  
 XX PA (IDEX-) IDEXX LAB INC.  
 XX PI Guo H, Lawton R, Mermer B, Aiyappa AP;  
 XX WPI; 2001-191542/19.  
 XX DR N-PSDB; AAF74300.  
 XX PT Novel canine interleukin 5 polynucleotide and polypeptides are used for  
 XX generating antibodies which are useful in treating allergies in dogs.  
 XX PS Claim 29; Page 46-47; 48pp; English.

CC The present invention provides the protein and coding sequences of the  
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
 CC cancer and inflammatory reactions in dogs. The present sequence is one  
 CC version of the IL-5 protein shown in the specification

XX SQ Sequence 134 AA;  
 Query Match 98.5%; Score 601; DB 4; Length 134;  
 Best Local Similarity 99.1%; Pred. No. 2.6e-63;  
 Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 FAVENPNRLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60  
 DB 20 FAVENPNRLVAETLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 79  
 QY 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115  
 DB 80 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLVFLGVINTEWTPES 134

RESULT 4

AAW08479  
ID AAW08479 standard; protein; 132 AA.  
XX AC AAW08479;  
XX DT 17-OCT-2003 (revised)  
XX DT 24-SEP-1997 (first entry)  
XX DE Ovine IL-5.  
XX KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
XX KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
XX KW immunosuppression; allergy; reproductive system; growth; early maturity;  
XX KW antibody; diagnosis; immunopotentiator;  
XX KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
XX KW secretion; IGM; IGA; bacterial endotoxin; gamma-interferon.  
XX OS Ovis aries.  
XX XX WO9700321-A1.  
XX PN 03-JAN-1997.  
XX PD 14-JUN-1996; 96WO-AU000360.  
XX PF 14-JUN-1995; 95AU-00003502.  
XX PR 27-OCT-1995; 95AU-00006244.  
XX XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX PA Seow H, Wood P;  
XX PI WPI: 1997-077528/07.  
XX DR N-PSDB; AAT50755, AAT50756.  
XX DR Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine  
XX PT adjuvants and to treat or prevent microbial infections in livestock.  
XX PT Claim 31; Page 39-40; 78pp; English.  
XX PS This protein sequence represents ovine interleukin-5 (IL-5). Ovine IL-5  
XX CC or IL-12 are used to treat and/or prevent infections in livestock (esp.  
XX CC cows and sheep), particularly where the animals are stressed, e.g. during  
XX CC transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for  
XX CC veterinary use (partic. weakly immunogenic subunit or synthetic peptide  
XX CC vaccines). They may also be used to treat cancer, immunosuppression and  
XX CC allergy, to enhance/suppress the reproductive system and to promote  
XX CC growth or early maturity. Optionally interleukin can be delivered from  
XX CC constructs or delivery cells and antibodies are useful in enzyme  
XX CC immunoassays for rapid diagnosis of infection. The interleukins are  
XX CC immunopotentiators, especially IL-5 promotes growth of early  
XX CC haematopoietic progenitor cells and generation of cytotoxic cells from  
XX CC thymocytes, also it stimulates production and secretion of IGM and IgA  
XX CC (in synergism with bacterial endotoxin). IL-12 induces production of  
XX CC gamma-interferon by, and proliferation of, T and NK cells and increases  
XX CC the (non-)specific cytolytic lymphocyte response. The genetic constructs  
XX CC can also be used for in vitro production of IL-5 or -12. (updated on 17-  
XX CC OCT-2003 to standardise OS field)  
XX SQ Sequence 132 AA;  
Query Match 79.8%; Score 487; DB 2; Length 132;  
Best Local Similarity 80.7%; Pred. No. 9.9e-50;  
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
QY 2 AVENPMRLVAETLLSTHRTWLTGDNLMIPTEPNKHQICKEVFGQIDTLKNQTAH 61  
DB 19 AVESTMRLVAETLLSTHRTWLTGDNLMIPTEPNKHQICKEVFGQIDTLKNQTAQ 78  
QY 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLOVFLGVINTEWTPES 115  
DB 79 GDVAVKIFRNLISLKEIYDILQKRCGGERWRVQFLDYLOVFLGVINTEWTPES 132

RESULT 5  
AAP93152  
ID AAP93152 standard; protein; 113 AA.  
XX AC AAP93152;  
XX DT 15-MAR-1992 (first entry)  
XX DE Sequence of human interleukin-5 (IL-5).  
XX KW B-cell growth factor; lymphokine; B-cell stimulating factor 2.  
XX OS Homo sapiens.  
XX PN GB2217328-A.  
XX PD 25-OCT-1989.  
XX PF 12-APR-1988; 88GB-00008524.  
XX PR 12-APR-1988; 88GB-00008524.  
XX PA (BREI-) BRITISH BIO-TECHN L.  
XX PI Edwards RM;  
XX XX WPI: 1989-311767/43.  
XX DR N-PSDB; AAN91647.  
XX DR Synthetic gene encoding human interleukin-5 - has restriction sites at  
XX PT frequent intervals to facilitate manipulation.  
XX PS Disclosure; Fig 3a; 2lpp; English.  
XX CC AAN91647 has restriction sites for HindIII, BspMI, NcoI, SpeI, BspMI.  
XX CC ApuII, XmaI, ClaI, Ball, PstI, DraII, BamHI and EcoRI. IL5 acts as a B-  
XX CC cell growth and differentiation factor  
XX SQ Sequence 113 AA;  
Query Match 58.5%; Score 357; DB 1; Length 113;  
Best Local Similarity 61.9%; Pred. No. 2.5e-34;  
Matches 70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;  
QY 3 VENPMRLVAETLLSTHRTWLTGDNLMIPTEPNKHQICKEVFGQIDTLKNQTAH 62  
DB 1 MEIPTSALVKETALLSTHRTWLTGDNLMIPTEPNKHQICKEVFGQIDTLKNQTAH 60  
QY 63 EAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYLOVFLGVINTEWTPES 115  
DB 61 GTVERLFKRLSLIKKYIDGQKCKGERRRNVQFLDYLOVFLGVINTEWTPES 113

RESULT 6  
AAO30459  
ID AAO30459 standard; protein; 287 AA.  
XX AC AAO30459;  
XX DT 22-SEP-2003 (first entry)  
XX DE hIL5.36 variant protein.  
XX KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
XX KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
XX KW IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.  
XX OS Homo sapiens.  
XX OS Unidentified.  
XX OS Chimeric.  
XX PF Key Location/Qualifiers



XX  
PI Honjo T, Takatu K, Severinson E;  
XX  
DR WPI; 1988-085927/13.  
XX  
XX Recombinant human B-cell differentiation factor - used for diagnosis or  
PT treatment of immunodeficiency diseases, various infections and cancers.  
XX  
XX  
XX Claim 8; Page 17; 5pp; English.  
XX  
XX Bcdf has an approx. molecular weight of 13,149. The Bcdf is useful in the  
CC diagnosis or treatment of e.g. immunodeficiency diseases which occur due  
CC to the deficiency of this factor in a living body and also in the  
CC treatment of various infections and cancers. (Updated on 25-MAR-2003 to  
CC correct PR field.)  
XX  
XX  
SQ Sequence 115 AA;  
Query Match 58.4%; Score 356; DB 1; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.4e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
QY 4 ENPMRLVAVETLLSTHRTWLIGDGNLMPTPENKQHLCIKVEFGIDTLKNQTAHGE 63  
Db 4 EIPTSLVKTETALLSTHRTLLIANETLRIPVPVHKHQLCTEIEIFQIGITLESQTVQGG 63  
QY 64 AVDKLFQNLSLIKHEHIERQKRCAGRWVTKFDLYQLQVFLGVINTEWTPES 115  
Db 64 TVERLFKNLSLIXKYYIDGQKKCGEERRRVNQFLDYQLQVFLGVINTEWTPES 115  
RESULT 9  
AAB45489  
ID AAB45489 standard; protein; 115 AA.  
AC AAB45489;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE Human interleukin-5 mature protein SEQ ID NO: 1.  
XX  
XX Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;  
XX cancer; eosinophilia; vaccine; allergic rhinitis.  
XX  
XX Homo sapiens.  
XX  
XX WO200065058-A1.  
XX  
XX 02-NOV-2000.  
XX  
XX 19-APR-2000; 2000WO-DK000205.  
XX  
XX 23-APR-1999; 99DK-00000552.  
XX 06-MAY-1999; 99US-0132811P.  
XX  
XX (MEBI-) M & E BIOTECH AS.  
XX  
XX Klysner S;  
XX  
XX WPI; 2000-672791/65.  
XX  
XX Down-regulating interleukin 5 (IL-5) activity in humans by administering  
PT IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or  
PT amelioration of asthma or other chronic allergic conditions.  
XX  
XX Claim 19; Page 118; 172pp; English.  
XX  
XX The present invention is concerned with methods of treating asthma,  
CC eosinophilia, allergic rhinitis and other allergic diseases. These  
CC involve the use of interleukin-5 (IL-5) analogues and modified IL-5  
CC proteins and their coding sequences to down-regulate IL-5 activity and  
CC thus reduce eosinophil numbers. The allergic diseases may be treated  
CC using autovaccines, nucleic acid vaccines or live vaccines. In addition,  
CC

CC it is possible that they may be used in the treatment of cancer and  
CC helminthic infections  
XX  
SQ Sequence 115 AA;  
Query Match 58.4%; Score 356; DB 3; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.4e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
QY 4 ENPMRLVAVETLLSTHRTWLIGDGNLMPTPENKQHLCIKVEFGIDTLKNQTAHGE 63  
Db 4 EIPTSLVKTETALLSTHRTLLIANETLRIPVPVHKHQLCTEIEIFQIGITLESQTVQGG 63  
QY 64 AVDKLFQNLSLIKHEHIERQKRCAGRWVTKFDLYQLQVFLGVINTEWTPES 115  
Db 64 TVERLFKNLSLIXKYYIDGQKKCGEERRRVNQFLDYQLQVFLGVINTEWTPES 115  
RESULT 10  
ABG94295  
ID ABG94295 standard; protein; 115 AA.  
XX  
AC ABG94295;  
XX  
DT 10-DEC-2002 (first entry)  
XX  
DE Human mature interleukin 5 protein.  
XX  
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;  
KW cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;  
KW vaccine; infectious disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200256905-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 21-JAN-2002; 2002WO-IB000166.  
XX  
XX 19-JAN-2001; 2001US-0262379P.  
XX 04-MAY-2001; 2001US-0289549P.  
XX 05-OCT-2001; 2001US-032598P.  
XX 07-NOV-2001; 2001US-0331045P.  
XX  
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
XX  
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;  
PI Piossek C;  
XX  
XX WPI; 2002-627351/67.  
XX  
XX Molecular antigen array used in the production of vaccines for infectious  
PT diseases.  
XX  
XX Disclosure; Page 422; 441pp; English.  
XX  
XX This invention relates to a novel ordered and repetitive antigen array  
CC used in the production of vaccines for infectious diseases. The invention  
CC also discloses a composition comprising a non-natural molecular scaffold  
CC comprising a core particle selected from a core particle of a non-natural  
CC origin and a core particle of natural origin and an organiser comprising  
CC at least one first attachment site, where the organiser is connected to  
CC the core particle by at least one covalent bond. Also disclosed is an  
CC antigen or antigenic determinant with at least one second attachment  
CC site, where the antigen or antigenic determinant is any old beta peptide  
CC (Abeta1-42) or its fragment and where the second attachment site is  
CC selected from an attachment site not naturally occurring with the antigen  
CC or antigenic determinant and an attachment site naturally occurring with  
CC the antigen or antigenic determinant, where the second attachment site is  
CC capable of association through at least one non-peptide bond to the first  
CC attachment site and where the antigen or antigenic determinant and the  
CC scaffold interact through the association to form an ordered and

CC repetitive antigen array. The invention also comprises a coat protein  
 CC capable of forming a capsid which comprises mutant Obeta coat proteins  
 CC having an amino acid sequence selected from five amino acid sequences  
 CC fully defined in the specification. The compounds of the invention may  
 CC have antimicrobial, antiallergic, immunomodulatory, cytostatic,  
 CC antiviral, antidiabetic, or hypoglycaemic activities and may be used in  
 CC immunisation and as a vaccine. The present sequence represents a protein  
 CC sequence used to create the compositions of the invention  
 XX Sequence 115 AA;

Query Match 58.4%; Score 356; DB 5; Length 115;  
 Best Local Similarity 62.5%; Pred. No. 3.4e-34;  
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
 QY 4 ENPMRLVAETLLSTHRTWLTGDNLMPTPENKQHQLCKEYFGIDTLKNOTAHGE 63  
 Db 4 EIPTSALVKETALLSTHRTLLIANETLRIPVPHKQHQLCTEIPFGIGTLESQTVQGG 63  
 QY 64 AVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 115  
 Db 64 TVERLFKNLSLIKYYIDGQKKCGEERRVNVQFLDYLVQVFLGVINTEWTPES 115

RESULT 11  
 ABG80607  
 ID ABG80607 standard; protein; 115 AA.

AC ABG80607;

DT 29-NOV-2002 (first entry)

DE Human mature Interleukin 5.

KW Molecular antigen array; vaccine; antigen; antimicrobial;  
 KW molecular-scaffold; amyloid beta; Abeta 1-42; influenza;  
 KW graft versus host disease; IGS-mediated allergic reaction; anaphylaxis;  
 KW adult respiratory distress syndrome; ARDS; Crohn's disease;  
 KW allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;  
 KW Grave's disease; systemic lupus erythematosus; osteoporosis;  
 KW inflammatory immune disease; myasthenia gravis; multiple sclerosis;  
 KW immunoproliferative disease lymphadenopathy; Alzheimer's disease;  
 KW angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;  
 KW rheumatoid arthritis; diabetes; infectious disease; factor Xa;  
 KW enterokinase; cysteine-containing linker.

OS Homo sapiens.

PN W0200256907-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-IB000168.

XX 19-JAN-2001; 2001US-0262379P.

PR 04-MAY-2001; 2001US-0288549P.

PR 05-OCT-2001; 2001US-0326998P.

PR 07-NOV-2001; 2001US-0331045P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (NOVS) NOVARTIS PHARMA AG.

PA (MAUR) MAURER P.

PA (LECH) LECHNER F.

PA (ORTM) ORTMANN R.

PA (LUJO) LUEGEND R.

PA (STAU) STAUFENBIEL M.

PA (FREV) FREY P.

XX Maurer P, Lechner F, Ortmann R, Luegend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
 XX WPI; 2002-636514/69.

PT Molecular antigen array used in the production of vaccines for infectious  
 PT diseases.  
 XX Disclosure; Page 399; 418pp; English.

XX The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a  
 CC core particle of a non-natural origin; and (2) a core particle of natural  
 CC origin; and (ii) an organiser comprising at least one first attachment  
 CC site, where the organiser is connected to the core particle by at least  
 CC one covalent bond; (b) an antigen or antigenic determinant with at least  
 CC one second attachment site, where the antigen or antigenic determinant is  
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
 CC attachment site is selected from: (i) an attachment site not naturally  
 CC occurring with the antigen or antigenic determinant; and (ii) an  
 CC attachment site naturally occurring with the antigen or antigenic  
 CC determinant, where the second attachment site is capable of association  
 CC through at least one non-peptide bond to the first attachment site; and  
 CC where the antigen or antigenic determinant and the scaffold interact  
 CC through the association to form an ordered and repetitively occurring  
 CC array. Also included is a process for producing a non-naturally occurring  
 CC ordered and repetitively occurring antigen array. The composition is used in  
 CC immunisation and as a vaccine for diseases such as influenza, graft  
 CC versus host disease, IGE-mediated allergic reactions, anaphylaxis, adult  
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 CC gravis, immunoproliferative disease lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, immunoblastic lymphadenopathy,  
 CC rheumatoid arthritis, diabetes, multiple sclerosis, Alzheimer's disease,  
 CC osteoporosis and infectious diseases. The present sequence is an antigen  
 CC for use in the array of the invention. The antigen is modified to possess  
 CC a cleavage site (enterokinase or factor Xa) and a Cysteine-containing N-  
 CC or C-terminal linker peptide which serves as the attachment point to a  
 CC virus like particle or bacterial protein (the scaffold protein)

XX Sequence 115 AA;

Query Match 58.4%; Score 356; DB 5; Length 115;

Best Local Similarity 62.5%; Pred. No. 3.4e-34;

Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLLSTHRTWLTGDNLMPTPENKQHQLCKEYFGIDTLKNOTAHGE 63

Db 4 EIPTSALVKETALLSTHRTLLIANETLRIPVPHKQHQLCTEIPFGIGTLESQTVQGG 63

QY 64 AVDKLFQNLSLIKEHIERQKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 115

Db 64 TVERLFKNLSLIKYYIDGQKKCGEERRVNVQFLDYLVQVFLGVINTEWTPES 115

RESULT 12

AAO30453

ID AAO30453 standard; protein; 115 AA.

XX AAO30453;

XX 22-SEP-2003 (first entry)

XX Human mature interleukin 5 (IL5) protein.

XX Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;  
 KW tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5;  
 KW IL5; human.

XX Homo sapiens.

XX W02003042244-A2.

XX 22-MAY-2003.

XX 15-NOV-2002; 2002WO-DK000764.



```
PR 16-NOV-2001; 2001DK-00001702.
PR 16-NOV-2001; 2001US-0331575P.
PA (PHAR-) PHARMEXA AS.
PA (KLYS/) KLYSNER S.
PA (NIEL/) NIELSEN F S.
PA (BRAT/) BRATT T.
PA (VOLD/) VOLDBOEG B.
PA (MOUR/) MOURITSEN S.
XX
XX Klyener S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX WPI; 2003-449558/42.
XX
XX New immunogenic analogue of a polymeric protein, useful for preparing a
XX composition for treating inflammatory diseases e.g. arthritis.
XX Disclosure; Page 105; 196pp; English.
XX
XX The invention relates to immunogenic analogues of multimeric proteins
XX such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
XX factor alpha (TNF, TNFalpha) and methods for production of immunogenic
XX analogues. The immunogenic analogue is useful for preparing a composition
XX for treating inflammatory diseases, e.g., arthritis. It is also used in
XX gene therapy. The present sequence is human mature IL5 protein. This
XX sequence is used to illustrate the method of the invention
XX
XX Sequence 115 AA;
XX
XX Query Match 58.4%; Score 356; DB 6; Length 115;
XX Best Local Similarity 62.5%; Pred. No. 3.4e-34;
XX Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
XX
XX 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMIPTEPNKHQLCIKVEFGIDTLKNQTAHGE 63
XX 4 EIPTSAVKETALLSTHRTLLIANETLRIPVPHKHQLCITEIFQIGITLESQTVQGG 63
XX
XX 64 AVDKLFQNLSLIKHIERQKRCAGERWRVTKFDLYQLVFLGVINTWPTES 115
XX 64 TVERLFKNLSLTKYIDGQKKCGEERRRVNQFLDYQLQELFVGNVTWETIES 115
XX
XX
XX RESULT 13
XX ABG94353
XX ID ABG94353 standard; protein; 123 AA.
XX AC ABG94353;
XX
XX 10-DEC-2002 (first entry)
XX
XX Human C-IL-5-S protein.
XX
XX Human; mouse; rat; antimicrobial; antiallergic; immunomodulatory;
XX cytostatic; antiviral; antidiabetic; hypoglycaemic; antigen array;
XX vaccine; infectious disease.
XX
XX Homo sapiens.
XX
XX WC020256905-A2.
XX
XX 25-JUL-2002.
XX
XX 21-JAN-2002; 2002WO-IB000156.
XX
XX 19-JAN-2001; 2001US-0262379P.
XX 04-MAY-2001; 2001US-0288549P.
XX 05-OCT-2001; 2001US-0328989P.
XX 07-NOV-2001; 2001US-0331045P.
XX
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Renner WA, Bachmann M, Tissot A, Maurer P, Lechner F, Sebbel P;
XX Piossek C;
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XX WPI; 2002-627351/67.
XX
XX Molecular antigen array used in the production of vaccines for infectious
XX diseases.
XX
XX Example 10; Page 440; 441pp; English.
XX
XX This invention relates to a novel ordered and repetitive antigen array
XX used in the production of vaccines for infectious diseases. The invention
XX also discloses a composition comprising a non-natural molecular scaffold
XX comprising a core particle selected from a core particle of a non-natural
XX origin and a core particle of natural origin and an organiser comprising
XX at least one first attachment site, where the organiser is connected to
XX the core particle by at least one covalent bond. Also disclosed is an
XX antigen or antigenic determinant with at least one second attachment
XX site, where the antigen or antigenic determinant is amyloid beta peptide
XX (Abeta1-42) or its fragment and where the second attachment site is
XX selected from an attachment site not naturally occurring with the antigen
XX or antigenic determinant and an attachment site naturally occurring with
XX the antigen or antigenic determinant, where the second attachment site is
XX capable of association through at least one non-peptide bond to the first
XX attachment site and where the antigen or antigenic determinant and the
XX scaffold interact through the association to form an ordered and
XX repetitive antigen array. The invention also comprises a coat protein
XX capable of forming a capsid which comprises mutant beta coat proteins
XX having an amino acid sequence selected from five amino acid sequences
XX fully defined in the specification. The compounds of the invention may
XX have antimicrobial, antiallergic, immunomodulatory, cytostatic,
XX antiviral, antidiabetic, or hypoglycaemic activities and may be used in
XX immunisation and as a vaccine. The present sequence represents a protein
XX sequence used to create the compositions of the invention
XX
XX Sequence 123 AA;
XX
XX Query Match 58.4%; Score 356; DB 5; Length 123;
XX Best Local Similarity 62.5%; Pred. No. 3.7e-34;
XX Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
XX
XX 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMIPTEPNKHQLCIKVEFGIDTLKNQTAHGE 63
XX 12 EIPTSAVKETALLSTHRTLLIANETLRIPVPHKHQLCITEIFQIGITLESQTVQGG 71
XX
XX 64 AVDKLFQNLSLIKHIERQKRCAGERWRVTKFDLYQLVFLGVINTWPTES 115
XX 72 TVERLFKNLSLTKYIDGQKKCGEERRRVNQFLDYQLQELFVGNVTWETIES 123
XX
XX
XX RESULT 14
XX ABG80665
XX ID ABG80665 standard; protein; 123 AA.
XX AC ABG80665;
XX
XX 29-NOV-2002 (first entry)
XX
XX Human IL-5/ N-terminal cysteine containing linker, human C-IL-5-S.
XX
XX Molecular antigen array; vaccine; antigen; antimicrobial; mutant;
XX molecular scaffold; amyloid beta; Abeta 1-42; influenza; mutein;
XX graft versus host disease; IGS-mediated allergic reaction; anaphylaxis;
XX adult respiratory distress syndrome; ARDS; Crohn's disease;
XX allergic asthma; acute lymphoblastic leukaemia; non-Hodgkin's lymphoma;
XX Grave's disease; systemic lupus erythematosus; osteoporosis;
XX inflammatory immune disease; myasthenia gravis; multiple sclerosis;
XX immunoproliferative disease lymphadenopathy; Alzheimer's disease;
XX angioimmunoproliferative lymphadenopathy; immunoblastic lymphadenopathy;
XX rheumatoid arthritis; diabetes; infectious disease; factor Xa;
XX enterokinase; cysteine-containing linker.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
```

PN WO200256907-A2.  
 XX 25-JUL-2002.  
 XX 21-JAN-2002; 2002WO-JB000168.  
 XX 19-JAN-2001; 2001US-0262379P.  
 PR 04-MAY-2001; 2001US-0288549P.  
 PR 05-OCT-2001; 2001US-0326998P.  
 PR 07-NOV-2001; 2001US-0331045P.  
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (NOVS) NOVARTIS PHARMA AG.  
 PA (MAUR) MAURER P.  
 PA (LECH) LECHNER F.  
 PA (ORTM) ORTMANN R.  
 PA (LUFO) LUEOEND R.  
 PA (STAU) STAUFENBIEL M.  
 PA (FREY) FREY P.  
 XX Maurer P, Lechner F, Ortmann R, Lueoend R, Staufenbiel M, Frey P;  
 PI Renner WA, Bachmann M, Tissot A, Sebbel P, Piossek C;  
 XX WPI; 2002-636514/68.  
 DR Molecular antigen array used in the production of vaccines for infectious  
 PT diseases.  
 PT Disclosure; Page 417; 418pp; English.  
 XX The invention relates to a composition comprising: (a) a non-natural  
 CC molecular scaffold comprising: (i) a core particle selected from: (1) a  
 CC core particle of a non-natural origin; and (2) a core particle of natural  
 CC origin; and (ii) an organiser comprising at least one first attachment  
 CC site, where the organiser is connected to the core particle by at least  
 CC one covalent bond; (b) an antigen or antigenic determinant with at least  
 CC one second attachment site, where the antigen or antigenic determinant is  
 CC amyloid beta peptide (Abeta 1-42) or its fragment, and where the second  
 CC attachment site is selected from: (i) an attachment site not naturally  
 CC occurring with the antigen or antigenic determinant; and (ii) an  
 CC attachment site naturally occurring with the antigen or antigenic  
 CC determinant, where the second attachment site is capable of association  
 CC through at least one non-peptide bond to the first attachment site; and  
 CC where the antigen or antigenic determinant and the scaffold interact  
 CC through the association to form an ordered and repetitive antigen array.  
 CC Also included is a process for producing a non-naturally occurring  
 CC ordered and repetitive antigen array. The composition is used in  
 CC immunisation and as a vaccine for diseases such as influenza, graft  
 CC versus host disease, IgE-mediated allergic reactions, anaphylaxis, adult  
 CC respiratory distress syndrome (ARDS), Crohn's disease, allergic asthma,  
 CC acute lymphoblastic leukaemia, non-Hodgkin's lymphoma, Grave's disease,  
 CC systemic lupus erythematosus, inflammatory immune diseases, myasthenia  
 CC gravis, immunoproliferative disease lymphadenopathy, immunoblastic lymphadenopathy,  
 CC angioimmunoproliferative lymphadenopathy, multiple sclerosis, Alzheimer's disease,  
 CC rheumatoid arthritis, diabetes, osteoporosis and infectious diseases. The antigen is modified to  
 CC possess a cleavage site (enterokinase or factor Xa) and a Cysteine-  
 CC containing N- or C-terminal linker peptide which serves as the attachment  
 CC point to a virus like particle or bacterial protein (the scaffold  
 CC protein)  
 XX Sequence 123 AA;  
 SQ  
 Query Match 58.4%; Score 356; DB 5; Length 123;  
 Best Local Similarity 62.5%; Pred. No. 3.7e-34;  
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
 QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMIPPEKNHQLCKEIVFGQIDTLKNQTAHGE 63  
 Db 12 EIPTSALVKETALLSTHRTLLIANETLRIPVPVKNHQLCTEIEIFQIGTLESQTVQGG 71  
 QY 64 AVDKLFQNLSLIKEHIEROKRCAGERRWRTKFLDYQLQVFLGVINTEWTPES 115

Db 72 TVERLFKNLSLIKKYIDGQKKCGERRRVNQFLDYQLQVFLGVINTEWTPES 123  
 RESULT 15  
 AAR92802  
 ID AAR92802 standard; protein; 134 AA.  
 XX AAR92802;  
 AC AAR92802;  
 XX 24-MAY-1996 (first entry)  
 DT Human interleukin-5.  
 XX Human interleukin-5.  
 DE Cytokine; mutein; interleukin-5; agonist; antagonist; diagnosis; therapy;  
 KW cancer; inflammation; degenerative disease.  
 XX Homo sapiens.  
 OS WO9604306-A2.  
 XX 15-FEB-1996.  
 PD 31-JUL-1995; 95WO-US008950.  
 PF 01-AUG-1994; 94US-00284393.  
 PR (SCHE) SCHERING CORP.  
 XX Zurawski SM, Zurawski G;  
 PI WPI; 1996-129335/13.  
 DR Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and murine  
 PT P600 contg. amino acid substitutions - useful for the diagnosis and  
 PT treatment of cancer, inflammation, etc.  
 XX Disclosure; Page 43; 52pp; English.  
 PS Muteins of human interleukin-5 (AAR92802) and other cytokines (see also  
 XX AAR92790-801) are obtd. by site-directed mutagenesis of natural cytokine  
 CC sequences at positions identified as critical for activity. The muteins  
 CC are useful in the screening of cytokine and cytokine receptor levels, and  
 CC in the diagnosis or treatment of e.g. inflammation, cancer, and  
 CC degenerative disorders  
 XX Sequence 134 AA;  
 SQ  
 Query Match 58.4%; Score 356; DB 2; Length 134;  
 Best Local Similarity 62.5%; Pred. No. 4.2e-34;  
 Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
 QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMIPPEKNHQLCKEIVFGQIDTLKNQTAHGE 63  
 Db 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVKNHQLCTEIEIFQIGTLESQTVQGG 82  
 QY 64 AVDKLFQNLSLIKEHIEROKRCAGERRWRTKFLDYQLQVFLGVINTEWTPES 115  
 Db 83 TVERLFKNLSLIKKYIDGQKKCGERRRVNQFLDYQLQVFLGVINTEWTPES 134  
 Search completed: August 25, 2004, 00:02:24  
 Job time : 83.1325 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 24, 2004, 23:59:38 ; Search time 20.7831 Seconds  
(without alignments)  
285.664 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 FAVENPMRLVAETLLST.....FLDYLOVFLGVINTEWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	115	4	US-09-322-409-86
2	610	100.0	115	4	US-09-451-527-86
3	610	100.0	134	4	US-09-322-409-81
4	610	100.0	134	4	US-09-451-527-81
5	601	98.5	134	4	US-09-371-615A-2
6	356	58.4	134	1	US-08-284-393B-13
7	356	58.4	134	3	US-08-759-628-9
8	356	58.4	134	4	US-09-371-615A-7
9	356	58.4	134	4	US-09-462-941-12
10	356	58.4	134	5	PCT-US95-08950-13
11	356	58.4	134	6	5324640-2
12	351	57.5	121	4	US-09-180-864-2
13	347	56.9	133	4	US-09-371-615A-8
14	72.5	11.9	686	4	US-09-914-259-33
15	72	11.8	15	5	PCT-US94-06655-4
16	71	11.6	323	4	US-09-134-000C-5535
17	69.5	11.4	976	3	US-08-560-005-2
18	69.5	11.4	976	3	US-09-195-868-14
19	69.5	11.4	976	3	US-09-418-540-2
20	69.5	11.4	976	4	US-09-969-528-2
21	69.5	11.4	1187	3	US-08-664-962B-8
22	69.5	11.4	1187	3	US-09-311-743-8
23	69.5	11.4	1189	3	US-09-195-868-15
24	69.5	11.4	1229	3	US-09-195-868-28
25	67.5	11.1	968	1	US-08-434-730-14
26	67.5	11.1	1185	3	US-08-664-962B-2
27	67.5	11.1	1185	3	US-09-311-743-2

28	67	11.0	2311	4	US-08-934-386-9	Sequence 9, Appli
29	66.5	10.9	312	4	US-09-107-532A-6369	Sequence 6369, Ap
30	66.5	10.9	589	4	US-09-543-681A-4194	Sequence 4194, Ap
31	66	10.8	2325	3	US-08-417-089-6	Sequence 6, Appli
32	66	10.8	2325	3	US-08-695-651-6	Sequence 6, Appli
33	66	10.8	2325	3	US-08-930-285-6	Sequence 6, Appli
34	66	10.8	2325	3	US-08-695-421-6	Sequence 6, Appli
35	66	10.8	2325	4	US-08-697-826A-10	Sequence 10, Appli
36	65.5	10.7	248	4	US-09-367-293-5	Sequence 5, Appli
37	65	10.7	300	4	US-09-328-352-6714	Sequence 6714, Ap
38	64.5	10.6	186	4	US-09-107-532A-6672	Sequence 6672, Ap
39	64.5	10.6	364	4	US-09-252-991A-18473	Sequence 18473, A
40	64.5	10.6	414	4	US-10-067-443-2	Sequence 2, Appli
41	64.5	10.6	439	4	US-10-067-443-19	Sequence 19, Appli
42	64.5	10.6	984	4	US-09-328-352-6926	Sequence 6926, Ap
43	64	10.5	260	4	US-09-107-532A-5350	Sequence 5350, Ap
44	64	10.5	283	4	US-09-540-236-3710	Sequence 3710, Ap
45	63.5	10.4	448	2	US-08-878-989-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-322-409-86  
; Sequence 86, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-CL  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-09-322-409-86

Query Match 100.0%; Score 610; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 4e-71;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAETLLSTHRTWLIGDNLMIPTPENKHQLCIKEVFGIDTLKQTA 60

Db 1 FAVENPMRLVAETLLSTHRTWLIGDNLMIPTPENKHQLCIKEVFGIDTLKQTA 60

QY 61 HGEAVDKLFLQNLSLIKHEIERQKRCAGRWVTKFLDYLOVFLGVINTEWTPES 115

Db 61 HGEAVDKLFLQNLSLIKHEIERQKRCAGRWVTKFLDYLOVFLGVINTEWTPES 115

RESULT 2

US-09-451-527-86  
; Sequence 86, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527

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; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-451-527-86

Query Match      100.0%; Score 610; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 4e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 60
Db 1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 60

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 115
Db 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 115

RESULT 3
US-09-322-409-81
; Sequence 81, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-322-409-81

Query Match      100.0%; Score 610; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 5e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 60
Db 20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 79

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 115
Db 80 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 134

RESULT 4
US-09-451-527-81
; Sequence 81, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
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; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-451-527-81

Query Match      100.0%; Score 610; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 5e-71;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 60
Db 20 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 79

Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 115
Db 80 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 134

RESULT 5
US-09-371-615A-2
; Sequence 2, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371,615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-09-371-615A-2

Query Match      98.5%; Score 601; DB 4; Length 134;
Best Local Similarity 99.1%; Pred. No. 7.3e-70;
Matches 114; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAVENPMNRLVAETLTLLSTHRTWLIGDGNLMIPPTENKQHQLCIKEVFQGITLKNQTA 60
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Qy 61 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 115
Db 80 HGEAVDKLFQNLSLIKHEIERQKRCAGRWRTKFLDYLOVFLGVINTWTPES 134

RESULT 6
US-08-284-393B-13
; Sequence 13, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
```

CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/284,393B  
FILING DATE: 01-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,030  
REFERENCE/DOCKET NUMBER: DX0389  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-284-393B-13

Query Match 58.4%; Score 356; DB 1; Length 134;  
Best Local Similarity 62.5%; Pred. No. 3.7e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMITPENKHNQHCICKEVFGQIDTLKNQTAHGE 63  
DB 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEIEFGIGTLESQTVQGG 82

QY 64 AVDKLFQNLSLIKHEIRKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115  
DB 83 TVERLFKNLSLIKXIDGKKCKGERRRVNQFLDYLOEFLGVNTEWIIES 134

RESULT 7  
US-08-759-628-9  
Sequence 9, Application US/08/759628  
Patent No. 6225446  
GENERAL INFORMATION:  
APPLICANT: Altmann, Scott W.  
APPLICANT: Rock, Fernando L.  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Kastelein, Robert A.  
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,628  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/008,574  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0552Q  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 20-134  
OTHER INFORMATION: /note= "peptide of Figure 1"  
US-08-759-628-9

Query Match 58.4%; Score 356; DB 3; Length 134;  
Best Local Similarity 62.5%; Pred. No. 3.7e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMITPENKHNQHCICKEVFGQIDTLKNQTAHGE 63  
DB 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEIEFGIGTLESQTVQGG 82

QY 64 AVDKLFQNLSLIKHEIRKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115  
DB 83 TVERLFKNLSLIKXIDGKKCKGERRRVNQFLDYLOEFLGVNTEWIIES 134

RESULT 8  
US-09-371-615A-7  
Sequence 7, Application US/09371615A  
Patent No. 6537781  
GENERAL INFORMATION:  
APPLICANT: IDEXX LABORATORIES  
TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
FILE OF INVENTION: CANINE INTERLEUKIN 5  
FILE REFERENCE: 03604001700US00  
CURRENT APPLICATION NUMBER: US/09/371,615A  
CURRENT FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Interleukin 5  
US-09-371-615A-7

Query Match 58.4%; Score 356; DB 4; Length 134;  
Best Local Similarity 62.5%; Pred. No. 3.7e-38;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMITPENKHNQHCICKEVFGQIDTLKNQTAHGE 63  
DB 23 EIPTSALVKETALLSTHRTLLIANETLRIPVPVHKHQLCTEIEFGIGTLESQTVQGG 82

QY 64 AVDKLFQNLSLIKHEIRKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115  
DB 83 TVERLFKNLSLIKXIDGKKCKGERRRVNQFLDYLOEFLGVNTEWIIES 134

RESULT 9  
US-09-462-941-12  
Sequence 12, Application US/09462941  
Patent No. 6608183  
GENERAL INFORMATION:  
APPLICANT: Cox III, George N  
APPLICANT: Bolder Biotechnology, Inc.



## RESULT 13

US-09-371-615A-8  
; Sequence 8, Application US/09371615A  
; Patent No. 6537781

## ; GENERAL INFORMATION:

; APPLICANT: IDEXX LABORATORIES  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING

; TITLE OF INVENTION: CANINE INTERLEUKIN 5

; FILE REFERENCE: 036040017000US00

; CURRENT APPLICATION NUMBER: US/09/371.615A

; CURRENT FILING DATE: 1999-08-10

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; OTHER INFORMATION: Interleukin 5

US-09-371-615A-8

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Best Local Similarity 56.9%; Score 347; DB 4; Length 133;

Matches 66; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

QY 2 AVENPMRLVAETLTILSTHRTWLTGDNLMIPTPENKHOLCIKEVFGIDTLKNOTAH 61

Db 20 AMIPKSTVVKELTQLSARALTSNETWRLPVTHKHQLCIGIFQGLDILKQTVR 79

QY 62 GEAVDKLFQNLISKEHIEKQKRCAGERWRVTKFLDYQVFLGVINTWTE 114

Db 80 GGTVEMLFQNLISLKKYIDRQKCGEERRRTQFLDYQVFLGVNTEWAVE 132

## RESULT 14

US-09-914-259-33

; Sequence 33, Application US/09914259

; Patent No. 6495336

; GENERAL INFORMATION:

; APPLICANT: Makowski, Lee

; APPLICANT: Hyman, Paul

; APPLICANT: Williams, Mark

; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

; FILE REFERENCE: 8471-010-999

; CURRENT APPLICATION NUMBER: US/09/914.259

; CURRENT FILING DATE: 2000-11-21

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 33

; LENGTH: 686

; TYPE: PRT

; ORGANISM: Strongylocentrotus purpuratus

US-09-914-259-33

## Query Match

Best Local Similarity 11.9%; Score 72.5; DB 4; Length 686;

Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMIPENKHQLC--IKEVFGIDTLKNOTAHGEAVDKLFQNLISKEHIERQKK 84

Db 15 GQGNL-----SQEQIITGTREVIKGLEQKNE--HNDILNSLYQSLKMLKDTGDSN 65

QY 85 RCAGERWRVTKFLDYQVFLG 105

Db 66 LVEEKTDIIEKSLSELELGLG 86

## RESULT 15

PCT-US94-06655-4

; Sequence 4, Application PC/TUS9406655

; GENERAL INFORMATION:

; APPLICANT: Chaiken, Irwin

; APPLICANT: Graddis, Thomas  
; APPLICANT: Myszka, David  
; TITLE OF INVENTION: Coiled-Coil Stem Loop Templates  
; NUMBER OF SEQUENCES: 12

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: Corporate Patents / P.O. Box 1539

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/06655

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Sutton, Jeffrey A.

; REGISTRATION NUMBER: 34028

; REFERENCE/DOCKET NUMBER: PS0164

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 270-5024

; TELEFAX: (215) 270-5090

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 1..15

; OTHER INFORMATION: /note="Corresponds to amino acids

; OTHER INFORMATION: 93-107 of human Interleukin 5 (helix D)."

PCT-US94-06655-4

## Query Match

Best Local Similarity 11.8%; Score 72; DB 5; Length 15;

Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 97 LDYQVFLGVINTEW 111

Db 1 LDYQVFLGVINTEW 15

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Job time : 21.7831 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2004, 00:05:39 ; Search time 78.0522 Seconds  
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463.015 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 FAVENPMRLVAETLLST.....FLDYQLVFLGVINTEWTPSS 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1295152 seqs, 314255058 residues

Total number of hits satisfying chosen parameters: 1295152

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	610	100.0	115	14	US-10-218-654-86
3	610	100.0	115	14	US-10-262-439-86
4	610	100.0	134	9	US-09-755-633-5
5	610	100.0	134	14	US-10-218-654-81
6	610	100.0	134	14	US-10-262-439-81
7	358	58.7	115	16	US-10-658-834A-588
8	357	58.5	115	16	US-10-658-834A-569
9	357	58.5	287	14	US-10-295-074-13
10	356	58.4	115	14	US-10-289-454-234
11	356	58.4	115	14	US-10-050-902-234
12	356	58.4	115	14	US-10-050-898-234
13	356	58.4	115	14	US-10-295-074-1
14	356	58.4	115	16	US-10-658-834A-208
15	356	58.4	115	16	US-10-658-834A-574

16	356	58.4	115	16	US-10-658-834A-580	Sequence 580, App
17	356	58.4	115	16	US-10-658-834A-587	Sequence 587, App
18	356	58.4	115	16	US-10-658-834A-589	Sequence 589, App
19	356	58.4	115	16	US-10-658-834A-595	Sequence 595, App
20	356	58.4	123	14	US-10-289-454-337	Sequence 337, App
21	356	58.4	123	14	US-10-050-902-337	Sequence 337, App
22	356	58.4	123	14	US-10-050-898-337	Sequence 337, App
23	356	58.4	134	14	US-10-289-454-233	Sequence 233, App
24	356	58.4	134	14	US-10-400-377-12	Sequence 12, Appl
25	356	58.4	134	14	US-10-400-708-12	Sequence 12, Appl
26	356	58.4	134	14	US-10-298-148-12	Sequence 12, Appl
27	356	58.4	134	14	US-10-050-902-233	Sequence 233, App
28	356	58.4	134	14	US-10-050-898-233	Sequence 233, App
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32	356	58.4	138	14	US-10-289-454-335	Sequence 335, App
33	356	58.4	138	14	US-10-050-902-335	Sequence 335, App
34	356	58.4	138	14	US-10-050-898-335	Sequence 335, App
35	356	58.4	285	14	US-10-295-074-9	Sequence 9, Appl
36	356	58.4	285	14	US-10-295-074-11	Sequence 11, Appl
37	356	58.4	287	14	US-10-295-074-15	Sequence 15, Appl
38	355	58.2	115	16	US-10-658-834A-568	Sequence 568, App
39	355	58.2	115	16	US-10-658-834A-575	Sequence 575, App
40	355	58.2	115	16	US-10-658-834A-581	Sequence 581, App
41	355	58.2	115	16	US-10-658-834A-585	Sequence 585, App
42	355	58.2	115	16	US-10-658-834A-596	Sequence 596, App
43	355	58.2	115	16	US-10-658-834A-597	Sequence 597, App
44	354	58.0	115	16	US-10-658-834A-576	Sequence 576, App
45	354	58.0	115	16	US-10-658-834A-582	Sequence 582, App

ALIGNMENTS

RESULT 1

US-09-755-633-10  
; Sequence 10, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-Cl-C1  
; CURRENT FILING DATE: 2001-01-05  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 10  
; TYPE: PRT  
; LENGTH: 115  
; ORGANISM: Canis familiaris  
US-09-755-633-10

Query Match 100.0%; Score 610; DB 9; Length 115;  
Best Local Similarity 100.0%; Pred. No. 1.9e-64;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	FAVENPMRLVAETLLSTRTWLIGDGNLMIPENKHNHLCIKKEYFQIGIDTLKNOTA	60
Qy	61	HGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFLDYQLVFLGVINTEWTPSS	115
Db	61	HGEAVDKLFQNLISLKEHIERQKRCAGERWRVTKFLDYQLVFLGVINTEWTPSS	115

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RESULT 2
US-10-218-654-86
; Sequence 86, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-86

Query Match      100.0%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFGIDTLKNQTA 60
DQ 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFGIDTLKNQTA 60
QY 61 HGEAVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115
DQ 61 HGEAVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115

RESULT 3
US-10-262-439-86
; Sequence 86, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-86

Query Match      100.0%; Score 610; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.9e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFGIDTLKNQTA 60
DQ 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFGIDTLKNQTA 60
QY 61 HGEAVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115
DQ 61 HGEAVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115

RESULT 4
US-09-755-633-5
; Sequence 5, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-755-633-5

Query Match      100.0%; Score 610; DB 9; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFGIDTLKNQTA 60
DQ 20 FAVENPNRLVAETLLTLLSTHRTWLIGDGNLMPTPENKQHQLCIKEVFGIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 115
DQ 80 HGEAVDKLFQNLSLIKHIERQKRCACGERWRVTKFLDYQLQVFLGVINTEWTPES 134

RESULT 5
US-10-218-654-81
; Sequence 81, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-218-654-81

Query Match      100.0%; Score 610; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
```

```
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60
DB 20 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 80 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 134

RESULT 6
US-10-262-439-81
; Sequence 81, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim. Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-81

Query Match 100.0%; Score 610; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60
DB 20 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 80 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 134

RESULT 7
US-10-658-834A-588
; Sequence 588, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-588

Query Match 58.7%; Score 358; DB 16; Length 115;
Best Local Similarity 62.5%; Pred. No. 1.9e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 4 ENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTAHGE 63
DB 4 BIPTSAVKETLALLSTHRTLLIANETLRIPVPVKNHQLCTEIRFQIGTLESQTVQGG 63
QY 64 AVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 64 TVERLFKNLSLIKYYIDGQKKCGERRRVNQFDLYQLVPLGVINTEWTPES 115

RESULT 8
US-10-658-834A-569
; Sequence 569, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-569

Query Match 58.5%; Score 357; DB 16; Length 115;
Best Local Similarity 62.5%; Pred. No. 2.5e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 4 ENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTAHGE 63
DB 4 BIPTSAVKETLALLSTHRTLLIANETLRIPVPVKNHQLCTEIRFQIGTLESQTVQGG 63
QY 64 AVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 64 TVERLFKNLSLIKYYIDGQKKCGERRRVNQFDLYQLVPLGVINTEWTPES 115

RESULT 9
US-10-295-074-13
; Sequence 13, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmex A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 287
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```
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60
DB 20 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 80 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 134

RESULT 6
US-10-262-439-81
; Sequence 81, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim. Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 81
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-262-439-81

Query Match 100.0%; Score 610; DB 14; Length 134;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 60
DB 20 FAVENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 80 HGEAVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 134

RESULT 7
US-10-658-834A-588
; Sequence 588, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-588

Query Match 58.7%; Score 358; DB 16; Length 115;
Best Local Similarity 62.5%; Pred. No. 1.9e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 4 ENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTAHGE 63
DB 4 BIPTSAVKETLALLSTHRTLLIANETLRIPVPVKNHQLCTEIRFQIGTLESQTVQGG 63
QY 64 AVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 64 TVERLFKNLSLIKYYIDGQKKCGERRRVNQFDLYQLVPLGVINTEWTPES 115

RESULT 8
US-10-658-834A-569
; Sequence 569, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding N
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-569

Query Match 58.5%; Score 357; DB 16; Length 115;
Best Local Similarity 62.5%; Pred. No. 2.5e-34;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 4 ENPMNLVAETLLTSLTHRTWLIGDGNLMPTPENKNHQLCIKEVFGQIDTLKNQTAHGE 63
DB 4 BIPTSAVKETLALLSTHRTLLIANETLRIPVPVKNHQLCTEIRFQIGTLESQTVQGG 63
QY 64 AVDKLFQNLSLIKEHIERQKRCACGERWRVTKFDLYQLVPLGVINTEWTPES 115
DB 64 TVERLFKNLSLIKYYIDGQKKCGERRRVNQFDLYQLVPLGVINTEWTPES 115

RESULT 9
US-10-295-074-13
; Sequence 13, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmex A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 13
; LENGTH: 287
```

TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Two human IL5 monomers joined by diglycine linker and including  
OTHER INFORMATION: eminally positioned P30 and P2 epitopes  
US-10-295-074-13

Query Match 58.4%; Score 357; DB 14; Length 287;  
Best Local Similarity 61.9%; Pred. No. 8.2e-34;  
Matches 70; Conservative 17; Mismatches 26; Indels 0; Gaps 0;  
QY 3 VENPMRLVAETLLSTHRTWLIGDGNLMIPTPENKQHOLCIKEVFGQIDTLKNOTAHG 62  
DB 43 LEITSALVKETALLSTHRTLLIANETLRIPVPHKHOLCTEIEFGIGTLESQTVQGG 102  
QY 63 EAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115  
DB 103 GTVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNTWIIIES 155

RESULT 10  
US-10-289-454-234  
Query Match 58.4%; Score 356; DB 14; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Bachmann, Martin  
APPLICANT: Jennings, Gary  
APPLICANT: Sonderegger, Ivo  
TITLE OF INVENTION: Antigen Arrays for Treatments of Allergic Eosinophilic Diseases  
FILE REFERENCE: 1700.0360001  
CURRENT APPLICATION NUMBER: US/10/289,454  
CURRENT FILING DATE: 2003-02-10  
PRIOR APPLICATION NUMBER: US 60/396,636  
PRIOR FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: PCT/IB02/00166  
PRIOR FILING DATE: 2002-01-21  
PRIOR APPLICATION NUMBER: US 10/050,902  
PRIOR FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US 60/331,045  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 386  
SOFTWARE: Patent in version 3.2  
SEQ ID NO 234  
LENGTH: 115  
TYPE: PRT  
ORGANISM: processed human IL-5  
US-10-289-454-234

Query Match 58.4%; Score 356; DB 14; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMIPTPENKQHOLCIKEVFGQIDTLKNOTAHG 63  
DB 4 EIPTSALVKETALLSTHRTLLIANETLRIPVPHKHOLCTEIEFGIGTLESQTVQGG 63  
QY 64 AVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115  
DB 64 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNTWIIIES 115

RESULT 11  
US-10-050-902-234  
Query Match 58.4%; Score 356; DB 14; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Renner, Wolfgang A.  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Maurer, Patrick  
APPLICANT: Lechner, Franziska  
APPLICANT: Sebbel, Peter  
APPLICANT: Piossek, Christine

TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0190004  
CURRENT APPLICATION NUMBER: US/10/050,902  
CURRENT FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US 60/262,379  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/288,549  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/326,998  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: US 60/331,045  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 234  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-050-902-234

Query Match 58.4%; Score 356; DB 14; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
QY 4 ENPMRLVAETLLSTHRTWLIGDGNLMIPTPENKQHOLCIKEVFGQIDTLKNOTAHG 63  
DB 4 EIPTSALVKETALLSTHRTLLIANETLRIPVPHKHOLCTEIEFGIGTLESQTVQGG 63  
QY 64 AVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115  
DB 64 TVERLFKNLSLIKKYIDGQKKCGEERRRVNQFLDYQLQVFLGVNTWIIIES 115

RESULT 12  
US-10-050-898-234  
Query Match 58.4%; Score 356; DB 14; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;  
GENERAL INFORMATION:  
APPLICANT: Renner, Wolfgang A.  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Maurer, Patrick  
APPLICANT: Lechner, Franziska  
APPLICANT: Sebbel, Peter  
APPLICANT: Piossek, Christine  
APPLICANT: Ortman, Rainer  
APPLICANT: Luond, Rainer  
APPLICANT: Staufenbiel, Matthias  
APPLICANT: Frey, Peter  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0190005  
CURRENT APPLICATION NUMBER: US/10/050,898  
CURRENT FILING DATE: 2002-01-18  
PRIOR APPLICATION NUMBER: US 60/262,379  
PRIOR FILING DATE: 2001-01-19  
PRIOR APPLICATION NUMBER: US 60/288,549  
PRIOR FILING DATE: 2001-05-04  
PRIOR APPLICATION NUMBER: US 60/326,998  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: US 60/331,045  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 350  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 234  
LENGTH: 115  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-050-898-234

Query Match 58.4%; Score 356; DB 14; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

	QY	4	ENPMNRLVASTLLTLLSTHRTWLIDGNGLMETPENKNHQCIKEVFQIGDITLKNOTAHGE	63
			: :	
	Db	4	EIPTSALVKETALLSTHRTLILANETLRIPVPVHKHQJCTBEIFGIGTLSEQTVOGG	63
			: :	
	QY	64	AVDKLFQNLSLIKEHIERQKRCRAGEWRVTKFDLYQLVGLVINTWTPTES	115
			: :	
	Db	64	TVERLFKNLSLIKVIQCKKKCGEERRVNQFDDYLQEELGVNMTWIIIES	115
			: ~:	

```

RESULT 13
US-10-295-074-1
; Sequence 1, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MINIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-295-074-1

```

Query Match	58.4%	Score 356;	DB 14;	Length 115;
Best Local Similarity	62.5%	Pred. No. 3.2e-34;		
Matches 70;	Conservative 16;	Mismatches 26;	Indels 0;	Gaps 0;

Qy	4	ENPMNRLVAETLLTLLSTHRTWLTCGDGNLMIPPTENKNHOLCIEVFQFGIDTILKNCTAHCE	63
Dd	4	EIPTSALVKETLLALLSTHRTLLANETRIPIPVVKHKNHOLCTEIRFOIGLSTLESQTQGG	63

[illegible]

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RESULT 14
US-10-658-834A-208
; Sequence 208, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Er
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank CAA28390
; DATABASE ENTRY DATE: 1995-03-21
US-10-658-834A-208

```

Query Match	58.4%	Score 356;	DB 16;	Length 115;
Best Local Similarity	62.5%;	Pred. NO. 3.28-34;		
Matches 70;	Conservative 16;	Mismatches 26;	Indels 0;	Gaps 0;

Qy	4	ENPMNELVATETLLSTHRTWLGDNLMIPPEKNKHQLCIKKVFQGGIDTLKQNTAHGE	63
Db	4	EPTSLVAKETLALSTHRTLLIATETLRIPVPEKHQLCETEEFQGGILESTVQGG	63
Qy	64	AYDKLFQNLSLKEHIEROKKRCACGERWRVTKFLDYLVQFLGVINTEWTPES	115
Db	64	TVYRLFKNLSLKKYIDGKKKCGGERARVNOFLDYLVQFLGVINTEWTPES	115

## RESULT 15

```

RES001.13
US-10-658-834A-574
Sequence 574, Application US/10658834A
Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Dritanefi, Lilia
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Re
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658
PRIORITY FILING DATE: 2003-09-08
CURRENT APPLICATION NUMBER: 60/457,135
PRIORITY FILING DATE: 2003-03-21
PRIORITY APPLICATION NUMBER: 60/409,898
PRIORITY FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version
SEQ ID NO 574
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-10-658-834A-574

```

Query Match 58.4%; Score 356; DB 16; Length 115;  
Best Local Similarity 62.5%; Pred. No. 3.2e-34;  
Matches 70; Conservative 16; Mismatches 26; Indels

QY	4	ENPNRLVABTLLSTHRTWLLGDGNLMP	PPENKNHOLCCKEVPGGTDLTKNQTAGE	63
DB	4	EITSAVKETALLSTHRTLLIANETLR	PPVHNHOLCQEIFGGTGLTSSQTVQGG	63
QY	64	AVDKLFNLSLIKEHIERKKRCAGRWRTK	FLDYQLVQLGVINTWPTES	115
DB	64	TVSRFLPNLSLIIKKYDGOKKKCGERRR	NPFLDYQLVQLGVINTWPTES	115

Search completed: August 25, 2004, 00:21:35  
Job time : 79.0522 secs

Blank Sheet

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: August 24, 2004, 23:55:53 ; Search time 22.6305 Seconds  
(without alignments)  
488.810 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 FAVENPMRLVAETLLTLLST.....FLDYLVQVFLGVINTWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*

1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	491	80.5	134	2 JC5116	interleukin-5 prec
2	356	58.4	134	1 A28477	interleukin-5 prec
3	347	56.9	133	1 ICM55	interleukin-5 prec
4	332	54.4	132	1 A48418	interleukin-5 prec
5	78.5	12.9	258	2 T47758	hypothetical prote
6	74.5	12.2	1232	2 B39432	Arp-dependent deox
7	73.5	12.0	253	2 T47757	hypothetical prote
8	73	12.0	1199	2 G69698	RNA polymerase (be
9	72.5	11.9	451	2 S33816	kinesin light chai
10	72.5	11.9	649	2 S33813	kinesin light chai
11	72.5	11.9	677	2 S33814	kinesin light chai
12	72.5	11.9	686	2 S33815	kinesin light chai
13	72	11.8	401	2 S28653	hypothetical prote
14	71	11.6	216	2 B69498	hypothetical prote
15	71	11.6	300	2 B64594	hypothetical prote
16	71	11.6	328	2 F64187	p-aminobenzoate sy
17	71	11.6	446	2 S76228	hypothetical prote
18	71	11.6	461	2 T28698	noc1 protein - fis
19	70	11.5	933	2 A59250	myosin - Acetabula
20	69.5	11.4	253	2 C97331	arac-type DNA-bind
21	69.5	11.4	331	2 G83876	hypothetical prote
22	69.5	11.4	1188	2 JC4889	phosphatidylinosit
23	69	11.3	215	2 F45355	ORF2 protein - Aut
24	69	11.3	345	2 A5	UPE1 protein - yea
25	69	11.3	759	2 F64662	trans-Golgi membra
26	69	11.3	1871	2 D96898	probable DNA Polym
27	69	11.3	1894	2 T02155	DNA-directed DNA p
28	68.5	11.2	190	2 S23712	interferon alpha-I
29	68.5	11.2	638	2 AE2115	hypothetical prote

30	68.5	11.2	709	2 T32089	hypothetical prote
31	68.5	11.2	1102	2 S65235	probable membrane
32	68	11.1	215	2 B72854	AcOrf-34 protein -
33	68	11.1	414	2 G84311	hypothetical prote
34	68	11.1	529	2 S35306	phytoene dehydroge
35	68	11.1	767	1 COZPCD	cdc10 start contro
36	68	11.1	1055	2 T10432	DNA-directed RNA p
37	68	11.1	1621	2 A82255	hypothetical prote
38	67.5	11.1	1189	2 JC6118	SH2-containing ino
39	67	11.0	215	2 T41780	ACMNPV orf34 - Bom
40	67	11.0	356	2 S15156	myosin heavy chain
41	67	11.0	570	2 AG1228	DNA polymerase bet
42	66.5	10.9	2311	2 T06161	acetyl-CoA carboxy
43	66.5	10.9	274	2 T21284	hypothetical prote
44	66.5	10.9	590	2 H71977	hypothetical prote
45	66.5	10.9	767	2 T37844	SCF complex protei

## ALIGNMENTS

### RESULT 1

JC5116  
interleukin-5 precursor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 02-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 20-Jun-2000  
C:Accession: JC5116  
R:Werten, B.; Gobright, E.; Seow, H.F.  
Gene 176, 273-274, 1996  
A:Title: The nucleotide sequence of the bovine interleukin-5-encoding cDNA.  
A:Reference number: JC5116; MUID:97075944; PMID:8918267  
A:Accession: JC5116  
A:Molecule type: mRNA  
A:Residues: 1-134 <MER>  
A:Cross-references: EMBL:Z67872; NID:g1113120; PIDN:CRA91779.1; PID:g1113121  
A:Experimental source: lymphocytes  
C:Comment: This protein plays a role in the eosinophilia associated with parasitic dise  
C:Genetics:  
A:Gene: IL-5  
C:Superfamily: interleukin-5  
C:Keywords: cytokine; glycoprotein; growth factor; homodimer; lymphokine; T-cell  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-134/Product: interleukin-5 #status predicted <MAT>  
F:63/D/sulfide bonds: interchain (to 105) #status predicted  
F:76.90/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:105/D/sulfide bonds: interchain (to 63) #status predicted

Query Match 80.5%; Score 491; DB 2; Length 134;  
Best Local Similarity 81.6%; Pred. No. 9.1e-42;  
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 2 AVENPMRLVAETLLTLLSTHETWLGNGNLMIPPTENKHOLCTKEVFQGIIDTLKNQTAH 61

DB 21 AVESPMRLVAETLLTLLSSHTLLIGDGNLMIPPTQHTNHLQICIEEVFQGIIDTLKNQTAQ 80

QY 62 GEANDKLPONLSLKEHIEROKKACAGRWVTKFDYLVQVFLGVINTWTPES 115

DB 81 GDAVKKIFQNLSLKEHIEROKKACAGRWVTKFDYLVQVFLGVINTWTPES 134

### RESULT 2

A28477  
interleukin-5 precursor - human  
N:Alternate names: B-cell growth factor II; cytotoxic T lymphocyte inducer; eosinophil  
C:Species: Homo sapiens (man)  
C:Date: 01-Dec-1989 #sequence\_revision 07-Jul-1995 #text\_change 22-Jun-1999  
C:Accession: A28477; A33883; A26112; A39881; JX0106; S15775  
R:Tanabe, T.; Konishi, M.; Mizuta, T.; Noma, T.; Honjo, T.  
J. Biol. Chem. 262, 16580-16584, 1987

A:Title: Molecular cloning and structure of the human interleukin-5 gene.  
A:Reference number: A28477; MUID:86059042; PMID:2824500  
A:Accession: A28477  
A:Molecule type: DNA





Cytokine 3, 72-81, 1991  
A:Title: The rat interleukin-5 gene: characterization and expression by retroviral gene  
A:Reference number: A48418; MUID:91355638; PMID:1653053  
A:Accession: A48418  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-132 <UB>  
A:Cross-references: EMBL:X54419; NID:g313254; PIDN:CAA38283.1; PID:g313255  
A:Experimental source: cell line TR5-1  
A:Note: sequence extracted from NCBI backbone (NCBI:63651, NCBI:63652)  
C:Superfamily: interleukin-5  
C:Keywords: cytokine; signal sequence; growth factor; homodimer; lymphokine; T-cell  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:45-74/88/Product: interleukin-5 #status predicted <MAT>  
F:61/Dsulfide bonds: interchain (to 103) #status predicted  
F:103/Dsulfide bonds: interchain (to 61) #status predicted

Query Match 54.4%; Score 332; DB 1; Length 132;  
Best Local Similarity 56.6%; Pred. No. 6.2e-26;  
Matches 64; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 2 AVENPMRLVAETLLSTHRTWLGDNLMIPENKQKHCQKVFQIDTLKQTAH 61  
DB 19 AMBIPMSTVVKETLIQLSTRALLTNETNRLPVPTRHQRQICIGIFQGLDILKQTVR 78  
QY 62 GEAVDFMLFQNLISLKEHIERKRCACGERWRVTKFDLYQLVFLGVINTEWTP 114  
DB 79 GGVTEILFQNLISLKYIDQKCKGEEKRKTHTFDLYQLVFLGVNTEWAME 131

RESULT 5  
T47758  
hypothetical protein F2413.60 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 28-Jul-2000  
C:Accession: T47758  
R:Nyakatura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, February 2000  
A:Reference number: Z24475  
A:Accession: T47758  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-258 <NYA>  
A:Cross-references: EMBL:AL138655  
A:Experimental source: cultivar Columbia; BAC clone F2413  
C:Genetics:  
A:Map position: 3  
A:Introns: 109/3  
A:Note: F2413.60  
C:Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 12.9%; Score 78.5; DB 2; Length 258;  
Best Local Similarity 26.8%; Pred. No. 2.5;  
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 9 RIVAEITLLSTHRTWLGDNLMIPENKQKHCQKVFQIDTLKQTAHGEA 64  
DB 161 KAVANYISTVSATR---LGDNEYVMQISGSKHNFISNVLGLEDRFVLVDMSSRSQ 217  
QY 65 VDKLFQNLISLKEHIERKRC 86  
DB 218 GERIFVTLHLQVEKIENYKLC 239

RESULT 6  
B39432  
ATP-dependent deoxyribonuclease chain A adda - Bacillus subtilis  
N:Alternate names: ATP-dependent exonuclease synthesis protein Adda  
C:Species: Bacillus subtilis  
C:Date: 21-Feb-1992 #sequence\_revision 21-Feb-1992 #text\_change 02-Feb-2001  
C:Accession: B39432; H69582  
R:Xoolistra, J.; Venema, G.

J. Bacteriol. 173, 3644-3655, 1991  
A:Title: Cloning, sequencing, and expression of Bacillus subtilis genes involved in ATP.  
A:Reference number: A39432; MUID:91267926; PMID:1646786  
A:Accession: B39432  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1232 <KOO>  
A:Cross-references: GB:M63489; NID:g142438; PIDN:AAA22201.1; PID:g142440  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertei, C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galles, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, R.; Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, Y.; Ogawa, K.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Serol, A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: H69582  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1232 <KUN>  
A:Cross-references: GB:Z39109; GB:AL009126; NID:G2633260; PIDN:CAB12903.1; PID:el183065  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: addA  
C:Keywords: nucleotide binding; P-loop  
F:30-37/Region: nucleotide-binding motif A (P-loop)

Query Match 12.2%; Score 74.5; DB 2; Length 1232;  
Best Local Similarity 22.2%; Pred. No. 38;  
Matches 24; Conservative 24; Mismatches 37; Indels 23; Gaps 4;

QY 3 VENPMRLVAETLLSTHRTWLG--DGNLMIPENKQKHCQKVFQIDTLKQTA 60  
DB 633 IDNPY----QDIPLASVLRSPVIGADENLSLRLENKKAPY-----YEAMKDYLA 679

QY 61 HGEAVDFMLFQNLISLKEHIERK-----KRCACGERWRVTKFDLYL 100  
DB 680 AGDRSDELYQKLTIFYGHLQKWRAPSKNHSVSELIWEVYRDTKMYDV 727

RESULT 7  
T47757  
hypothetical protein F2413.50 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 28-Jul-2000  
C:Accession: T47757  
R:Nyakatura, G.; Partmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;  
submitted to the Protein Sequence Database, February 2000  
A:Reference number: Z24475  
A:Accession: T47757  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-253 <NYA>  
A:Cross-references: EMBL:AL138655  
A:Experimental source: cultivar Columbia; BAC clone F2413  
C:Genetics:  
A:Map position: 3  
A:Introns: 104/3  
A:Note: F2413.50  
C:Superfamily: Arabidopsis thaliana hypothetical protein F2413.60

Query Match 12.0%; Score 73.5; DB 2; Length 253;  
Best Local Similarity 27.1%; Pred. No. 7.6;  
Matches 23; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 9 RLVAETLLTSLTHTWLTGNGNLMPTPENKNHOLCIKEVFGQID-----TLKNQTAH 61  
 Db 156 KAVASYLSTVATR---LGNENVRVQVSSSKIHNFISNVLGIEEDGFVLDVSSRSQ 212  
 QY 62 GEAVDKLFQNLISLKEHIERQKRC 86  
 Db 213 GE---RLFYTLHLQVENMDYKINC 234

## RESULT 8

G69698  
 RNA polymerase (beta' subunit) rpoC - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 02-Sep-2000  
 C:Accession: G69698  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
 A.; Ehrlich, S.D.; Emerson, P.T.; Ehtian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
 A:Authors: Laubert, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel  
 Y, M.; Ogawa, K.; Ogiwara, B.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A:Reference number: A69580; MUID:9804033; PMID:9384377  
 A:Accession: G69698  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-1199 <KUN>  
 A:Cross-references: GB:299104; GB:AL009126; NID:92632267; PID:CAB11884.1; PID:e1182041;  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: rpoC  
 C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 12.0%; Score 73; DB 2; Length 1199;  
 Best Local Similarity 34.7%; Pred. No. 51;  
 Matches 26; Conservative 12; Mismatches 31; Indels 6; Gaps 4;

QY 35 TPENKNHOLCIKEVFGQIDTLKN--QTAKG-EAVDKLFQNLISLKE-HIERQKRCAGE 89  
 Db 142 TPLEKKQLLSEKVRAYLDYKNGKQFQASMGAEAIHKLQDIDLVKEVDMLKEELKTSQQ 201

QY 90 -RWRVTKFLDYQLVF 103  
 Db 202 RRTAIRKRLVLEAF 216

## RESULT 9

S33816  
 kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)  
 C:Species: Strongylocentrotus purpuratus (purple urchin)  
 C:Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-Sep-1997  
 C:Accession: S33816  
 R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
 J. Mol. Biol. 231, 155-158, 1993  
 A:Title: Sequences of sea urchin kinesin light chain isoforms.  
 A:Reference number: S33813; MUID:93267648; PMID:8496962  
 A:Accession: S33816  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-451 <WED>  
 A:Cross-references: EMBL:L08259; NID:g161531; PID:g161532

Query Match 11.9%; Score 72.5; DB 2; Length 451;  
 Best Local Similarity 25.9%; Pred. No. 19;  
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMPTPENKNHOLC--IKEVFGQIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKK 84  
 Db 15 GQGNL-----SQEQITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKDDTPGDSN 65  
 QY 85 RCAGERWRVTKFLDYQLVFLG 105  
 Db 66 LVEEKTDIIEKSLSLGLG 86

## RESULT 10

S33813  
 kinesin light chain - sea urchin (Strongylocentrotus purpuratus)  
 C:Species: Strongylocentrotus purpuratus (purple urchin)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Sep-1997  
 C:Accession: S33813  
 R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
 J. Mol. Biol. 231, 155-158, 1993  
 A:Title: Sequences of sea urchin kinesin light chain isoforms.  
 A:Reference number: S33813; MUID:93267648; PMID:8496962  
 A:Accession: S33813  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-849 <WED>  
 A:Cross-references: EMBL:L10233; NID:g161525; PID:g161526

Query Match 11.9%; Score 72.5; DB 2; Length 649;  
 Best Local Similarity 25.9%; Pred. No. 28;  
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMPTPENKNHOLC--IKEVFGQIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKK 84  
 Db 15 GQGNL-----SQEQITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKDDTPGDSN 65  
 QY 85 RCAGERWRVTKFLDYQLVFLG 105  
 Db 66 LVEEKTDIIEKSLSLGLG 86

## RESULT 11

S33814  
 kinesin light chain - sea urchin (Strongylocentrotus purpuratus)  
 C:Species: Strongylocentrotus purpuratus (purple urchin)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Sep-1997  
 C:Accession: S33814  
 R:Wedaman, K.P.; Knight, A.E.; Kendrick-Jones, J.; Scholey, J.M.  
 J. Mol. Biol. 231, 155-158, 1993  
 A:Title: Sequences of sea urchin kinesin light chain isoforms.  
 A:Reference number: S33813; MUID:93267648; PMID:8496962  
 A:Accession: S33814  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-877 <WED>  
 A:Cross-references: EMBL:L10234; NID:g161527; PID:g161528

Query Match 11.9%; Score 72.5; DB 2; Length 677;  
 Best Local Similarity 25.9%; Pred. No. 30;  
 Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 27 GDGNLMPTPENKNHOLC--IKEVFGQIDTLKNQTAHGEAVDKLFQNLISLKEHIERQKK 84  
 Db 15 GQGNL-----SQEQITGTREVIKGLEQLKNE--HNDILNSLYQSLKMLKDDTPGDSN 65  
 QY 85 RCAGERWRVTKFLDYQLVFLG 105  
 Db 66 LVEEKTDIIEKSLSLGLG 86

## RESULT 12

S33815  
 kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)  
 C:Species: Strongylocentrotus purpuratus (purple urchin)  
 C:Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 01-Dec-2000

Search completed: August 25, 2004, 00:06:25  
Job time : 23.6305 secs

Blank sheet

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 23:41:12 ; Search time 12.9317 Seconds  
(without alignments)  
463.052 Million cell updates/sec

Title: US-10-787-382-10  
Perfect score: 610  
Sequence: 1 FAVENPMNLVAETLLST.....FLDYQLVFLGVINTWTPES 115

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	610	100.0	134	1 IL5_CANFA	Q95476 canis fami
2	510	83.6	134	1 IL5_FELCA	Q77515 felis silve
3	494	81.0	134	1 IL5_HORSE	Q02899 equus cabal
4	491	80.5	134	1 IL5_BOVIN	P52173 bos tauris
5	487	79.8	132	1 IL5_SHEEP	Q28586 ovis aries
6	372	61.0	135	1 IL5_CAVPO	Q08997 cavia porce
7	361	59.2	134	1 IL5_CERTO	P46685 cercocobus
8	358	58.7	132	1 IL5_MERUN	Q62575 meriones un
9	356	58.4	134	1 IL5_HUMAN	P05113 homo sapien
10	354	58.0	132	1 IL5_SIGHI	Q9819 sigmodon hi
11	352	57.7	134	1 IL5_MAGMU	P48093 macaca mula
12	347	56.9	133	1 IL5_MOUSE	P04401 mus musculu
13	346	56.7	139	1 IL5_MACEU	Q9xt91 macropus eu
14	332	54.4	132	1 IL5_RAT	Q08125 rattus norv
15	94.5	15.5	590	1 MP41_MXVVL	Q9801 myxoma viru
16	74.5	12.2	1232	1 ADDA_BACSU	P23478 bacillus eu
17	73	12.0	1199	1 RPOC_BACSU	P37871 bacillus eu
18	72.5	11.9	686	1 KLC_STRPU	Q05090 strongyloce
19	72	11.8	401	1 Y148_METSM	P22344 methanobrev
20	71.5	11.7	437	1 SECV_STRGB	Q59912 streptomyce
21	71	11.6	216	1 Y037_ARCFU	Q28292 archaeoglob
22	71	11.6	328	1 Y870_HARIN	Q57597 haemophilus
23	71	11.6	461	1 TIPA_SCHPO	P79055 schizosacch
24	69	11.3	346	1 UFE1_YEAST	P41834 saccharomyc
25	68.5	11.2	349	1 EGC2_BUCBU	Q8d4q0 vibrio vuln
26	68	11.1	169	1 HSCB_BUCBP	Q89a17 buchnera ap
27	68	11.1	215	1 Y034_NPVAC	P21287 autographa
28	68	11.1	529	1 CRT1_MYXAC	Q02861 myxococcus
29	68	11.1	767	1 CC10_SCHPO	P01129 schizosacch
30	68	11.1	1055	1 RPOC_PEDAC	P77917 pediococcus
31	67.5	11.1	439	1 ARLY_THETIN	Q8r7c3 thermococ
32	66.5	10.9	767	1 CUL1_SCHPO	Q13790 schizosacch
33	66	10.8	119	1 RPOZ_CAUCR	P58056 caulobacter

34 66 10.8 864 1 SVL\_WIGBR Q8d333 wiggleswort  
35 65.5 10.7 248 1 NAG1\_CANAL Q04802 candida alb  
36 85.5 10.7 889 1 SEC3\_DROME Q9v9g4 drosophila  
37 65 10.7 163 1 CYPH\_UROFA Q00660 uromyces fa  
38 65 10.7 295 1 SYGA\_BACSU P54380 bacillus su  
39 65 10.7 664 1 DHSA\_HUMAN P31040 homo sapien  
40 65 10.7 738 1 ST11\_YEAST P23561 saccharomyc  
41 64.5 10.6 225 1 YP83\_MYCPN P75197 mycoplasma  
42 64 10.5 295 1 EFTS\_BACAA Q81w9 bacillus an  
43 64 10.5 366 1 YP59\_STAM Q99tt7 staphylococ  
44 64 10.5 429 1 ARLY\_PYRAE Q8zu95 pyrobaculum  
45 64 10.5 430 1 TEK2\_MOUSE Q92297 mus musculu

#### ALIGNMENTS

RESULT 1  
IL5\_CANFA

ID IL5\_CANFA STANDARD; PRT; 134 AA.  
AC Q95J76;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Interleukin-5 precursor (Il-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN IL5.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_taxid=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21334408; PubMed=11440633;  
RA Yang S., Sellins K.S., Weber E., McCall C.;  
RT "Canine interleukin-5: molecular characterization of the gene and  
RT expression of biologically active recombinant protein.";  
RL J. Interferon Cytokine Res. 21:361-367(2001)  
CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
CC developing B-cells to immunoglobulin secreting cells (By  
CC similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-5 family.  
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CC  
CC EMBL; AF331920; AAL10715.1; -.  
CC EMBL; AF331919; AAL10715.1; -.  
CC InterPro; IPR009079; 4.helix\_cytokine.  
CC InterPro; IPR000186; Interleukin\_5.  
CC Pfam; PF02025; IL5; 1.  
CC PRINTS; PR00432; INTERLEUKIN5.  
CC ProDom; PD006721; Interleukin\_5; 1.  
CC Cytokine; Growth factor; Glycoprotein; Signal.  
CC SIGNAL 1 21  
CC CHAIN 22 134  
CC INTERLEUKIN-5.  
CC DISULFID 63 63  
CC INTERCHAIN (WITH C-105) (BY SIMILARITY).  
CC DISULFID 105 105  
CC INTERCHAIN (WITH C-63) (BY SIMILARITY).  
CC CARBOHYD 76 76  
CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC CARBOHYD 90 90  
CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
CC SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;

Query Match 100.0%; Score 610; DB 1; Length 134;

Best Local Similarity 100.0%; Pred. No. 2.le-55;

Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 FAVENPMNLVAETLLTLLSTHRTWLGDNLMIPTPENKHNHOLCIKEVFOGIDTLKNQTA 60
Db 20 FAVENPMNLVAETLLTLLSTHRTWLGDNLMIPTPENKHNHOLCIKEVFOGIDTLKNQTA 79
QY 61 HGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 115
Db 80 HGEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 134

RESULT 2
IL5_FELCA
ID IL5_FELCA STANDARD; PRT; 134 AA.
AC 077515; 062740;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Felis silvestris catus (Cat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98452719; PubMed=9781459;
RA Padraig P.A., Qin Y., Wells T.N.C., Solway J., Camoretti-Mercado B.;
RL "Sequence and structural analysis of feline interleukin-5 cDNA.";
RT Am. J. Vet. Res. 59:1263-1269(1998).
RN [2]
RP SEQUENCE OF 12-128 FROM N.A.
RA Harley R., Day M.J., Gruffydd-Jones T.J., Harbour D.A., Helps C.R.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells (By
CC similarity).
CC -!- SUBUNIT: Homodimer, disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC
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CC
CC EMBL; AF025436; AAC64505.1; -.
CC EMBL; AF051372; AAC05752.1; -.
CC HSP; P05113; IHL.
CC InterPro; IPR000186; Interleukin_5.
CC Pfam; PF02025; IL5; 1.
CC PRINTS; PR00432; INTERLEUKIN5.
CC ProDom; PD06721; Interleukin_5; 1.
CC Cytokine; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 19 BY SIMILARITY.
CC CHAIN 20 134 INTERLEUKIN-5.
CC DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
CC FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
CC FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 104 105 KC -> NF (IN REF. 2).
CC FT CONFLICT 108 111 ERWR -> KWK (IN REF. 2).
CC FT CONFLICT 114 114 K -> N (IN REF. 2).
CC FT CONFLICT 117 117 D -> N (IN REF. 2).
CC FT CONFLICT 121 121 V -> F (IN REF. 2).
CC FT CONFLICT 125 126 VI -> LL (IN REF. 2).
CC SEQUENCE 134 AA; 87D18DB8F8C8920 CRC64;

Query Match 83.68; Score 510; DB 1; Length 134;
Best Local Similarity 84.28; Pred. No. 3.4e-45;
Matches 96; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 AVENPMNLVAETLLTLLSTHRTWLGDNLMIPTPENKHNHOLCIKEVFOGIDTLKNQTAH 61
Db 21 AVQSPMNLVAETLLTLLSTHRTWLGDNLMIPTPENKHNHOLCIKEVFOGIDTLKNQTV 80
QY 62 GEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 115
Db 81 GDAVKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 134

RESULT 3
IL5_HORSE
ID IL5_HORSE STANDARD; PRT; 134 AA.
AC 002599;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX VANDERGRIFT E.V., HOROV D.W.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RL "FUNCTION: Factor that induces terminal differentiation of late-
RL developing B-cells to immunoglobulin secreting cells (By
RL similarity).
RL -!- SUBUNIT: Homodimer, disulfide-linked (By similarity).
RL -!- SUBCELLULAR LOCATION: Secreted.
RL -!- SIMILARITY: Belongs to the IL-5 family.
RL
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RL
RL EMBL; U91947; AAB51382.1; -.
RL HSP; P05113; IHL.
RL InterPro; IPR000186; Interleukin_5.
RL Pfam; PF02025; IL5; 1.
RL PRINTS; PR00432; INTERLEUKIN5.
RL ProDom; PD06721; Interleukin_5; 1.
RL Cytokine; Growth factor; Glycoprotein; Signal.
RL SIGNAL 1 19 BY SIMILARITY.
RL CHAIN 20 134 INTERLEUKIN-5.
RL DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).
RL FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).
RL FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
RL FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
RL SEQUENCE 134 AA; 2914840E3E7A006D CRC64;

Query Match 81.08; Score 494; DB 1; Length 134;
Best Local Similarity 84.18; Pred. No. 1.5e-43;
Matches 95; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 AVENPMNLVAETLLTLLSTHRTWLGDNLMIPTPENKHNHOLCIKEVFOGIDTLKNQTAH 61
Db 21 AVQSPMNLVAETLLTLLSTHRTWLGDNLMIPTPENKHNHOLCIKEVFOGIDTLKNQTV 80
QY 62 GEAVDKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 114
Db 81 GDAVKLFQNLSLIKEHIEROKKRCAGRWRTKFLDYLVQVFLGVINTEWTPES 133

RESULT 4
IL5_BOVIN

```

ID IL5\_BOVIN STANDARD; PRT; 134 AA.  
AC P52173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN IL5.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]\_TaxID=9913;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=97075944; PubMed=8918267;  
RA Mertens B., Gobright E., Sew H.F.;  
RT "The nucleotide sequence of the bovine interleukin-5 encoding cDNA."  
RL Gene 176:273-274 (1996).  
CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
developing B-cells to immunoglobulin secreting cells (By  
similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-5 family.  
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CC -----  
DR EMBL; Z67872; CA91779.1; -.  
DR PIR; JCS116; JCS116.  
DR HSSP; P05113; 1HUL.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKIN5.  
DR ProDom; PD006721; Interleukin\_5.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 134  
FT DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).  
FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).  
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 134 AA; 15229 MW; 0B3A2328EE7431F4 CRC64;  
Query Match 80.5%; Score 491; DB 1; Length 134;  
Best Local Similarity 81.6%; Pred. No. 3e-43;  
Matches 93; Conservative 12; Mismatches 9; Indels 0; Gaps 0;  
QY 2 AVENPMNLVAETLLTSLTHRTWLGDNLMIPENKNHOLCIKEVFGIDTLKNQTAH 61  
DB 21 AVESTMNLVAETLLTSLTHRTWLGDNLMIPENKNHOLCIKEVFGIDTLKNQTAH 80  
QY 62 GEAVDKLFQNLSLIKEHIEROKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 115  
DB 81 GDAVKKTFQNLSLIKEHIEROKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 134

RESULT 5  
IL5\_SHEEP  
ID IL5\_SHEEP STANDARD; PRT; 132 AA.  
AC Q28586;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).

GN IL5.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]\_TaxID=9940;  
RP SEQUENCE FROM N.A.  
RA Bryson C.E., Viney E., Brandon M., Boyd A.W.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]\_TaxID=9940;  
RP SEQUENCE FROM N.A.  
RA Seow H.-F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;  
RT "Cloning of ovine interleukin-5 cDNA."  
RL submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
developing B-cells to immunoglobulin secreting cells (By  
similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the IL-5 family.  
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CC -----  
DR EMBL; U17053; AAB60629.1; -.  
DR EMBL; U17052; AAB60629.1; JOINED.  
DR EMBL; U35038; AAC9991.1; -.  
DR HSSP; P05113; 1HUL.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKIN5.  
DR ProDom; PD006721; Interleukin\_5.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 132  
FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).  
FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).  
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 132 AA; 14974 MW; D783P2B720E249D9 CRC64;  
Query Match 79.8%; Score 487; DB 1; Length 132;  
Best Local Similarity 80.7%; Pred. No. 7.5e-43;  
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
QY 2 AVENPMNLVAETLLTSLTHRTWLGDNLMIPENKNHOLCIKEVFGIDTLKNQTAH 61  
DB 19 AVESTMNLVAETLLTSLTHRTWLGDNLMIPENKNHOLCIKEVFGIDTLKNQTAH 78  
QY 62 GEAVDKLFQNLSLIKEHIEROKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 115  
DB 79 GDAVKKTFQNLSLIKEHIEROKRCACGERWRVTKFLDYQLQVFLGVINTWTPES 132

RESULT 6  
IL5\_CAVPO  
ID IL5\_CAVPO STANDARD; PRT; 135 AA.  
AC Q08587;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
DE (Eosinophil differentiation factor).  
GN IL5.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.





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CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
CC EMBL; L37780; AAA65675.1; -.
CC DR HSSP; P05113; IHUL.
CC DR InterPro; IPR000186; Interleukin_5.
CC DR Pfam; PF020235; IL5_1.
CC DR PRINTS; PR00432; INTERLEUKINS.
CC DR ProDom; PD006721; Interleukin_5; 1.
CC KW Cytokine; Growth factor; Glycoprotein; Signal.
CC FT SIGNAL 1 17 POTENTIAL.
CC FT CHAIN 18 132 INTERLEUKIN-5.
CC FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
CC FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
CC FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 132 AA; 15164 MW; 60CE3852F9F84261 CRC64;
CC -----
CC Query Match 58.7%; Score 358; DB 1; Length 132;
CC Best Local Similarity 61.1%; Pred. No. 1.1e-29;
CC Matches 69; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
CC -----
CC QY 2 AVENPMRLVAETLTLLSTHRTWLIGDNLMIPTPENKHEQICKEVFGIDTLKNQTAH 61
CC DB 19 ALBIPMSAVVKETLIQLSTHRLTSLNETVRLPVPTHKNEHQLCGIFQGLDILKNQTAH 78
CC -----
CC QY 62 GEAVDKLFQNLISLKHIEROKRCAGERRVTKFDLYQLQVFLGVINTWETPE 114
CC DB 79 GGAVETLFQNLISLKHIEROKRCAGERRVTKFDLYQLQVFLGVINTWETPE 131
CC -----
CC RESULT 9
CC IL5_HUMAN
CC ID IL5_HUMAN STANDARD; PRT; 134 AA.
CC AC P05113; Q13840;
CC DT 13-AUG-1987 (Rel. 05, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
CC DE (Eosinophil differentiation factor) (B cell differentiation factor 1).
CC GN IL5.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=87066782; PubMed=3024129;
CC RA Azuma C., Tanabe T., Konishi M., Kinashi T., Noma T., Matsuoka F.,
CC RA Yacita Y., Takatsu K., Hammarstrom L., Smith C.I.E., Severinson E.,
CC RA Honjo T.;
CC RT "Cloning of cDNA for human T-cell replacing factor (interleukin-5)
CC RT and comparison with the murine homologue."
CC RL Nucleic Acids Res. 14:9149-9158(1986).
CC [2]
CC RN SEQUENCE FROM N.A.
CC RX MEDLINE=88059042; PubMed=2824500;
CC RA Tanabe T., Konishi M., Mizuta T., Noma T., Honjo T.;
CC RT "Molecular cloning and structure of the human interleukin-5 gene."
CC RL J. Biol. Chem. 262:16580-16584(1987).
CC [3]
CC RN SEQUENCE FROM N.A.
CC RX MEDLINE=88016145; PubMed=3498940;
CC RA Campbell H.D., Tucker W.Q.J., Hort Y., Martinson M.E., Mayo G.,
CC RA Clutterbuck E.J., Sanderson C.J., Young I.G.;
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RT "Molecular cloning, nucleotide sequence, and expression of the gene
RT encoding human eosinophil differentiation factor (interleukin 5).";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6629-6633(1987).
[4]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=88041112; PubMed=2823259;
CC RA Yokota T., Coffman R.L., Hagiwara H., Rennick D.M., Takebe Y.,
CC RA Yokota K., Gemmell L., Shrader B., Yang G., Meyerson P., Luh J.,
CC RA Hoy P., Pene J., Briere F., Spits H., Banchereau J., de Vries J.,
CC RA Lee F.D., Arai N., Arai K.;
CC RT "Isolation and characterization of lymphokine cDNA clones encoding
CC mouse and human IGA-enhancing factor and eosinophil
CC colony-stimulating factor activities: relationship to interleukin
CC 5.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 84:7388-7392(1987).
[5]
CC RN SEQUENCE FROM N.A.
CC RA Honjo T., Takatsu K., Severinson E.;
CC RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
[6]
CC RN SEQUENCE FROM N.A.
CC RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
CC RA Nickerson D.A.;
CC RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[7]
CC RN SEQUENCE OF 20-134, AND DISULFIDE BONDS.
CC RX MEDLINE=90299868; PubMed=2361960;
CC RA Minamitake Y., Kodama S., Katayama T., Adachi H., Tanaka S.,
CC RA Tsujimoto M.;
CC RT "Structure of recombinant human interleukin 5 produced by Chinese
CC hamster ovary cells.";
CC RL J. Biochem. 107:292-297(1990).
[8]
CC RN DISULFIDE BONDS.
CC RX MEDLINE=91243978; PubMed=2037074;
CC RA Proudfoot A.E.I., Davies J.G., Turcatti G., Wingfield P.T.;
CC RT "Human interleukin-5 expressed in Escherichia coli: assignment of the
CC disulfide bridges of the purified unglycosylated protein.";
CC RL FEBS Lett. 283:61-64(1991).
[9]
CC RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
CC RX MEDLINE=93247642; PubMed=8483502;
CC RA Milburn M.V., Hassell A.M., Lambert M.H., Jordan S.R.,
CC RA Proudfoot A.E.I., Graber P., Wells T.N.C.;
CC RT "A novel dimer configuration revealed by the crystal structure at
CC 2.4-A resolution of human interleukin-5.";
CC RL Nature 363:1172-1176(1993).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -!- DATABASE: NAME=R&D Systems' cytokine mini-reviews; IL5;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=207".
CC -----
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CC -----
CC EMBL; X04688; CAA28390.1; -.
CC DR EMBL; J03478; AAA74469.1; -.
CC DR EMBL; J02971; AAA98620.1; -.
CC DR EMBL; X12705; CAA31210.1; -.
CC DR EMBL; X12706; CAA31211.1; -.
CC DR EMBL; AF353265; AAK19759.1; -.
CC DR PIR; A28477; A28477.
CC DR PDB; 1HUL; 07-DEC-95.
CC DR Genew; HGNC:6016; IL5.
CC MIM; 147850; -.
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DR GO: GO:0005576; C:extracellular; TAS.
DR GO: GO:0005137; F:interleukin-5 receptor binding; TAS.
DR GO: GO:0009626; P:hypermotile response; TAS.
DR GO: GO:0009694; P:inflammatory response; TAS.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS: PR00432; INTERLEUKIN5.
DR ProDom: PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 134
FT DISULFID 63 63
FT DISULFID 105 105
FT CARBOHYD 22 22
FT CARBOHYD 47 47
FT CARBOHYD 88 88
FT CONFLICT 26 38
FT HELIX 39 40
FT TURN 41 45
FT TURN 46 46
FT TURN 51 54
FT STRAND 60 62
FT HELIX 64 77
FT TURN 82 82
FT HELIX 83 103
FT TURN 104 105
FT STRAND 108 111
FT HELIX 112 128
FT TURN 129 129
SQ SEQUENCE 134 AA; 15238 MW; DC984467179556A3 CRC64;

Query Match 58.4%; Score 356; DB 1; Length 134;
Best Local Similarity 62.5%; Pred. No. 1.9e-29;
Matches 70; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 4 ENPMRLVAETLTLLSTHRTWLIGDGNLMTPTENKKNHOLCIKEVFGIDTLKNQTAHCE 63
Db 23 EIPTSALVKTETALLSTHRTLLTANETLRFPVPHKHQLCTEIEFGIGTLESQVQGG 82

QY 64 AVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
Db 83 TVERLFNLSLIKXYIDGKKCKGERRRVNQFLDYQLQVFLGVNTEWIES 134

RESULT 10
IL5_SIGHI STANDARD; PRT; 132 AA.
AC Q9ES19;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=20510033; PubMed=11054577;
RA Houard S., Jacquet A., Haumont M., Daminet V., Milican F., Glineur F.,
RT "cloning, expression and purification of recombinant cotton rat
interleukin-5.";
RL Gene 257:149-155 (2000).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.

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DR EMBL: AF148211; AAC16722.1; -.
DR HSP: P05113; IHUL.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS: PR00432; INTERLEUKIN5.
DR ProDom: PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 132
FT DISULFID 61 61
FT DISULFID 103 103
FT CARBOHYD 45 45
FT CARBOHYD 74 74
FT CARBOHYD 88 88
FT SEQUENCE 132 AA; 15434 MW; B328B81B2371FEB9 CRC64;

Query Match 58.0%; Score 354; DB 1; Length 132;
Best Local Similarity 59.6%; Pred. No. 2.9e-29;
Matches 68; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAETLTLLSTHRTWLIGDGNLMTPTENKKNHOLCIKEVFGIDTLKNQTA 60
Db 18 FAVEPMHTVVKETLIQLSTHRLTSTNEVTRPVPHKHQLCTEIEFGIGTLESQVQGG 77

QY 61 HGEAVDKLFQNLSLIKHEIRQKRCAGRWRTKFLDYQLQVFLGVINTWTPTE 114
Db 78 RGGVETVLFQNLSLIKKYIDRQKCKGERRRTRQFLDYQLQVFLGVNTEWTE 131

RESULT 11
IL5_MACMU STANDARD; PRT; 134 AA.
AC P48093;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954 (1995).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
developing B-cells to immunoglobulin secreting cells (By
similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.

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 CC -----  
 DR EMBL; U19848; AAA86710.1; -  
 DR HSSP; P05113; 1HUL  
 DR InterPro; IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR ProDom; PD06721; Interleukin\_5; 1.  
 CC CytoKine; Growth factor; Glycoprotein; Signal.  
 KW SIGNAL 1 19 BY SIMILARITY.  
 FT CHAIN 20 134 INTERLEUKIN-5.  
 FT DISULFID 63 63 INTERCHAIN (WITH C-105) (BY SIMILARITY).  
 FT DISULFID 105 105 INTERCHAIN (WITH C-63) (BY SIMILARITY).  
 FT CARBOHYD 22 22 O-LINKED (BY SIMILARITY).  
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 134 AA; 15150 MW; DC985ECF4BAB86A3 CRC64;  
 Query Match 57.7%; Score 352; DB 1; Length 134;  
 Best Local Similarity 62.5%; Pred. No. 4.7e-29;  
 Matches 70; Conservative 15; Mismatches 27; Indels 0; Gaps 0;  
 QY 4 ENPMNRLVAETLLSTHRTWLTGDNLMIPENKNHQLCIKEVFGQIDTLKNQTAHGE 63  
 Db 23 EIPASALVKETALLSTHRTLLANETLRIPVPHKHQLCTEIEIFQIGITLESQIVQGG 82  
 QY 64 AVDXLFQNLISLKEHIEROKKRCAGRWRTKFLDYQLVFLGVINTEWTPES 115  
 Db 83 TVBERLFNLSLIRKYGQKKCGEERRVNPQLDYQLVFLGVINTEWTPES 134  
 RESULT 12  
 IL5\_MOUSE  
 ID IL5\_MOUSE STANDARD; PRT; 133 AA.  
 AC P04401;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell  
 DE growth factor II) (BCGF-II) (Eosinophil differentiation factor)  
 DE (Cytotoxic T lymphocyte inducer).  
 IL5 OR IL-5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88254802; PubMed=3133208;  
 RA Campbell H.D., Sanders C.J., Wang Y., Hort Y., Martinson M.E.,  
 RA Tucker W.O.J., Stellwagen A., Strath M., Young I.G.;  
 RT "Isolation, structure and expression of cDNA and genomic clones for  
 RT murine eosinophil differentiation factor: Comparison with other  
 RT eosinophilopoietic lymphokines and identity with interleukin-5";  
 RL Eur. J. Biochem. 174:345-352(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=87065032; PubMed=3024009;  
 RA Kinashi T., Harada N., Severinson E., Tanabe T., Sideras P.,  
 RA Konishi M., Azuma C., Tomimaga A., Bergstedt-Lindqvist S.,  
 RA Takahashi M., Matsuda F., Yaota Y., Takatsu K., Honjo T.;  
 RT "Cloning of complementary DNA encoding T-cell replacing factor and  
 RT identity with B-cell growth factor II";  
 RL Nature 324:70-73(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90180853; PubMed=3078564;  
 RA Mizuta T.R., Tanabe T., Nakakubo H., Noma T., Honjo T.;  
 RT "Molecular cloning and structure of the mouse interleukin-5 gene";  
 RL Growth Factors 1:51-57(1988).  
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-

CC developing B-cells to immunoglobulin secreting cells.  
 CC -!- SUBUNIT: Homodimer; disulfide-linked.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-5 family.  
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 CC -----  
 CC EMBL; X06270; CAA29606.1; -  
 CC EMBL; X06271; CAA29607.1; -  
 CC EMBL; X04601; CAA28266.1; -  
 CC PIR; S00807; ICMS5.  
 CC HSSP; P05113; 1HUL.  
 CC MGD; MGI:96557; IL5.  
 DR InterPro; IPR000186; Interleukin\_5.  
 DR Pfam; PF02025; IL5; 1.  
 DR PRINTS; PR00432; INTERLEUKINS.  
 DR ProDom; PD06721; Interleukin\_5; 1.  
 CC CytoKine; Growth factor; Glycoprotein; Signal.  
 KW SIGNAL 1 20  
 FT CHAIN 21 133 INTERLEUKIN-5.  
 FT DISULFID 62 62 INTERCHAIN (WITH C-104) (BY SIMILARITY).  
 FT DISULFID 104 104 INTERCHAIN (WITH C-62) (BY SIMILARITY).  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 133 AA; 15410 MW; C6DC091682452A24 CRC64;  
 Query Match 56.9%; Score 347; DB 1; Length 133;  
 Best Local Similarity 58.4%; Pred. No. 1.5e-28;  
 Matches 66; Conservative 18; Mismatches 29; Indels 0; Gaps 0;  
 QY 2 AVENPMNRLVAETLLSTHRTWLTGDNLMIPENKNHQLCIKEVFGQIDTLKNQTAH 61  
 Db 20 AVEIPMSVTVKETTQLSAHALLTSNETMELPVTNKHQLCIGEIFQGLDILKNQTVR 79  
 QY 62 GEAVDXLFQNLISLKEHIEROKKRCAGRWRTKFLDYQLVFLGVINTEWTPES 114  
 Db 80 GGTVEMLFQNLISLIRKYGQKKCGEERRVNPQLDYQLVFLGVINTEWTPES 132  
 RESULT 13  
 IL5\_MOUSE  
 ID IL5\_MOUSE STANDARD; PRT; 139 AA.  
 AC Q9XT91;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF)  
 DE (Eosinophil differentiation factor).  
 IL5.  
 OS Macropus eugenii (Tamar wallaby).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.  
 OX NCBI\_TaxID=9315;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99432005; PubMed=10501836;  
 RA Hawken R.J., Maccarone P., Toder R., Marshall Graves J.A.,  
 RA Maddox J.F.;  
 RT "Isolation and characterization of marsupial IL5 genes";  
 RL Immunogenetics 49:942-948(1999).  
 CC -!- FUNCTION: Factor that induces terminal differentiation of late-  
 CC developing B-cells to immunoglobulin secreting cells (By  
 CC similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-5 family.

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CC -----
DR EMBL; AF064209; AAD37462.1; -.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 139 INTERLEUKIN-5.
FT DISULFID 64 64 INTERCHAIN (WITH C-106) (BY SIMILARITY).
FT DISULFID 106 106 INTERCHAIN (WITH C-64) (BY SIMILARITY).
FT CARBOHYD 48 48 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 139 AA; 15784 MW; CE16342A68F10622 CRC64;
Query Match 56.78; Score 346; DB 1; Length 139;
Best Local Similarity 57.63; Pred. No. 2e-28;
Matches 68; Conservative 20; Mismatches 26; Indels 4; Gaps 1;
QY 2 AVENPMRLVAETLLTSLTHTLIGDGNLMIPPTENKHQLCIKVEFGQIDTLKNQTAH 61
DB 22 ATGNFVSRVLTETLSLTARTLLIGNGTLRISIPDPQNHPLCIEBIFQIGETLKNQTA 81
QY 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTPES 115
DB 82 ENVVEKIFQNLSSLGKVIYAKKCGERRRVEQFLDYLEEFRTINIEWNTWTVES 139
RESULT 14
IL5_RAT
ID IL5_RAT STANDARD; PRT; 132 AA.
AC Q08125;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell
DE growth factor II) (SCGF-II) (Eosinophil differentiation factor)
DE (Cytotoxic T lymphocyte inducer).
GN IL5 OR IL-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RX MEDLINE=91355638; PubMed=1633053;
RA Ueberli K.T., Li W., Guin Z., Richter G., Raabe T.,
RA Diamantstein T., Blanckenstein T.;
RT "The rat interleukin-5 gene: characterization and expression by
RT retroviral gene transfer and polymerase chain reaction.";
RL Cytokine 3:72-81(1991).
CC -!- FUNCTION: Factor that induces terminal differentiation of late-
CC developing B-cells to immunoglobulin secreting cells.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-5 family.
CC -----
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CC -----
DR EMBL; X54419; CAA38283.1; -.
DR PIR; A48418; A48418.
DR HSSP; P05113; 1HUL.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKIN5.
DR ProDom; PD006721; Interleukin_5; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 132 INTERLEUKIN-5.
FT DISULFID 61 61 INTERCHAIN (WITH C-103) (BY SIMILARITY).
FT DISULFID 103 103 INTERCHAIN (WITH C-61) (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 132 AA; 15207 MW; 214A928B94C047031 CRC64;
Query Match 54.43; Score 332; DB 1; Length 132;
Best Local Similarity 56.63; Pred. No. 5.1e-27;
Matches 64; Conservative 18; Mismatches 31; Indels 0; Gaps 0;
QY 2 AVENPMRLVAETLLTSLTHTLIGDGNLMIPPTENKHQLCIKVEFGQIDTLKNQTAH 61
DB 19 AMEIPMTVTKETLIQLSTHRLTSTNETWRLPVPTKHNHQLCIGEIFQSLDILKNQTV 78
QY 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTWTP 114
DB 79 GGTVEILFQNLISLKKYIDGKCKGERRKTRHFLDYQLQVFLGVNTEWAME 131
RESULT 15
MP44 MYXVL
ID MP44 MYXVL STANDARD; PRT; 590 AA.
AC Q908Q1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable metalloendopeptidase Gl-type (EC 3.4.24.-).
GN M045L.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20032073; PubMed=10562494;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus.";
RL Virology 264:298-318(1999).
CC -!- FUNCTION: Seems to be involved in viral proteins maturation by
CC cleavage at Ala-Gly--Xaa motifs (By similarity).
CC -!- COFACTOR: Binds 1 zinc ion (potential).
CC -!- SIMILARITY: Belongs to peptidase family M44.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF170726; AAF14933.1; -.
DR MEROPS; M44.001; -.
DR InterPro; IPR005072; Peptidase_M44.
DR Pfam; PF03410; Peptidase_M44; 1.
KW Hydrolase; Metalloprotease; Zinc.
FT METAL 41 41 ZINC (CATALYTIC) (POTENTIAL).
FT ACT_SITE 44 44 POTENTIAL.
```

```
FT METAL      45      ZINC (CATALYTIC) (POTENTIAL).
SQ SEQUENCE  590 AA; 68224 MW; 1DEE178930C75984 CRC64;

Query Match      15.5%; Score 94.5; DB 1; Length 590;
Best/Local Similarity 25.7%; Pred. No. 0.054;
Matches 36; Conservative 23; Mismatches 38; Indels 43; Gaps 7;

QY      5 NPMNRLVAETLLSTHRTWLIGDGNLMPTP-----ENKNHQ----LCIKVFOGI 52
Db      185 NTFGRLPACPLTIPCTVRT-IIGKTIIMFSPFYVMVRVPSLHNILSILCLYEIYHLV 243

QY      53 DTLKNQTANGEVD-KLFQNLSLIKEH-----IERQKKFCAGERWRVTKF 96
Db      244 DY-----ETVDNKLTYTFIFIHEHYERFLQSSGRNLNLTYYKKIRLCYGGDFLMVY 295

QY      97 LDYLQV-----FLGVINTE 110
Db      296 LSPFCIRHDFDYLTIVNTD 315
```

Search completed: August 25, 2004, 00:02:58  
Job time : 13.9317 secs

Blank

Sheet

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 24, 2004, 23:54:03 ; Search time 66.9679 Seconds  
(without alignments)  
541.821 Million cell updates/sec

Title: US-10-787-382-10

Perfect score: 610

Sequence: 1 FAVENPMRLVAETLLST.....FLDYQLVFLGVINTEWTPES 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_virus.\*

16: sp\_bacteriap.\*

17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	134	Q95J76	Q95J76 canis famil
2	563	92.3	118	Q9TV10	Q9TV10 canis famil
3	505	82.8	134	Q9TSD7	Q9TSD7 felis silve
4	501	82.1	134	Q9MTN5	Q9MTN5 sus scrofa
5	382	62.6	134	Q8MKH1	Q8MKH1 salmairi sci
6	325	53.3	132	Q9X2C9	Q9X2C9 rattus norv
7	109.5	18.0	40	Q9XT92	Q9XT92 smnthopsis
8	78.5	12.9	258	Q9M1K0	Q9M1K0 arabidopsis
9	76.5	12.5	158	Q96575	Q96575 leucophaea
10	75	12.3	292	Q8PUD3	Q8PUD3 mechanosarc
11	73.5	12.0	253	Q9M1K1	Q9M1K1 arabidopsis
12	73	12.0	248	Q8VR0	Q8VR0 helianthus
13	73	12.0	623	Q7XRA0	Q7XRA0 oryza sativ
14	73	12.0	661	Q921P5	Q921P5 mus musculu
15	73	12.0	664	Q8K2B3	Q8K2B3 mus musculu
16	72.5	11.9	229	Q9CLF5	Q9CLF5 pasteurella

## ALIGNMENTS

RESULT 1

Q95J76 PRELIMINARY; PRT; 134 AA.

AC Q95J76; ID Q95J76; PRELIMINARY; PRT; 134 AA.

DT 01-DEC-2001 (TRENBLrel. 19, Created)

DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Interleukin-5.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

[1] SEQUENCE FROM N.A.

RP MEDLINE=21334408; PubMed=11440633;

RA Yang S., Sellins K.S., Weber E., McCall C.;

RT "Canine interleukin-5: molecular characterization of the gene and

RT expression of biologically active recombinant protein.";

RL J. Interferon Cytokine Res. 21:361-367(2001).

DR EMBL; AF331920; AAL10716.1; -

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR00186; Interleukin\_5.

DR Pfam; PF02025; IL5; 1

DR PRINTS; PR00432; INTERLEUKIN\_5.

DR ProDom; PDOM6721; Interleukin\_5; 1.

SQ SEQUENCE 134 AA; 15307 MW; 003C86D94D6FF4C6 CRC64;

Query Match 100.0%; Score 610; DB 6; Length 134;

Best Local Similarity 100.0%; Pred. No. 3.3e-56;

Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVENPMRLVAETLLSTRTWLIGGNLMITPENKNHQLCIKEVFOQIDILKNQTA 60

20 FAVENPMRLVAETLLSTRTWLIGGNLMITPENKNHQLCIKEVFOQIDILKNQTA 79

QY 61 HGEAVDKLQNLISLIKEHIERKQKRCACERWRTKFLDYQLVFLGVINTEWTPES 115

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Db 80 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 134
|||||
RESULT 2
Q9TV10 ID Q9TV10 PRELIMINARY; PRT; 118 AA.
AC Q9TV10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-5 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT "Cloning and sequencing of canine interleukin-5";
PL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091133; AAD46991.1; -.
DR HSSP; P05113; IHUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
FT NON TER 1
FT TER 118
SQ SEQUENCE 118 AA; 13507 MW; 36A5563DD67C968C CRC64;

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Query Match 92.38; Score 563; DB 6; Length 118;
Best Local Similarity 93.78; Pred. No. 2.4e-51;
Matches 104; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FAVENPNRLVAETLLSTHRTWLGDNLMIPTEPNKHQLCIKEVFQGITLKNQTA 60
|||||
Db 8 FAVENPNRLVAETLLSTHRTWLGDNLMIPTEPNKHQLCIKEVFQGITLKNQTA 67
|||||
Qy 61 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 111
|||||
Db 68 HGEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 118
|||||

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RESULT 3
Q9TSD7 ID Q9TSD7 PRELIMINARY; PRT; 134 AA.
AC Q9TSD7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 5
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandegrift E., Hughes K.J., O'Reilly K.L.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068770; AAC27616.1; -.
DR HSSP; P05113; IHUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15176 MW; 9A118B78F8CAC820 CRC64;

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Query Match 82.88; Score 505; DB 6; Length 134;
Best Local Similarity 84.18; Pred. No. 3.5e-45;
Matches 95; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETLLSTHRTWLGDNLMIPTEPNKHQLCIKEVFQGITLKNQTAH 61
|||||
Db 21 AVQSPMRLVAETLLSTHRTWLGDNLMIPTEPNKHQLCIKEVFQGITLKNQTV 80
|||||
Qy 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTP 114
|||||
Db 81 GDAVEKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 133
|||||

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RESULT 4
Q9MYM5 ID Q9MYM5 PRELIMINARY; PRT; 134 AA.
AC Q9MYM5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin-5.
GN IL-5.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20130134; PubMed=10663563;
RA Sylvain H., Matvienko O., Leonchiks A., Alving K., van der Ploeg I.;
RT "Molecular cloning, expression, and purification of pig interleukin-5";
RL Immunogenetics 51:59-64(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Johnsen C.K., Grondahl-Hansen J., Johansen R., Jungersen G.,
RA Heegaard P.M.H.;
RT "Sus scrofa mRNA for interleukin-5";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010088; CAB70611.2; -.
DR HSSP; P05113; IHUL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000186; Interleukin_5.
DR Pfam; PF02025; IL5; 1.
DR PRINTS; PR00432; INTERLEUKINS.
DR ProDom; PD006721; Interleukin_5; 1.
SQ SEQUENCE 134 AA; 15191 MW; B485D562A028A899 CRC64;

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```

Query Match 82.18; Score 501; DB 6; Length 134;
Best Local Similarity 85.18; Pred. No. 9.1e-45;
Matches 97; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETLLSTHRTWLGDNLMIPTEPNKHQLCIKEVFQGITLKNQTAH 61
|||||
Db 21 AVENTMRLVAETLLSTHRTWLGDNLMIPTEPNKHQLCIKEVFQGITLKNQTA 80
|||||
Qy 62 GEAVDKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEWTPES 115
|||||
Db 81 GDAVEKLFQNLISLKEHIERQKRCAGRWRTKFLDYQLQVFLGVINTEW 134
|||||

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RESULT 5
Q8MKH1 ID Q8MKH1 PRELIMINARY; PRT; 134 AA.
AC Q8MKH1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```



DE Interleukin-5.  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.  
OX NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21972723; PubMed=11976788;  
RA Herold J.M., Laverne A., Kazanji M.;  
RT "Molecular cloning, characterization, and quantification of squirrel  
RT monkey (Saimiri sciureus) Th1 and Th2 cytokines";  
RL Immunogenetics 54:20-29(2002).  
DR EMBL; AF294756; AAK92043.1; -.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKIN5.  
DR PRODOM; PD006721; Interleukin\_5; 1.  
SQ SEQUENCE 134 AA; 15210 MW; EAFACCA5DB48767C CRC64;  
  
Query Match 62.6%; Score 382; DB 6; Length 134;  
Best Local Similarity 68.2%; Pred. No. 2.9e-32;  
Matches 75; Conservative 11; Mismatches 24; Indels 0; Gaps 0;  
  
Qy 6 PMRLVAETLTLTLLSHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNTAH 65  
Db 25 PTAALVKETLTLTLLSHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNTAH 65  
Qy 66 DKLFQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTEWTPES 115  
Db 85 EKLQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTEWTPES 134  
  
RESULT 6  
Q9R2C9 PRELIMINARY; PRT; 132 AA.  
AC Q9R2C9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin-5 precursor.  
GN IL-5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Lou M;  
RA Pierrot C.;  
RT "Cloning, expression of rat IL-5 and production of neutralizing  
RT antiserum: comparative study of IL-5 activity expressed in E.coli and  
RT baculovirus system";  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ011299; CA09587.1; -.  
DR HSP; P05113; 1HUL.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKIN5.  
DR PRODOM; PD006721; Interleukin\_5; 1.  
KW Signal.  
FT SIGNAL.  
FT CHAIN.  
SQ SEQUENCE 132 AA; 15191 MW; 81A87CB4C04702B CRC64;  
  
Query Match 53.3%; Score 325; DB 11; Length 132;  
Best Local Similarity 55.8%; Pred. No. 2.7e-26;  
Matches 63; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Qy 2 AVENPMRLVAETLTLTLLSHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNTAH 61  
Db 19 AVEIPMSVTVKTELTLTLLSHRTWIGDGNLMPTPENKNHOLCIKEVFGQIDTLKNTVR 78  
Qy 62 CEAVDKLQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTEWTP 114  
Db 79 GGTVEIPQNLSLKEHIEROKKACGERWVTKFLDYQLVFLGVINTEWTP 131  
  
RESULT 7  
Q9XT92 PRELIMINARY; PRT; 40 AA.  
AC Q9XT92;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Interleukin-5 (Fragment).  
GN IL5.  
OS Smnithopsis macroura (Stripe-faced dunnart).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.  
OX NCBI\_TaxID=9302;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99432005; PubMed=10501836;  
RA Hawken R.J., Maccarone P., Toder R., Marshall Graves J.A.,  
RA Maddox J.F.;  
RT "Isolation and characterization of marsupial IL5 genes";  
RL Immunogenetics 49:942-948(1999).  
DR EMBL; AF064208; AAD37461.1; -.  
DR HSP; P05113; 1HUL.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005137; F:interleukin-5 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000186; Interleukin\_5.  
DR Pfam; PF02025; IL5; 1.  
DR PRINTS; PR00432; INTERLEUKIN5.  
DR PRODOM; PD006721; Interleukin\_5; 1.  
FT NON\_TER 1 40  
FT NON\_TER 1 40  
SQ SEQUENCE 40 AA; 4695 MW; 54B93064203EA70B CRC64;  
  
Query Match 18.0%; Score 109.5; DB 6; Length 40;  
Best Local Similarity 53.8%; Pred. No. 0.00029;  
Matches 21; Conservative 9; Mismatches 8; Indels 1; Gaps 1;  
  
Qy 52 IDTLKNTAHGEAVDKLFQNLSLKEHIEROKKACGER 90  
Db 1 IETLKNQTAEDNVVERIFQNFSLKEHITTKQC-GEK 38  
  
RESULT 8  
Q9MIK0 PRELIMINARY; PRT; 258 AA.  
AC Q9MIK0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Putative bHLH transcription factor).  
GN F2413.60.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nyakatura G., Fartmann B., Dauner D., Steir W., Holland R.,  
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F.,  
RA Salanoubat M.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]

```

RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
RA Jacoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
RT "Basic-helix-loop-helix (bHLH) transcription factors in Arabidopsis
thaliana.";
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (bHLH) FAMILY OF
TRANSSCRIPTION FACTORS.
DR EMBL; AL138655; CAB72168.1; -;
DR EMBL; AF488577; AAM10941.1; -;
DR PIR; T47758; T47758.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SMO0353; HLH; 1.
DR PROSITE; PS00888; HLH_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 258 AA; 29004 MW; 2AE6CBF05422D3E0 CRC64;

Query Match 12.9%; Score 78.5; DB 10; Length 258;
Best Local Similarity 26.8%; Pred. No. 4.6;
Matches 22; Conservative 15; Mismatches 38; Indels 7; Gaps 2;

QY 9 RLVAETLTLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFQID---TLKNQTAHGEA 64
DB 161 KAVANYISTVSATR---LGNENVQISSKIHNFISNLSGLIEDRFLVDMSSRSQ 217

QY 65 VDKLFQNLSLIKHEIRQKRC 86
DB 218 GERLFYTLHLQVKEIKYKLC 239

RESULT 9
ID O96575 PRELIMINARY; PRT; 158 AA.
AC O96575;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaposome-associated protein SNAP-25-2 (fragment).
GN SNAP-2.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9259578; PubMed=10327594;
RX Uchard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
RT variability in the cockroach Leucophaea maderae";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
DR EMBL; AF091599; AAC69875.1; -;
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SMC0337; t_SNARE; 1.
DR PROSITE; PSS0192; t_SNARE; 1.
FT NON_TER
SQ SEQUENCE 158 AA; 17926 MW; 6ABE26EBA70D0358 CRC64;

Query Match 12.5%; Score 76.5; DB 5; Length 158;
Best Local Similarity 24.0%; Pred. No. 4.2;
Matches 23; Conservative 16; Mismatches 32; Indels 25; Gaps 3;

QY 2 AVENPMRLVAETLTLLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFQIDTLKNQTAH 61
DB 76 AREDEMEENVQVNTMIGLNRLNAIDMGSEL-----ENQNRQ-----IDRIKNAES 122

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QY 62 GEAVDKLFQNLSLIKHEIRQKRCAGERWRVTKFL 97
DB 123 NE-----ERHDSRTNKKLNSQFKIQKFI 146

RESULT 10
Q8PUD3 PRELIMINARY; PRT; 292 AA.
ID Q8PUD3;
AC Q8PUD3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MM2402.
GN MM2402.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013483; AAM32098.1; -;
DR InterPro; IPR007160; DUF362.
DR Pfam; PF04015; DUF362; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 292 AA; 31887 MW; 496D34C3BE9B0420 CRC64;

Query Match 12.3%; Score 75; DB 17; Length 292;
Best Local Similarity 27.6%; Pred. No. 12;
Matches 32; Conservative 12; Mismatches 32; Indels 40; Gaps 5;

QY 5 NPMRLVAE-TLTLSTHRTWLIGDGNLMPTPENKNHQLCIKEVFQIDTLKN---QT 59
DB 66 NPGKIIVAEKSMITLDTKE-----VLKKLGLWQV 94

QY 60 AHGEAVDKLFQNLSLIKHEIRQKRCAGERWRVTKFL---DYLQVFLGVINTEWT 112
DB 95 AEGEGVDEILTFDHLKREHVEPEKAYSWPFGFDVPEFLGSVDY-TIALPVIKHTWT 149

RESULT 11
Q9MIK1 PRELIMINARY; PRT; 253 AA.
ID Q9MIK1;
AC Q9MIK1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Putative bHLH transcription factor).
GN F2413.50.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Quettier F.,
RA Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

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[3]
RN SEQUENCE FROM N.A.
RP Jakoby M.J., Heim M.A., Bailey P., Martin C., Weisshaar B.;
RA "Basic-helix-loop-helix (bHLH) transcription factors in Arabidopsis
RT thaliana.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (bHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
DR EMBL; AL138655; CAB72167.1; -.
DR EMBL; AF488576; AAM10940.1; -.
DR PIR; T47757; T47757.
DR HSP; P22415; IAN4.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH_1.
DR SMART; SMO0353; HLH; 1.
DR PROSITE; PSS0888; HLH_2; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 253 AA; 28714 MW; 9DE64B574869394A CRC64;

Query Match 12.0%; Score 73.5; DB 10; Length 253;
Best Local Similarity 27.1%; Pred. No. 15;
Matches 23; Conservative 15; Mismatches 34; Indels 13; Gaps 3;

QY 9 RLVAETLLTSLTHTWLGNGNLMIPENKHNQLCIKVEFGQID-----TLKNQTAH 61
D 156 KAVASYLSTVSATR--LGDNEVMQVSSSKIHNFISNVLGGIEEDGFVLVDVSSRSQ 212
QY 62 GEAVDKLFQNLISLKEHIERQKKRC 86
D 213 GE---RLFYTLHLQVENMDYKINC 234

RESULT 12
Q8RVRO PRELIMINARY; PRT; 248 AA.
AC Q8RVRO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MADS-box transcription factor HAM75.
GN HAM75.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Peredovik; TISSUE=flower;
RA Shulga O.A., Skryabin K.G., Angenent G.C.;
RT "Sunflower MADS-box transcription factor HAM75.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF462152; AAL83209.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SMO0432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
SQ SEQUENCE 248 AA; 28526 MW; 7D31DE7670915E0D CRC64;

Query Match 12.0%; Score 73; DB 10; Length 248;

Best Local Similarity 24.1%; Pred. No. 17;
Matches 26; Conservative 24; Mismatches 44; Indels 14; Gaps 4;

QY 8 NRLVAETLLTSLTHTWLGNGNLMIPENKHNQLCIKVEFGQIDTLKNQTAH-----61
D 95 NKLKSRAELLQRNHRHYM-GEIESLSLKEIQNLEQDGLGNIRTKNKLHESISSEL 153
QY 62 ---GEAVDKLFQNLISLKEHIERQKKRCAGE--RRVTKFELDYLOVEL 104
D 154 QKKGKAIQEQ--QNTTLTKKIKERKDKTIPONTQWENHYVDHDTTFL 199

RESULT 13
Q7XRAO PRELIMINARY; PRT; 623 AA.
AC Q7XRAO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNB0085F13.15 protein.
GN OSJNB0085F13.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Ding C.W.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Feng Q.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.Y., Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606620; CAB02768.1; -.
SQ SEQUENCE 623 AA; 67335 MW; A4980874AE0FBA87 CRC64;

Query Match 12.0%; Score 73; DB 10; Length 623;
Best Local Similarity 27.0%; Pred. No. 49;
Matches 31; Conservative 23; Mismatches 43; Indels 18; Gaps 6;

QY 3 VENPMNRLVAETLLTSLTHTWLGNGNLMIPTP---ENKNHQLCIKVEFGQIDTLKNQT 59
D 341 VPHPV--LCTESGRAMASHHSMILEALSAIPEQDEDTTHRLISK--IQDLSKQPRT 396
QY 60 AH----GEAVDKLFQNLISLKEH-IEROX-----KRCAGERWRVTKFELDYLOVF 103
D 397 AHTVNGGGGVDAHSHAVELKKGKGIEMYLKAKLSKRVGTGDANGIYTHMNLVSF 451

RESULT 14
Q921P5 PRELIMINARY; PRT; 661 AA.
AC Q921P5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN SDHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011301; AAH11301.1; -.
DR HSP; P00363; 1KF6.
```

DR MGD; MGI:1914195; Sdha.  
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR0013953; FAD\_bind2.  
DR InterPro; IPR001327; FAD\_Pyr\_redox.  
DR InterPro; IPR003952; FRD/SDH\_FAD\_BS.  
DR InterPro; IPR001100; Pyr\_redox.  
DR InterPro; IPR004112; Succ\_DH flav\_C.  
DR Pfam; PF00890; FAD binding 2; 1.  
DR Pfam; PF02910; succ DH flav\_C; 1.  
DR PRINTS; PR00368; FADPNE.  
DR PRINTS; PR00411; PNDRDTASEI.  
DR PROSITE; PS00504; FRD\_SDH\_FAD\_BINDING; 1.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 661 AA; 72326 MW; 0572C189951983EE CRC64;  
  
Query Match 12.0%; Score 73; DB 11; Length 661;  
Best Local Similarity 26.5%; Pred.No. 53;  
Matches 22; Conservative 17; Mismatches 42; Indels 2; Gaps 2;  
  
QY 32 MIPTPENKNHOLCIKEVFGQIDTLK-NQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGER 90  
DB 559 LVETLEQLNMLCALQTIYGAERKESGAHAREDKYRVDEYDYSKPIQGGQKKPFGEH 618  
QY 91 WRVTKFLDYQLVFLGVINTEWTP 113  
DB 619 WR-KHTLSYVDIKTKVTLRYRP 640  
  
RESULT 15  
Q8K2B3 PRELIMINARY; PRT; 664 AA.  
AC Q8K2B3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Succinate dehydrogenase complex).  
GN Sdha.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognath.; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body, Embryo, Pancreas, and Testis;  
RX MEDLINE=22354683; PubMed=12456851;  
RA The PANTOM Consortium.  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
DR EMBL; BC031849; AAH31849.1; -  
DR EMBL; AK029520; BAC26491.1; -  
DR EMBL; AK034928; BAC28884.1; -  
DR EMBL; AK049590; BAC33821.1; -  
DR EMBL; AK050475; BAC34276.1; -  
DR EMBL; AK075990; BAC36101.1; -  
DR MGD; MGI:1914195; Sdha.  
DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR003953; FAD bind2.  
DR InterPro; IPR001327; FAD\_Pyr\_redox.  
DR InterPro; IPR003952; FRD/SDH\_FAD\_BS.  
DR InterPro; IPR001100; Pyr\_redox.  
DR InterPro; IPR004112; Succ\_DH flav\_C.  
DR Pfam; PF00890; FAD binding 2; 1.  
DR Pfam; PF02910; succ DH flav\_C; 1.  
DR PRINTS; PR00368; FADPNE.

DR PRINTS; PR00411; PNDRDTASEI.  
DR PROSITE; PS00504; FRD\_SDH\_FAD\_BINDING; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 664 AA; 72595 MW; DCE1535163C9449 CRC64;  
  
Query Match 12.0%; Score 73; DB 11; Length 664;  
Best Local Similarity 26.5%; Pred.No. 53;  
Matches 22; Conservative 17; Mismatches 42; Indels 2; Gaps 2;  
  
QY 32 MIPTPENKNHOLCIKEVFGQIDTLK-NQTAHGEAVDKLFQNLSLIKEHIERQKKRCAGER 90  
DB 562 LVETLEQLNMLCALQTIYGAERKESGAHAREDKYRVDEYDYSKPIQGGQKKPFGEH 621  
QY 91 WRVTKFLDYQLVFLGVINTEWTP 113  
DB 622 WR-KHTLSYVDIKTKVTLRYRP 643  
  
Search completed: August 25, 2004, 00:05:33  
Job time : 68.9679 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 290.939 Seconds  
(without alignments)  
8907.036 Million cell updates/sec

Title: US-10-787-382-4  
Perfect score: 610  
Sequence: 1 caaggcaaacactgaacatt.....acagatgaatatatttgag 610

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_29Jan04.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002s.\*  
7: geneseqn2003as.\*  
8: geneseqn2003bs.\*  
9: geneseqn2003cs.\*  
10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610	100.0	610	3	Az55546 Canine in
2	610	100.0	610	3	Az55547 Canine in
3	405.8	66.5	838	3	Az44265 Porcine I
4	402	65.9	402	3	Az55548 Canine in
5	402	65.9	402	3	Az55549 Canine in
6	401.8	65.9	405	4	Aaf74300 Canine in
7	379	62.1	816	3	Aa34857 Human ade
8	379	62.1	816	3	Aa13338 Human int
9	379	62.1	816	3	Aaf20979 Human low
10	379	62.1	816	7	Abz96673 Human nuc
11	379	62.1	816	7	Acf63368 Human int
12	379	62.1	4057	3	Aa34858 Human ade
13	379	62.1	4057	3	Aaf20980 Human low
14	379	62.1	4057	7	Abz96674 Human nuc
15	364.4	59.7	520	2	Aat50755 Ovine IL-
16	345	56.6	345	3	Az55550 Canine ma
17	345	56.6	345	3	Az55551 Canine ma
18	344.2	51.5	399	2	Aat50756 Ovine IL-
19	293.8	48.2	393	4	Aaf74306 Canine in
20	276.6	45.3	858	8	Aal61293 hIL5-P2-P
21	275.6	45.2	402	1	Aan81380 A human B
22	275.6	45.2	858	8	Aal61294 hIL5-P30-
23	252	41.3	252	4	Aaf74305 Canine in

24 249.4 40.9 385 3 AAA43842  
25 232.4 38.1 864 8 AAL61296  
26 232 38.0 370 1 AAN91647  
27 231.4 37.9 864 8 AAL61295  
28 221 36.2 1945 9 ADB53890  
29 217.6 35.7 1533 1 AAN82431  
30 217.6 35.7 1534 2 AAT89013  
31 217.6 35.7 1623 2 AAT14925  
32 217.6 35.7 1623 2 AAV64062  
33 209.6 34.4 481 1 AAN80461  
34 207.4 34.0 377 2 AAV01595  
35 206.4 33.8 399 2 AAV64061  
36 206.4 33.8 402 2 AAT14921  
37 196.4 32.2 348 2 AAT14922  
38 194.6 31.9 342 2 AAT14923  
39 194.2 31.8 339 2 AAT14924  
40 181.4 29.7 375 3 AAC68870  
41 178.6 29.3 357 3 AAC68871  
42 172.2 28.2 381 3 AAC68867  
43 168.6 27.6 375 3 AAC68872  
44 166.4 27.3 399 3 AAC68873  
45 166 27.2 444 3 AAC68875

## ALIGNMENTS

## RESULT 1

AZ55546  
ID AZ55546 standard; cDNA; 610 BP.  
AC  
AC AZ55546;  
DT 14-MAR-2000 (first entry)  
DE Canine interleukin-5 (IL-5) cDNA.  
XX  
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
XX Canis familiaris.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 29..433  
FT /\*tag= a  
FT /product= "Canine IL-5"  
XX  
XX WO9961618-A2.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-C087306P.  
XX  
XX (HESK-) HESKA CORP.

Sim G, Yang S, Dreitz MJ, Wonderling RS;

WPI; 2000-072623/06.

P-PSDB; AAY58219.

Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease.

Claim 1h; Page 223-224; 264pp; English.

Sequences AZ55546-25551 represent cDNA sequences encoding canine interleukin-5 (IL-5). The invention relates to canine IL-4, canine or feline IL-5, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins,

CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targetting

XX Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;

Query Match 100.0%; Score 610; DB 3; Length 610;

Best Local Similarity 100.0%; Pred. No. 2.9e-171; Indels 0; Gaps 0;

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 60

DB 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 60

QY 61 TCTTGGGGCTGCCCTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 120

DB 61 TCTTGGGGCTGCCCTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 120

QY 121 AGAGACCTTGACACTGCTTCCACTCATCGAATTCGCTGATAGGCGATGGAACTGTAT 180

DB 121 AGAGACCTTGACACTGCTTCCACTCATCGAATTCGCTGATAGGCGATGGAACTGTAT 180

QY 181 GATTCTTACTCCTGAAATTAATAATCACTCACTGCTGATTAAGAGAGTTTTCAGGGTAT 240

DB 181 GATTCTTACTCCTGAAATTAATAATCACTCACTGCTGATTAAGAGAGTTTTCAGGGTAT 240

QY 241 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300

DB 241 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300

QY 301 GTCTTTTAATAAGAACACATAGAGCCCAAAAAAGAGTGTGAGGAGAAAGATGGAG 360

DB 301 GTCTTTTAATAAGAACACATAGAGCCCAAAAAAGAGTGTGAGGAGAAAGATGGAG 360

QY 361 AGTGACAAAGTTCCTAGACTACTCTGCAAGTATTTCTTGTGTATATAAACACCGAGTGGAC 420

DB 361 AGTGACAAAGTTCCTAGACTACTCTGCAAGTATTTCTTGTGTATATAAACACCGAGTGGAC 420

QY 421 ACCGAAAGTTGAGAACAAACCGGCTTATTTGTAGTGAAGATTTTGGAGAAAGTGGTTT 480

DB 421 ACCGAAAGTTGAGAACAAACCGGCTTATTTGTAGTGAAGATTTTGGAGAAAGTGGTTT 480

QY 481 TTGGCGATGAGATGAGGCGCAACCAAGTAGTAGGACTTAAATGGCCAGTATAACTTAAGC 540

DB 481 TTGGCGATGAGATGAGGCGCAACCAAGTAGTAGGACTTAAATGGCCAGTATAACTTAAGC 540

QY 541 TTCAGACAAAGTAATAATTTTCAGGCATCCTACTACTTATCATTTCACAGATGAAA 600

DB 541 TTCAGACAAAGTAATAATTTTCAGGCATCCTACTACTTATCATTTCACAGATGAAA 600

QY 601 TATATTTGAG 610

DB 601 TATATTTGAG 610

RESULT 2

ID AA255547/c

XX AA255547 standard; cDNA; 610 BP.

AC AA255547;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA complement.

DE

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX Canis familiaris.  
 XX Key Location/Qualifiers  
 FH complement(178.582)  
 FT /\*tag= a  
 FT /product= "Canine IL-5"  
 XX WO9961618-A2.  
 XX 02-DEC-1999.  
 XX 28-MAY-1999; 98WO-US011942.  
 XX 29-MAY-1999; 98US-0087306P.  
 XX (HESK-) HESKA CORP.  
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX WPI; 2000-072623/06.  
 XX P-PSDB; AA558219.  
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 PT Claim 1h; Page 224-225; 264pp; English.  
 CC Sequences AA255546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targetting

SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;

Query Match 100.0%; Score 610; DB 3; Length 610;

Best Local Similarity 100.0%; Pred. No. 2.9e-171; Indels 0; Gaps 0;

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 60

DB 610 CAAGGCAAACTGAACTTTCAGAGCTATGAGAACTCTCTGAAATTTGAGTTTGTCTAGC 551

QY 61 TCTTGGGGCTGCCCTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 120

DB 550 TCTTGGGGCTGCCCTATGTTTCTGCTTTGCTGTAGAAATCCCATGAATAGCTGTGGC 491

QY 121 AGAGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGAACTGTAT 180

DB 490 AGAGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGAACTGTAT 431

QY 181 GATTCTTACTCCTGAAATTAATAATCACTCACTGCTGATTAAGAGAGTTTTCAGGGTAT 240

DB 430 GATTCTTACTCCTGAAATTAATAATCACTCACTGCTGATTAAGAGAGTTTTCAGGGTAT 371

QY 241 AGACACATTTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300

Db 370 AGACATTTGAAGAACCAAACTGCCACGGGAGGCTGGGATAAATATTTCCAAACTT 311  
QY 301 GTCTTTTAATAAAGAAACACATAGAGCGCCAAAGGAGGTTGTCAGGAGAAAGATGGAG 360  
Db 310 GTCTTTTAATAAAGAAACACATAGAGCGCCAAAGGAGGTTGTCAGGAGAAAGATGGAG 251  
QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACAACCGAGTGGAC 420  
Db 250 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACAACCGAGTGGAC 191  
QY 421 ACCGGAAAGTTGAGAACAAACCGGCTTATTTAGTGGAAAGATTTTGGAGAAAGATGGTTT 480  
Db 190 ACCGGAAAGTTGAGAACAAACCGGCTTATTTAGTGGAAAGATTTTGGAGAAAGATGGTTT 131  
QY 481 TTTGGCGATGAGAAATGAGGGCCAAACACAGTAGGAGCTTAATGGCCAGTATACTAAGC 540  
Db 130 TTTGGCGATGAGAAATGAGGGCCAAACACAGTAGGAGCTTAATGGCCAGTATACTAAGC 71  
QY 541 TTCAGAGACAAAGTAATAATTTTCAGGCATCCTACTACTTTATTCACCTTCACAGATGAAA 600  
Db 70 TTCAGAGACAAAGTAATAATTTTCAGGCATCCTACTACTTTATTCACCTTCACAGATGAAA 11  
QY 601 TATATTTGAG 610  
Db 10 TATATTTGAG 1

RESULT 3  
AAZ44265  
ID AAZ44265 standard; DNA; 838 BP.  
AC AAZ44265;  
XX  
DT 31-MAR-2000 (first entry)  
XX  
DE Porcine IL-5 DNA.  
XX  
KW Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;  
KW tenial cysticercosis; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.  
XX  
OS Sus scrofa.  
XX  
XX CN1231339-A.  
XX  
XX 13-OCT-1999.  
XX  
XX 29-JAN-1999; 99CN-00113447.  
XX  
XX 29-JAN-1999; 99CN-00113447.  
XX  
XX (JYTW-) UNIV NO 2 MILITARY MEDICAL PLA.  
XX  
XX Sun S, Dai J;  
XX  
XX WPI; 2000-087904/08.  
XX  
XX Nucleic acid vaccine for cysticercosis co-contracted by human and pig.  
XX  
XX Claim 3; Page 9; 21pp; Chinese.

This invention describes a novel nucleic acid vaccine for preventing and curing human and pork cysticercosis. The invention involves the formation of a eukaryotic expression plasmid from fusion transcript expression unit consisting of three protective antigen genes (cC1, cC3 and cC4) of pig tenial cysticercosis and coexpression unit of related cell factor gamma interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The production and purification process of said nucleic acid vaccine is simple and convenient, the physical and chemical properties of the vaccine are stable, and the vaccine is easy to store and transport, and possesses effective immunological protective function for human and pig cysticercosis. This sequence represents the pig IL-5 gene used in the method of the invention

XX Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;  
SQ  
Query Match 66.5%; Score 405.8; DB 3; Length 838;  
Best Local Similarity 84.8%; Pred. No. 2.2e-110;  
Matches 498; Conservative 0; Mismatches 67; Indels 22; Gaps 3;  
QY 1 CAAGCGCAACACTGAAACATTTTCAGAGCTATGAGAAATCTTCTGAAATTTGAGTTTGCCTAGC 60  
Db 17 CAAGCGCAACACTGAGCAATTTGAGAGCATGAGAAATCTTCTGCAATTTGAGTTTGCCTAGC 76  
QY 61 TCTTGGGCTGCCTATGTTTCTGCTTTTGTGTAGAAAAATCCCATGAAATAGATGCTGTGGC 120  
Db 77 TCTTGGGCTGCCTATGTTTCTGCAATTTGTAACAAAGTCCCATGAAATAGATGCTGTGGC 136  
QY 121 AGAGACCTTGACACTGCTCTCCACTCATCGAATCTGCTGATAGCCGATGGAAACCTGAT 180  
Db 137 AGAGACCTTTGCACTGCTCTCCACTCATCGAATCTGCTGATAGCCGATGGAAACCTGAT 196  
QY 181 GATTCCTACTCTCTGAAATAAATAAATCAACCACTGTGCATTAAGAAGTTTTTTCAGGGTAT 240  
Db 197 GATTCCTACTCTCTGAAACATCAATCAACCACTGTGCATTAAGAAGTTTTTTCAGGGTAT 256  
QY 241 AGACACATTTGAAGAACCAACTGCCACGGGAGGCTGTGGATRAAACTATTTCCAAACTT 300  
Db 257 AGACACATTTGAAGAAATCGCACTGTGCCGGGGGATGCTGTGAAAGGTTTTTCCGAAACTT 316  
QY 301 GTCCTTAATAAAGAAACACATAGAGCGCCAAAGGAGGTTGTCAGGAGAAAGATGGAG 360  
Db 317 GTCCTTAATAAAGAAACACATAGAGCGCCAAAGGAGGTTGTCAGGAGAAAGATGGAG 376  
QY 361 AGTGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACAACCGAGTGGAC 420  
Db 377 AGTAAAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACAACCTGAGTGGAC 436  
QY 421 ACCGGAAGTTGAGAACCAACCGGCTTATTTAGTGGAAAGATTTTGGAGAAAGAA----- 474  
Db 437 AATGAAAGTTGAGATGAATGAATGAACTGGGTTATTCAGTGAAGATTTCTGTAGGAGAGAGAA 496  
QY 475 -TGGTTTTTGGCGATGAGAAATGAGGGCCAAACCAACAGTAGGAGCTTAATGGCCAGTATA 533  
Db 497 TCTTATTTTTCGAATGAGAAATGAGGGCCAAAC-----AAGGTCAGTGTGA 542  
QY 534 ACTAAGCTTCAGAGACAAAGTAATAATTTTCAGGCATCCTACTACTTTT 580  
Db 543 ATTAACCTCAGATGCAAAAG-CAATTTTTCAGGCATCCTACTACTTTT 588

RESULT 4  
AAZ55548  
ID AAZ55548 standard; cDNA; 402 BP.  
XX  
XX AC AAZ55548;  
XX  
XX 14-MAR-2000 (first entry)  
XX  
XX Canine interleukin-5 (IL-5) cDNA coding region.  
XX  
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
XX Canis familiaris.  
XX  
XX WO9961618-A2.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-0087306P.  
XX  
XX (HESK-) HESKA CORP.  
XX

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX WPI: 2000-072623/06.  
 DR P-PSDB; AAY58219.  
 XX  
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 XX Claim 1h; Page 225; 264pp; English.  
 PS  
 CC Sequences AA255546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX  
 SQ Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;  
 Query Match 65.9%; Score 402; DB 3; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGCTGCCCTATGTTCTGCTTT 88  
 DB 1 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGCTGCCCTATGTTCTGCTTT 60  
 QY 89 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
 DB 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
 QY 149 CGAATTTGGCTGTAGCGGATGGAACTTGATGATCTTCTGAAATTAATATCAT 208  
 DB 121 CGAATTTGGCTGTAGCGGATGGAACTTGATGATCTTCTGAAATTAATATCAT 180  
 QY 209 CAATGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 268  
 DB 181 CAATGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
 QY 269 GGGAGGCTGTGATTAACATTTCCAACTTCTTTAATAAAGAACACATAGAGCG 328  
 DB 241 GGGAGGCTGTGATTAACATTTCCAACTTCTTTAATAAAGAACACATAGAGCG 300  
 QY 329 CAAAAAAGAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388  
 DB 301 CAAAAAAGAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
 QY 389 GTATTCTTGGTGTATTAACACCCGATGGACACCGGAAAGT 430  
 DB 361 GTATTCTTGGTGTATTAACACCCGATGGACACCGGAAAGT 402  
 RESULT 5  
 AA255549/c  
 ID AA255549 standard; cDNA; 402 BP.  
 XX  
 AC AA255549;  
 XX  
 DT 14-MAR-2000 (first entry)  
 XX  
 XX Canine interleukin-5 (IL-5) cDNA coding region complement.

XX  
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO9961618-A2.  
 XX  
 PD '02-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-US011942.  
 XX  
 PR 29-MAY-1998; 98US-0087306P.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX WPI: 2000-072623/06.  
 DR P-PSDB; AAY58219.  
 XX  
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 PS Claim 1h; Page 226; 264pp; English.  
 XX  
 CC Sequences AA255546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX  
 SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;  
 Query Match 65.9%; Score 402; DB 3; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-109;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGCTGCCCTATGTTCTGCTTT 88  
 DB 402 ATGAGATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGCTGCCCTATGTTCTGCTTT 343  
 QY 89 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
 DB 342 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 293  
 QY 149 CGAATTTGGCTGTAGCGGATGGAACTTGATGATCTTCTGAAATTAATATCAT 208  
 DB 282 CGAATTTGGCTGTAGCGGATGGAACTTGATGATCTTCTGAAATTAATATCAT 223  
 QY 209 CAATGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 268  
 DB 222 CAATGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 163  
 QY 269 GGGAGGCTGTGATTAACATTTCCAACTTCTTTAATAAAGAACACATAGAGCG 328  
 DB 162 GGGAGGCTGTGATTAACATTTCCAACTTCTTTAATAAAGAACACATAGAGCG 103  
 QY 329 CAAAAAAGAGGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388



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Db 102 CAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 43
Qy 389 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 430
Db 42 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGT 1
RESULT 6
AAF74300
ID AAF74300 standard; DNA; 405 BP.
XX AAF74300;
AC AAF74300;
DT 04-MAY-2001 (first entry)
DE Canine interleukin-5 coding sequence #1.
XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW inflammatory reaction; ds.
XX Canis sp.
XX WO200111049-A2.
PN 15-FEB-2001.
PD 09-AUG-2000; 2000WO-US021651.
XX 10-AUG-1999; 99US-00371615.
XX (IDEX-) IDEXX LAB INC.
PA Guo H, Lawton R, Mermer B, Aliyappa AP;
XX WPI; 2001-191542/19.
DR P-PSDB; AAB72615.
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT generating antibodies which are useful in treating allergies in dogs.
XX Claim 31; Page 46; 48pp; English.
XX The present invention provides the protein and coding sequences of the
CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
CC cancer and inflammatory reactions in dogs. The present sequence is one
CC version of the IL-5 coding sequence shown in the specification
XX Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;
SQ Query Match 65.9%; Score 401.8; DB 4; Length 405;
Best Local Similarity 99.5%; Pred No. 2.6e-109;
Matches 403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 29 ATGAGATGCTTCTGAATTTGAGTTTCTAGTCTTGGGCTGCCTATGTTTCTGCCTTT 88
Db 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGTCTTGGGCTGCCTATGTTTCTGCCTTT 60
Qy 89 GCTCTAGAAATCCCATGATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 148
Db 61 GCTCTAGAAATCCCATGATAGACTGGTGGCAGACCTTGACATGCTCTCCACTCAT 120
Qy 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTACTCTGAAAAATAAAATCAC 208
Db 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTACTCTGAAAAATAAAATCAC 180
Qy 209 CAACCTGTCATTAAGAAGTTTTTCAGGGTATAGACACATTAAGACCAACTGCCAC 268
Db 181 CAACCTGTCATTAAGAAGTTTTTCAGGGTATAGACACATTAAGACCAACTGCCAC 240
Qy 269 GGGGAGGCTGGGTAACATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328
Db 241 GGGGAGGCTGGGTAACATTTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
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Qy 329 CAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 388
Db 301 CAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360
Qy 389 GTATTTCTTGGTGTATATAACACCGAGTGGACACCGGAAAGTTGA 433
Db 361 GTATTTCTTGGTGTATATAACACCGAGTGGACAAATGGAAGTTGA 405
RESULT 7
AAA34857
ID AAA34857 standard; DNA; 816 BP.
XX AAA34857;
AC AAA34857;
DT 28-JUL-2000 (first entry)
DE Human adenosine receptor related polynucleotide SEQ ID NO:2546.
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
XX WO200009525-A2.
PN 24-FEB-2000.
PD 03-AUG-1999; 99WO-US017712.
XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
PA Nyce JW;
PI WPI; 2000-205971/18.
DR New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX Disclosure; Page 716; 1343pp; English.
PS The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
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CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
 Query Match 62.1%; Score 379; DB 3; Length 816;  
 Best Local Similarity 79.1%; Pred. No. 2.1e-102;  
 Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;  
 QY 2 AAGCAACACCTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 61  
 DB 18 AAGCAACACGAGACGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTGCTAGCT 77  
 QY 62 CTTGGGGTGCCTATGTTTCTGCTTTGCTGTGAAATCCCATGATAGACTGGTGGCA 121  
 DB 78 CTTGGAGTGCCTACGTGTATGCCATCCACAGAAATTCCTCAAGTGCATTGGTGA 137  
 QY 122 GAGACCTTGACATGCTCTCCACTATCGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 181  
 DB 138 GAGACCTTGGCAGCTGCTTTCTACTATCGAACTCTGCTGATAGCAATGAGACTCTCAGG 197  
 QY 182 ATTCCTACTCTGAAAATAAAATCACCACCTGTGCATTAAGAAAGTTTTCAGGGTATA 241  
 DB 198 ATTCCTGTCTGTACATAAAATCACCACCTGTGCATTAAGAAATCTTTCAGGGAATA 257  
 QY 242 GACACATTAAGAACCAAACTGCCCGGAGGCTGTGGATAACTATTCCTCAAACTTG 301  
 DB 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGCTACTGTGAAAGACTATTTCAAAACCTTG 317  
 QY 302 TCTTTAATAAAGAACACATAGAGCGCAAAAGGTTGTGAGAGAAAGATGGAGA 361  
 DB 318 TCTTTAATAAAGAAATACATTTGCGGCCAAAGAAAGTTGTGAGAGAAAGACGAGA 377  
 QY 362 GTGCAAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGACA 421  
 DB 378 GTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTTGGTGTATTAAGAACCGAGTGGATA 437  
 QY 422 CCGAAAAGTTGAGAACAAACCGGCTTATTTAGTGGAGAGATTTTGGAGAGAAATG--GTT 479  
 DB 438 ATAGAAAGTTGAGACTAACTGTTTGTTCAGCCAAAGATTTTGGAGAGAGAGACATT 497  
 QY 480 TTTTGGCGATGAGAAATGAGGGCCAAACACAGTAGGCACTTAATGGCCAGTATACTAAG 539  
 DB 498 TTACTGCAGTGAGAAATGAGGGCCAAAGAGAGTCAAGCCCTTAATTTTCAATATAATTA 557  
 QY 540 CTTTCAGAGACAAAGTAATATTTTCAGGCATCTACTACTATCA 584  
 DB 558 CTTTCAGAGGAAAGTAATATTTTCAGGCATCTACTACTATCA 602

## RESULT 8

AA13338  
 ID AAA13338 standard; cDNA; 816 BP.  
 XX  
 AC AAA13338;  
 XX  
 DT 25-JUL-2000 (first entry)  
 XX  
 DE Human interleukin-5 (IL-5) nucleotide sequence.  
 XX  
 KW Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;  
 KW antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;  
 KW allergic conjunctivitis; inhibitor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6048726-A.  
 XX  
 PD 11-APR-2000.  
 XX  
 PF 15-MAY-1998; 98US-00079839.  
 XX

PR 15-MAY-1998; 98US-00079839.  
 XX (WELT/) WELTMAN J K.  
 PA (KARI/) KARIM A S.  
 XX  
 PI Weltman JK, Karim AS;  
 XX  
 DR WPI; 2000-302784/26.  
 XX  
 PT Oligonucleotide comprising non-natural internucleoside linkage, useful  
 PT for inhibiting interleukin-5 expression and treating inflammatory  
 PT diseases, asthma, allergic rhinitis, allergic conjunctivitis.  
 XX  
 PS Disclosure; Col 3-4; 11pp; English.  
 XX  
 CC This sequence represents the human interleukin-5 (IL-5) encoding  
 CC nucleotide sequence. Interleukin-5 is involved in eosinophilic  
 CC inflammation and inflammatory disorders. The present invention relates to  
 CC an IL-5 antisense oligonucleotide (see AAI3337) which inhibits the  
 CC expression of IL-5. The antisense oligonucleotide has at least one non-  
 CC natural internucleoside linkage. The oligonucleotide is able to inhibit  
 CC IL-5 secretion in a dose dependent manner, and is useful for inhibiting  
 CC IL-5 expression and therefore treating inflammatory diseases, asthma,  
 CC allergic rhinitis, allergic conjunctivitis and inflammatory skin diseases  
 CC such as eczema  
 XX  
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
 Query Match 62.1%; Score 379; DB 3; Length 816;  
 Best Local Similarity 79.1%; Pred. No. 2.1e-102;  
 Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;  
 QY 2 AAGCAACACCTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 61  
 DB 18 AAGCAACACGAGACGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTGCTAGCT 77  
 QY 62 CTTGGGGTGCCTATGTTTCTGCTTTGCTGTGAAATCCCATGATAGACTGGTGGCA 121  
 DB 78 CTTGGAGTGCCTACGTGTATGCCATCCACAGAAATTCCTCAAGTGCATTGGTGA 137  
 QY 122 GAGACCTTGACATGCTCTCCACTATCGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCT 181  
 DB 138 GAGACCTTGGCAGCTGCTTTCTACTATCGAACTCTGCTGATAGCAATGAGACTCTCAGG 197  
 QY 182 ATTCCTACTCTGAAAATAAAATCACCACCTGTGCATTAAGAAAGTTTTCAGGGTATA 241  
 DB 198 ATTCCTGTCTGTACATAAAATCACCACCTGTGCATTAAGAAATCTTTCAGGGAATA 257  
 QY 242 GACACATTAAGAACCAAACTGCCCGGAGGCTGTGGATAACTATTCCTCAAACTTG 301  
 DB 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGCTACTGTGAAAGACTATTTCAAAACCTTG 317  
 QY 302 TCTTTAATAAAGAACACATAGAGCGCAAAAGGTTGTGAGAGAAAGATGGAGA 361  
 DB 318 TCTTTAATAAAGAAATACATTTGCGGCCAAAGAAAGTTGTGAGAGAAAGACGAGA 377  
 QY 362 GTGCAAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCGAGTGGACA 421  
 DB 378 GTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTTGGTGTATTAAGAACCGAGTGGATA 437  
 QY 422 CCGAAAAGTTGAGAACAAACCGGCTTATTTAGTGGAGAGATTTTGGAGAGAAATG--GTT 479  
 DB 438 ATAGAAAGTTGAGACTAACTGTTTGTTCAGCCAAAGATTTTGGAGAGAGAGACATT 497  
 QY 480 TTTTGGCGATGAGAAATGAGGGCCAAACACAGTAGGCACTTAATGGCCAGTATACTAAG 539  
 DB 498 TTACTGCAGTGAGAAATGAGGGCCAAAGAGAGTCAAGCCCTTAATTTTCAATATAATTA 557  
 QY 540 CTTTCAGAGACAAAGTAATATTTTCAGGCATCTACTACTATCA 584  
 DB 558 CTTTCAGAGGAAAGTAATATTTTCAGGCATCTACTACTATCA 602

RESULT 9  
ID AAF20979 standard; DNA; 816 BP.  
XX AAF20979;  
XX AAF20979;  
XX 14-MAR-2001 (first entry)  
XX Human low adenosine antisense oligonucleotide related sequence #2546.  
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
XX respiratory obstruction; pulmonary obstruction; impeded respiration;  
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
XX pulmonary hypertension; emphysema; pulmonary transplantation; bronchitis;  
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
XX cancer; ss.  
XX Homo sapiens.  
XX W0200062736-A2.  
XX 26-OCT-2000.  
XX 24-MAR-2000; 2000WO-US008020.  
XX 06-APR-1999; 99US-0127958P.  
XX (UVEC-) UNIV EAST CAROLINA.  
XX (NYCE-) NYCE J W.  
XX Nyce JW;  
XX WPI; 2000-679539/66.  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
XX adenosine receptors during metabolism, useful e.g. for treating cancers  
XX and respiratory obstructions.  
XX Disclosure; Page 788; 1592pp; English.  
XX The present invention describes low adenosine (A) content antisense  
XX oligonucleotides and compositions (I) comprising them. In the antisense  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
XX The antisense oligonucleotides and (I) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with  
XX lung/respiratory disorders and malignancies, such as stimulating and  
XX activating peptide factors and transmitters, transcription factors,  
XX immunoglobulins and antibodies, antibody receptors, cytokines and  
XX chemokines, endogenously produced specific and non-specific enzymes,  
XX binding proteins, adhesion molecules and their receptors, cytokine and  
XX chemokine receptors, adenosine receptors, bradykinin receptors, central  
XX nervous system (CNS) and peripheral nervous and non-nervous system  
XX receptors, CNS and peripheral nervous and non-nervous system peptide  
XX transmitters, defensins, growth factors, vasoactive peptides and  
XX receptors, binding proteins and malignancy associated proteins. The  
XX antisense oligonucleotides may be used in this way to treat disorders  
XX including respiratory obstruction (especially pulmonary obstruction  
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
XX surfactant hypoproduction which are associated with a disease or  
XX condition selected from pulmonary vasoconstriction, inflammation,  
XX allergies, asthma, impeded respiration, respiratory distress syndrome  
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,  
XX and/or cancer. AAF19434 to AAF21543 represent human polynucleotide  
XX fragments and antisense oligonucleotides used in the exemplification of  
XX the present invention

XX Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
SQ Query Match 62.1%; Score 379; DB 3; Length 816;  
Best Local Similarity 79.1%; Pred. No. 2.1e-102;  
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;  
XX 2 AAGCGAAACACTGAAACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCT 61  
XX 18 AAGCGAAACACTGAAACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCT 77  
XX 62 CTTGGGGCTGCTATGTTTCTGCTTCTGCTAGTAAATCCCATGAATAGACTGGTGACA 121  
XX 78 CTTGGAGTGTGCTAGCTGTATGCCATCCCAAGAAATTTCCCAAGTGCATTTGGTGAAA 137  
XX 122 GAGACCTTGGACACTCTCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGGAACCTGATG 181  
XX 138 GAGACCTTGGACACTCTCTCTCTCATCGAACTCTGCTGATAGCAATGAGACTCTGAGG 197  
XX 182 ATTCTTACTCTCTGAAATATAAATCAACCACTGTGCATTAAGAAAGTTTTCAGGGTATA 241  
XX 198 ATTCTTACTCTCTGAAATATAAATCAACCACTGTGCATTAAGAAAGTTTTCAGGGTATA 257  
XX 242 GACACATTTGAAGAACCAAACTGCCCAAGGAGGCTGTGGATAAACTATTCAAAACCTTG 301  
XX 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAAGACTATTCAAAACCTTG 317  
XX 302 TCTTTTAAATAAGAAACACATAGAGCGCCAAAAGAGTGTGCAAGGAAAGATGAGAGA 361  
XX 318 TCTTTTAAATAAGAAATACATTGACGGCCAAAAGAGTGTGGAAAGAAAGACGAGA 377  
XX 362 GTGCAAAAGTTCTTAGACTACTCTGCAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACA 421  
XX 378 GTAAACCAATTCCTTAGACTACTCTGCAAGAGTTTCTTGGTGTAAATAAACACCGAGTGGATA 437  
XX 422 CCGGAAAGTTGAGAAACAAACCGGCTTATTGTAGTGGAAAGTTTTCGAGAAAGAAATG -GTT 479  
XX 438 ATAGAAAGTTGAGACTAAACTGGTTTGTGAGCCAAAGATTTTGGAGGAGAAAGACATT 497  
XX 480 TTTTGGGATGAGATGAGGGCCAAACACAGTAGGACTTAAATGCGCCAGTATACTAAG 539  
XX 498 TTACTGCACTGAGAAATGAGGGCCAAAGAGAGTCAAGGCTTAAATTTTCAATATATATTTAA 557  
XX 540 CTTTCAGAGACAAAGTAAATATTTTCAGGCATCTCTACTCTTTATCA 594  
XX 558 CTTTCAGAGGAAAGTAAATATTTTCAGGCATCTCTACTCTTTGCGCA 602  
RESULT 10  
ID ABZ96673 standard; DNA; 816 BP.  
XX ABZ96673;  
XX 17-OCT-2003 (first entry)  
XX Human nucleic acid sequence.  
XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ublquinone; antiinflammatory; anti-allergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.  
XX Homo sapiens.  
XX W0200285308-A2.  
XX 31-OCT-2002.  
XX 23-APR-2002; 2002WO-US013135.  
XX



CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,  
CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative  
CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,  
CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,  
CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),  
CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,  
CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,  
CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant  
CC melanoma, and malignant nasal polyps. The nutritional supplement is  
CC useful for supplementing the diet of an individual, and the cosmetic  
CC composition is useful for improving the appearance of the skin in an  
CC individual with a skin disorder. ACF63279 to ACF63410 represent  
CC nucleotide sequence given in the exemplification of the present invention  
XX  
SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
  
Query Match 62.1%; Score 379; DB 7; Length 816;  
Best Local Similarity 79.1%; Pred. No. 2.1e-102;  
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;  
  
QY 2 AAGGCAAACTGAAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGATTTGCTAGCT 61  
DB 18 AAGGCAAACTGAAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGATTTGCTAGCT 77  
  
QY 62 CTTGGGCTGCTATGTTTCTGCTTTCGCTTGTGAGAAAATCCCATGATGACTGTGGCA 121  
DB 78 CTTGGAGCTGCTACGTGTATGCTATCCCAAGAAATTTCCCAAGTGCATTTGGTGA 137  
  
QY 122 GAGACCTTGACACTGCTCTCACTCATCGAACTTGGCTGATAGCGATGGACCTGATG 181  
DB 138 GAGACCTTGACACTGCTCTCACTCATCGAACTTGGCTGATAGCGATGGACCTGATG 197  
  
QY 182 ATTCTACTCTCTGAAATATAAAATACCAACTGTGCATTAAGAAATTTTTCAGGATATA 241  
DB 198 ATTCTCTCTCTGTAATAAAATACCAACTGTGCATTAAGAAATTTTTCAGGGAATA 257  
  
QY 242 GACACATTTGAGAACCAAGTCCCGGAGGCTGTGATTAATCTTCCAAACTTG 301  
DB 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGACTATTTCAAAACCTTG 317  
  
QY 302 TCCTTAATAAAGAAACACATAGAGCGCCAAAAAAGGTTGTGAGGAGAAATGAGAGATGAGGA 361  
DB 318 TCCTTAATAAAGAAATACATTGACGGCCAAAAAAGGTTGTGAGGAGAAATGAGAGATGAGGA 377  
  
QY 362 GTGCAAAAGTTCTAGACTACCTGCAAGTATTTCTTGTGTTATTAACACCGAGTGGACA 421  
DB 378 GTAACCAATTTCTAGACTACCTGCAAGTATTTCTTGTGTTATTAACACCGAGTGGATA 437  
  
QY 422 CCGGAAAGTTGAGAACCAACCGGCTTATTTAGTGGAGAGATTTTGGAGAGAAATG--GTT 479  
DB 438 ATGAAAGTTGAGACTAACTAACTGTTTGTTCAGCCCAAGATTTTGGAGGAGAGACATT 497  
  
QY 480 TTTTGGCGATCAGAAATGAGGCGCAACCAAGTGGAGCTTAATGCGCAGTATACTAAG 539  
DB 498 TTACTGCAGTGAAGATGAGGCGCAACCAAGTGGAGCTTAATTTCAATATAATTTAA 557  
  
QY 540 CTTGAGACAAAGTAAATTTTCAGGCACTCTTACTATTATCA 584  
DB 558 CTTGAGGAGGAAGTAAATTTTCAGGCACTCTTACTATTATCA 602

RESULT 12  
AAA34858  
ID AAA34858 standard; DNA; 4057 BP.  
XX  
AC AAA34858;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2547.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 717-718; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasize to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3313 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;

Query Match 62.1%; Score 379; DB 3; Length 4057;  
Best Local Similarity 79.1%; Pred. No. 4.1e-102;  
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;  
  
QY 2 AAGGCAAACTGAAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGATTTGCTAGCT 61  
DB 3259 AAGGCAAACTGAAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGATTTGCTAGCT 3318  
  
QY 62 CTTGGGCTGCTATGTTTCTGCTTTCGCTTGTGAGAAAATCCCATGATGACTGTGGCA 121  
DB 3319 CTTGGAGCTGCTACGTGTATGCCATCCCAAGAAATTTCCCAAGTGCATTTGGTGA 3378  
  
QY 122 GAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGACCTGATG 181  
DB 3379 GAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGACCTGATG 3438

Qy	182	ATTCTCTACTCTGAAATATAAAATTCACCAACTGTGCATTTAAAGAAAGTTTTTTCAGGGTATA	241
Db	3439	ATTCTCTGTCTGTACATAAAATTCACCAACTGTGCATGTGAAGAAATCTTTTCAGGGAATA	3498
Qy	242	GACACATTGAAGAACCAACTGCGCCACGGGGAGGCTGTGGATAAATATTTCCAAAACTTG	301
Db	3499	GGCACACTGGAGAGTCAAACTGTGTCAGGGGGTACTGTGGAAGACATTTCAAAAACTTG	3558
Qy	302	TCCTTTATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAGA	361
Db	3559	TCCTTTATAAAGAAATACATTGACGGCCAAAAAAGGTGTGCAGGAGAAAGACGGAGA	3618
Qy	362	GTGACAAAGTTCTCTAGACTACTCTCCAAGTATTTCTTCGTGTAAATAAACACCGAGTGGACA	421
Db	3619	GTAACCAATTCCTAGACTACTCTCAGAGTTTCTTCGTGTATGTAACACCGAGTGGATA	3678
Qy	422	CCGAAAGTTGAGAACAAACCGGCTTATGTAGTGGAAATTTTGGAGAGAAGATGGTTTT	481
Db	3679	ATAGAAAGTTGAGACTAACTGGTTTGTTCGAGCCAAAGATTTTGGAGGAGAAAGGACATT	3738
Qy	482	TT--GGCGATGAGAAATGAGGGCCCAACCAACAGTAGGGACATTATGCGCCAGTATAACTAAG	539
Db	3739	TTACTGCAGTGAGAAATGAGGCCCAAGAAAGATCGACGCCCTTAATTTTCAATATAATTAA	3798
Qy	540	CTTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTATCA	584
Db	3799	CTTCAGAGGGAAGTAAATATTTTCAGGCATACTGACACTTTGCCA	3843

RESULT 13

RESUL 13  
AAF20980  
ID AAF20980 standard; DNA: 4057 BP.

14-MAR-2001 (first entry)

XX DE Human low adenosine antisense oligonucleotide related sequence #2547:

Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
human; airway disorder; bronchoconstriction; lung inflammation;  
surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
respiratory obstruction; pulmonary obstruction; impeded respiration;  
surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
cancer; ss.

AA  
OS  
Homo sapiens.

AA  
PN  
WO200062736-A2.

26-OCT-2000.

XX  
PF  
24-MAR-2000: 2000WO-US008020.XX  
PR 06-APR-1999: 99IIS-0127958P-XX  
PA (IVEC-) INTV EAST CAROLINA

PA (UYEC-) UNIV EAST  
PA (NYCE/) NYCE J W.

XX  
PT  
NVCB :TW:XX  
DP WPT: 2000-679539/66

XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.

PS Disclosure: Page 788-789: 1592pp: English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;

Query Match 62.1%; Score 379; DB 3; Length 4057;

Best Local Similarity 79.1%; Pred. No. 4.1e-102;

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Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;
```

QY 2 AAGCAAACACTGAACATTTACAGAGCTATGAGAACTTCTGAATTTGAGTTTCCTAGCT 61

Db 3259 AAGGCAAACGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTGAGTTTGCTAGCT 3318

QY 62 CTTGGGGCTGCCTATGTTTCTGCCTTTGCTGTAGAAATCCCATGAAATAGACTGGTGGCA 121

Db 3319 CTTGGAGCTGCC<sup>T</sup>ACGTGTATGCCATCCCCACAGAAATTCCCACAAGTGCA<sup>T</sup>TGGTGAA 3378

QY 122 GAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGGATGGGAACCTGATG 181

Db 3379 GAGACCTGGCACTGCTTTCTACTCATCGAACTCTGCTGATAGCCAAATGAGACTCTGAGG 3438

QY 182 ATTCTACTCCTGAAAATAAAAATCACCACTGTGCATTAAAGAAGTTTTTCAGGTATA 241

Db 3439 ATTCCTGTTCCGTACATAAAATCACCAACTGTGCACTGAAGAAATCTTTCAGGGAATA 3498

242 GACACATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAACTTG 301

Db 3499 GGACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAACTTG 3558

302 TCTTTAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAGA 361

D<sub>b</sub> 3559 TCCTTAATAAGAAATACATTGACGGCCAAAAAAGTGTGGAGAAGAAAGACGGAGA 3618

362 GTGACAAAGTTCCTAGACTACCTGCAAGTATTCTTGGTGTAATAAACACCGAGTGGACA 421

D<sub>b</sub> 3619 GTAAACCAATTCCTAGACTACCTGCAAGAGTTTCTTGGTGTAATGAACACCGAGTGGATA 3678

422 CCGGAAAGTTGAGAACAAAACCGGCTTATTGTAGTGGAGAGATTTTGGAGGAAGAAATGGTTTT 481

3679 ATACAGCCTTACGCTACCTGTTCTTCCGCCAGAGATTGGAGGAGAGGACATT 3738

482 TT--GGCGATGAGGAATGAGGGCCACCAACAGTAGGGGACTTAATGGCCAGTATACTAAG 539

3739 TTACTGCGTGAGAAATGAGGGCCAGAAAGAGTCAGGCCCTTAAATTTTCAATATAATTTAA 3798

QY	540	CTTCAGAGCAAGTAATTTTCAGGCATCTCTACTACTATTATCA	584
DB	3799	CTTCAGAGCAAGTAATTTTCAGGCATCTCTACTACTATTATCA	3843
RESULT 14			
ID	ABZ96674		
XX	ABZ96674 standard; DNA; 4057 BP.		
XX	ABZ96674;		
CC	17-OCT-2003 (first entry)		
DT	Human nucleic acid sequence.		
DE	Human; antisense; lung dysfunction; nasal airway dysfunction;		
XX	antiinflammatory steroid; ubiquinone; antiinflammatory; anti allergic;		
KW	antiinflammatory steroid; ubiquinone; immunosuppressive; gene therapy;		
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;		
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;		
KW	lung inflammation; respiratory disease; ds.		
OS	Homo sapiens.		
XX	WO200285308-A2.		
PN	31-OCT-2002.		
PD	23-APR-2002; 2002WO-US013135.		
XX	24-APR-2001; 2001US-0286137P.		
PF	(EPIC-) EPIGENESIS PHARM INC.		
XX	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;		
PI	Miller S, Tang L, Shahabuddin S;		
PT	WPI; 2003-229219/22.		
PT	Pharmaceutical composition for treating ailments associated with impaired		
PT	respiration, has oligo(s) antisense to specific gene(s) or its		
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or		
PT	ubiquinone.		
XX	Disclosure; SEQ ID NO 11916; 872pp; English.		
XX	The invention relates to a novel pharmaceutical composition, which has a		
CC	first active agent comprising an oligonucleotide antisense to the		
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,		
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of		
CC	junctions of genes encoding a polypeptide associated with lung and/or		
CC	nasal airway dysfunction and a second active agent comprising an		
CC	antiinflammatory steroid and ubiquinone. A composition of the invention		
CC	has antiinflammatory, anti allergic, antiasthmatic, hypotensive,		
CC	immunosuppressive, and cytostatic activity. The composition may have a		
CC	use in antisense gene therapy. The composition is useful for treating or		
CC	preventing a respiratory, lung or malignant disease or condition, also		
CC	for enhancing the prophylactic or therapeutic respiratory effect of an		
CC	antiinflammatory steroid in a subject, for reducing or depleting levels		
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine		
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or		
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,		
CC	lung inflammation, lung allergies, or a respiratory disease or condition.		
CC	Note: The sequence data for this patent is not represented in the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences		
XX	Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;		
SQ	Query Match		
	Best Local Similarity 62.1%; Score 379; DB 7; Length 4057;		
	Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;		

QY	2	AAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGATGATTTGAGTTTCTAGCT	61
DB	3259	AAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGATGATTTGAGTTTCTAGCT	3318
QY	62	CTTGCGGCTGCTATGTTTCTGCTTGTAGAAAATCCCATGGAATAGACTGGTGCA	121
DB	3319	CTTGCGGCTGCTATGTTTCTGCTTGTAGAAAATCCCATGGAATAGACTGGTGCA	3378
QY	122	GAGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGAACTGATG	181
DB	3379	GAGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGAACTGATG	3438
QY	182	ATTCTACTCTCTGAAAATATAAATCAGCAACTGTCATTAAGAAAGTTTTTCAGGGTATA	241
DB	3439	ATTCTACTCTCTGAAAATATAAATCAGCAACTGTCATTAAGAAAGTTTTTCAGGGTATA	3498
QY	242	GACCATTTGAAGAACCAACTGCTCCACGGGAGGCTGTGATATAAACTATTCCAAAACCTTG	301
DB	3499	GCCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAGCTATTCAAAAACCTTG	3558
QY	302	TCCTTAATAAAGAACACATAGACGGCCCAAAAAAGGTTGTCAGGAGAAAGATGGAGA	361
DB	3559	TCCTTAATAAAGAACACATAGACGGCCCAAAAAAGGTTGTCAGGAGAAAGATGGAGA	3618
QY	362	GTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGTATAATAAACACCGAGTGGACA	421
DB	3619	GTAAACCAATTTCTTAGACTACCTGCAAGTATTTCTTGGTGTATAATAAACACCGAGTGGACA	3678
QY	422	CCGGAAGTTGAGAACCAAAACCGGCTTATTGTAGTGGAGATTTTGGGAGAGAAATGGTTTT	481
DB	3679	ATAGAAAGTTGAGACTAAACTGGTTTGTGAGCCAAAGATTTTGGAGGAGAAAGGACATT	3738
QY	482	TT--GGCGATGAGAAATGAGGGCCCAACCAACAGTAGAGGACTTAATGGCCAGTATTAACAAAG	539
DB	3739	TTACTGCACTGAGAAATGAGGGCCCAAGAGAGTACAGGCTTAATTTCAATATAATTAA	3798
QY	540	CTTCAGAGCAAGTAATTTTCAGGCATCTCTACTACTATTATCA	584
DB	3799	CTTCAGAGCAAGTAATTTTCAGGCATCTCTACTACTATTATCA	3843
RESULT 15			
ID	AAU50755 standard; DNA; 520 BP.		
XX	AAU50755;		
DT	17-OCT-2003 (revised)		
DT	24-SEP-1997 (first entry)		
XX	Ovine IL-5 gene.		
KW	Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;		
KW	livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;		
KW	immunosuppression; allergy; reproductive system; growth; early maturity;		
KW	antibody; diagnosis; immunopotentiator;		
KW	early haematopoietic progenitor cell; cytotoxic cell; thymocyte;		
KW	secretion; IgM; IGA; bacterial endotoxin; gamma-interferon; ss.		
OS	Ovis aries.		
XX	Location/Qualifiers		
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CDS	/tag= a		
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FT	/tag= b		
FT	/number= 1		
FT	184..216		
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FT	/number= 2		
FT	217..345		
FT	/tag= d		

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FT exon /number= 3
FT 346...480
FT /*tag= e
FT /number= 4
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PN WO9700321-A1.
XX
XX 03-JAN-1997.
XX
XX 14-JUN-1996; 96WO-AU000360.
XX
XX 14-JUN-1995; 95AU-00003502.
PR 27-OCT-1995; 95AU-00006244.
XX
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
XX Seow H, Wood P;
XX
XX WPI; 1997-077528/07.
DR P-PSDB; AAW08479.
XX
XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
XX adjuvants and to treat or prevent microbial infections in livestock.
XX
XX Claim 6; Page 39-40; 78pp; English.
XX
XX The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).
XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in
XX livestock (esp. cows and sheep), particularly where the animals are
XX stressed, e.g. during transport. IL-5 and IL-12 can also be used as
XX adjuvants in vaccines for veterinary use (partic. weakly immunogenic
XX subunit or synthetic peptide vaccines). They may also be used to treat
XX cancer, immunosuppression and allergy, to enhance/suppress the
XX reproductive system and to promote growth or early maturity. Optionally
XX interleukin can be delivered from constructs or delivery cells and
XX antibodies are useful in enzyme immunoassays, for rapid diagnosis of
XX infection. The interleukins are immunopotentiators, especially IL-5
XX promotes growth of early haematopoietic progenitor cells and generation
XX of cytotoxic cells from thymocytes, also it stimulates production and
XX secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12
XX induces production of gamma-interferon by, and proliferation of, T and NK
XX cells and increases the (non-)specific cytolytic lymphocyte response. The
XX genetic constructs can also be used for in vitro production of IL-5 or -
XX 12. (Updated on 17-Oct-2003 to standardise OS field)
XX
XX Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;

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Search completed: August 30, 2004, 21:48:17  
Job time : 292.939 secs

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Query Match 59.7%; Score 364.4; DB 2; Length 520;
Best Local Similarity 83.9%; Pred. No. 4e-98;
Matches 426; Conservative 0; Mismatches 76; Indels 6; Gaps 1;

QY 2 AAGGCAACACTGACATTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTAGCT 61
DB 13 AAGGCAACCTGAACTTTGAGATTCAGAGTCAAGAGATGATCTGGTTTGACCTTTGTAGCT 72
QY 62 CTTGGGGTGCCTATGTTTCTGCTTTGTCTAGAAAATCCCATGAATAGACTGGTGCA 121
DB 73 CTTGGAGCTGCTATGTTTGTGCCAATGCTGTAGAAAGTACCATGAATAGACTGGTGCA 132
QY 122 GAGACCTTGACATGCTCTCCACTCATCGAATCTGGCTGATAGCGGATGGGAACCTGATG 181
DB 133 GAGACCTTGACATGCTCTCCACTCATCGAATCTGGCTGATAGCGGATGGGAACCTGATG 192
QY 182 ATTCTCTACTCTGAAAATAAAATACCAACTGTGCAATTAAGAAAGTTTTCAGGGTATA 241
DB 193 ATTCTCTACTCTGAGCATACAAATCACCAACTATGCAATTAAGAAAGTCTTTCAGGGAATA 252
QY 242 GACACATTGAAGAACCAACTGCCACGGGGAGGCTGTGGNTAAACTATTCCAAAACCTTG 301
DB 253 GACACATTGAAGAAATCAAACTGCACAAGGGGATGCTGTGAAAAAATAATTCGNAACCTTG 312
QY 302 TCTTTAATAAAGAACACATAGAGCCCAAAAAAAGGTGTGCAGGAGAAAGATGGAGA 361

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DB 313 TCTTTAATAAAGAAATACATAGACCTCCAAAAAGGAAGTGTGGAGGAGAAAGATGGAGA 372
QY 362 GTGACAAAAGTTCTCTAGACTACCTGCAAGTATTTCTTGGTCTAATAAAACACCGAGTGGACA 421
DB 373 GTGAAACAATTCCTCGACTACCTGCAAGTATTTCTTGGTGTGATAAACACAGAGTGGACG 432
QY 422 CCGGAAAGTTGAGAACAAACCGGCTTATGTAGTGGAAAGATTTT-----GGAGAAAGAT 475
DB 433 ATGGAAAGCTGAGATCTACCTCTCTCACTGTAGTGAAGTTTCTTGGAGGAGGAGAAAGAT 492
QY 476 GGTTTTGTGGCGATGAGAAATGAGGGCCA 503
DB 493 GTTTTAATTTGAGTCAGAAATGAGGGCCA 520

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 21:24:28 ; Search time 2049.32 Seconds  
(without alignments)  
8888.782 Million cell updates/sec

Title: US-10-787-382-4  
Perfect score: 610  
Sequence: 1 caaggcaaacactgaacatt.....acagatgaataatttgag 610

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_esti.\*  
10: gb\_estc.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_lam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vri.\*  
28: gb\_gssi.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307.8	50.5	456	14	CD559532
C 2	307.2	50.4	456	14	CD559686
C 3	303.4	49.7	470	14	CD559687
4	303.4	49.7	492	14	CD559533

5	301	49.3	478	14	CD559534
6	300.8	49.3	463	14	CD559535
7	299.2	49.0	489	14	CD559536
C 8	293	48.0	467	14	CD559688
C 9	292.4	47.9	473	14	CD559689
C 10	292.2	47.9	467	14	CD559690
11	280.2	45.9	405	29	AY412020
12	278.4	45.6	477	14	CD559608
13	277.8	45.5	622	29	CE331159
14	276.2	45.3	405	29	AY412021
15	195	32.0	399	29	AY412022
C 16	164.8	27.0	503	13	BQ598873
17	48.2	7.9	1201	9	AL550373
C 18	43.8	7.2	1044	13	EX415231
C 19	43.8	7.2	1101	29	CNS017KX
20	42.4	7.0	1025	13	EX441235
21	42.4	7.0	1201	13	EX396080
22	41.8	6.9	432	9	AA560540
23	41.4	6.8	1201	9	AL547091
C 24	40.8	6.7	677	29	CG032226
25	40.6	6.7	522	12	BE670794
C 26	40.6	6.7	1026	13	EX461051
27	40.6	6.7	1201	13	EX387694
28	40.4	6.6	926	28	BH135042
29	40.2	6.6	623	28	AQ576964
30	40.2	6.6	666	28	AQ326668
31	40.2	6.6	1159	13	EX394939
32	40.2	6.6	1201	13	EX461310
33	40	6.6	317	14	CD087271
34	40	6.6	711	29	CC080466
35	40	6.6	1101	29	CNS0182P
36	39.8	6.5	535	28	AZ370501
C 37	39.8	6.5	565	28	AZ650499
38	39.6	6.5	1201	13	EX334478
C 39	39.4	6.5	1101	29	CNS0183C
40	39.2	6.4	603	12	BJ328562
41	39.2	6.4	619	12	BJ328648
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43	39.2	6.4	905	29	CNS00D59
44	39	6.4	843	28	BH085356
C 45	39	6.4	948	14	CD242046

ALIGNMENTS

RESULT 1  
CD559532  
LOCUS  
DEFINITION  
AGENCY: 14497057 NIH\_MGC 195 Homo sapiens cDNA clone  
IMAGE: 6971772 5', mRNA sequence.  
ACCESSION  
CD559532  
VERSION  
EST.  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CD559532 456 bp mRNA linear EST 11-JUN-2003  
AGENCY: 14497057 NIH\_MGC 195 Homo sapiens cDNA clone  
IMAGE: 6971772 5', mRNA sequence.

CD559532.1 GI:31585600  
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgs.nci.nih.gov/

1 (bases 1 to 456)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NTH

Bldg. 31 Em10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:



QY 246 CATTGAAGAACCAACTGCCACGGGAGGCTGTGATTAACATATTCAAAACCTTGCTTT 305  
 Db 216 CACTGGAGAGTCAAACTGTCAAGGGGGTACTGTGGAAGACTATTCAAAACCTTGCTTT 157  
 QY 306 TAATAAAGACACATAGAGCCCAAAAAAAGGTGTGCAGGAAGATCGAGAGTGA 365  
 Db 156 TAATAAAGAAATACATTGACGGCCAAAAAAGGTGTGGAAGAAAGACGAGAGTAA 97  
 QY 366 CAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACACCGAGTGCACCGG 425  
 Db 96 ACCAATTCCTAGACTACCTGCAAGAGTTTCTTGTTGTAATAAACACCGAGTGCATAATAG 37  
 QY 426 AAGTTGAGACAAACCGGCTATTCTAGTGGAGA 461  
 Db 36 AAGTTGAGACTAACTGGTTGTTGTCAGCCAAAGA 1

RESULT 3  
 CD559687/c  
 LOCUS  
 DEFINITION  
 AGENCOURT\_14497029 NIH\_MGC\_195 Homo sapiens cDNA clone  
 IMAGE:6971771 5', mRNA sequence.  
 CD559687  
 CD559687.2 GI:38453484  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 470)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585755.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat

CDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: IRBK1 row: 5 column: 10  
 High quality sequence start: 14  
 High quality sequence stop: 470.

## FEATURES

Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGE:6971771"  
 /tissue\_type="mixed"  
 /lab\_host="DH5A (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 195"  
 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/CiOntech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, MCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at

## ORIGIN

Query Match 49.7%; Score 303.4; DB 14; Length 470;  
 Best Local Similarity 80.5%; Pred. No. 4.3e-64;  
 Matches 355; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
 QY 6 CAAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTTCTGCTAGCTCTTG 65  
 Db 469 CAAACGAGACAGTTTTCAGAGCCCATGAGAGTGTCTTCGCAATTTGAGTTTCTGCTAGCTCTTG 410  
 QY 66 GGGCTGCTATGTTTCTGCTGCTATGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGA 125  
 Db 409 GAGCTGCTAGCTGTATGCCATCCCAAGAAATTTCCCAAGTGCATTGGTGAAGAGAGA 350  
 QY 126 CTTTGACACTGCTCTCCACTCATCGAACTTGGCTGTAGCGGATAGCGGATGGAACTGATGATTC 185  
 Db 349 CTTTGGCACTGCTTCTTACTCATCGAACTCTGCTGTATAGCCCAATGAGACTCTGAGGATTC 290  
 QY 186 CTACTCTGAAAATAAATAATCACCACCTGTGCATTAAGAAGTGTTCAGGGTATAGACA 245  
 Db 289 CTGTTCTCTGTACATAAATAATCACCACCTGTGCATGAAAGAAATCTTCAGGGATAGGCA 230  
 QY 246 CATTGAAGAACCAACTGCCACCGGAGGCTGTGGATAAACTATTCAAAACCTTGCTTT 305  
 Db 229 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGACTATTCAAAAACCTTGCTCT 170  
 QY 306 TAATAAAGACACATAGAGCCCAAAAAAAGGTGTGCAGGAAGATGGAGAGTGA 365  
 Db 169 TAATAAAGAAATACATTGACGGCCAAAAAAGTGTGGAGAAAGAACGCGAGAGTAA 110  
 QY 366 CAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTTGTAATAAACACCGAGTGCACCGG 425  
 Db 109 ACCAATTCCTAGACTACCTGCAAGAGTTTCTTGTTGTAATAAACACCGAGTGCATAATAG 50  
 QY 426 AAGTTGAGACAAACCGGCT 446  
 Db 49 AAGTTGAGACTAAACTGGTT 29

## RESULT 4

CD559533

LOCUS

DEFINITION

AGENCOURT\_14496993 NIH\_MGC\_195 Homo sapiens cDNA clone

IMAGE:6971771 5', mRNA sequence.

CD559533

CD559533.2 GI:38558947

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 492)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585601.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

CDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK1 row: 5 column: 10

High quality sequence start: 14

High quality sequence stop: 492.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES  
source

Location/Qualifiers  
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/clone="IMAGE:6971771"  
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/lab\_host="DH5A (TI phage-resistant)"  
/clone\_lib="NIH\_MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 49.7%; Score 303.4; DB 14; Length 492;  
Best Local Similarity 80.5%; Pred. No. 4.3e-64;  
Matches 355; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 6 CAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTG 65  
DB 33 CAACCGCAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTG 92

QY 66 GGGCTGCTATGTTTCTGCTTCTGCTGTAGAAAATCCCATGATACACTGGTGGCAGAGA 125  
DB 93 GAGCTGCTACGTGTATGCCATCCACAGAAATCCCAAGTGCATTTGGTGAAGAGA 152

QY 126 CTTGACACTGCTCTCAGCTATCGAATCTGGTGTATAGCGGATGGAAACCTGATGATTC 185  
DB 153 CTTGGCACTGCTTCTACTCATCGAACTCTGCTGATAGCAATGAGACTCTGAGGATTC 212

QY 186 CTACTCTGAAATAAATAACCAACTGTCATTAAGAAGTTTTCAGGGTATAGACA 245  
DB 213 CTGTTCTGTACATAAATACCAACTGTGCTGCACTGAAGAAATCTTTCAGGGAATAGGA 272

QY 246 CATTGAAGAACCAACTGCCCGGAGGCTGTGGATAAATATTTCCAAAACCTTGTCTT 305  
DB 273 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACATTTTCAAAAACCTTGTCTT 332

QY 306 TAATAAAGACACATAGACGCCAATAAAGAGTGTGCAGAGAAAGATGAGAGTCA 365  
DB 333 TAATAAAGAAATACATTGACGGCCAAATAAAGTGTGGAGAAGAAAGACCGAGAGTAA 392

QY 366 CAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTGTATAAACACCGAGTGGACACCGG 425  
DB 393 ACCAATTCCTAGACTACCTGCAAGTATTTCTTGGTGTATGAACACCGAGTGGATAATAG 452

QY 426 AAAGTTGAGAACAAACCGGCT 446  
DB 453 AAAGTTGAGACTAAACTGTT 473

RESULT 5  
LOCUS CD559534  
DEFINITION AGENCOURT\_14496928 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971770 5', mRNA sequence.  
ACCESSION CD559534  
VERSION CD559534.2 GI:38558949  
KEYWORDS EST.

SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 478)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585602.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBK1 row: g column: 09

High quality sequence start: 3

High quality sequence stop: 478.

Location/Qualifiers

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/clone\_lib="NIH\_MGC 195"

/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:

loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the

complete open reading frame (based on known gene sequences

available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30

cells lines or pooled total RNA from 10 different tissues

(from BD Biosciences/Clontech and Washington University).

PCR products are directionally cloned into the loxP sites

of the pDNR-Dual vector. Library constructed by Dr.

Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For

information on which gene each clone represents, please

visit our anonymous ftp site at

[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)

a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 49.3%; Score 301; DB 14; Length 478;  
Best Local Similarity 80.1%; Pred. No. 1.7e-63;  
Matches 366; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

QY 6 CAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTAGCTCTTG 65  
DB 22 CAACCGCAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTG 81

QY 66 GGGCTGCTATGTTTCTGCTTCTGCTGTAGAAAATCCCATGATACACTGGTGGCAGAGA 125  
DB 82 GAGCTGCTACGTGTATGCCATCCCAAGAAATTTCCCAAGTGCATTTGGTGAAGAGA 141

QY 126 CTTGACACTGCTCTCAGCTATCGAATCTGGTGTATAGCGGATGGAAACCTGATGATTC 185  
DB 142 CTTGGCACTGCTTCTACTCATCGAACTCTGCTGATAGCAATGAGACTCTGAGGATTC 201

QY 186 CTACTCTGAAATAAATAACCAACTGTCGCAATTAAGAAGTTTTCAGGGTATAGACA 245  
DB 202 CTGTTCTGTACATAAATACCAACTGTGCTGCACTGAAGAAATCTTTCAGGGAATAGGCA 261

QY 246 CATTGAAGAACCAACTGCCCGGAGGCTGTGGATAAATATTTCCAAAACCTTGTCTT 305

Db 262 CACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAGAAGCTATTCAAAAACTTGTCT 321  
QY 306 TATATAAGACACATAGAGCGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTCA 365  
Db 322 TATAAAGAATAACATAGCGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTCA 380  
QY 366 CAAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGTATAAACCACCGAGTGACACCG 425  
Db 381 ACCAAATCTTAGACTACCTGCAAGTATTTCTTGGTGTATAAACCACCGAGTGATAATAG 440  
QY 426 AAGTTGAGAACAAACCGGCTTATTGTAGTGGAGAT 462  
Db 441 AAGTTGAGAACAAACCGGCTTATTGTAGTGGAGAT 477

CD559535 463 bp mRNA linear EST 26-NOV-2003  
LOCUS AGENCOURT\_14496865 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971769 5', mRNA sequence.  
CD559535  
ACCESSION CD559535.2 GI:38589950  
VERSION 1  
KEYWORDS Homo sapiens (human)  
SOURCE EST  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 463)  
NTH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585603.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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High quality sequence stop: 463.  
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/clones="IMAGE:6971769"  
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/clone\_lib="NIH MGC 195"  
/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBKI.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBKI.presv.dat)  
a Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 49.3%; Score 300.8; DB 14; Length 463;  
Best Local Similarity 79.8%; Pred. No. 1.9e-63;  
Matches 367; Conservative 0; Mismatches 92; Indels 1; Gaps 1;  
QY 4 GGCAACACTGAACTTCAGAGCTATCAGAAATCTCTGAAATTTGAGTTTGTAGTCTCT 63  
Db 3 GACAACGCAGAAAGCTTCAGAGCCATGAGATGCTTCTGCATTTGAGTTTGTAGTCTCT 62  
QY 64 TGGGGCTCCCTATGTTTCTGCTTTTGTGTAGAAAAATCCCAATGAATAGACTGGTGGGAGA 123  
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Db 243 CACACTGGAGAGTCAAACCTGTGCAAGGGGTACTGTGGAAAGACTATTTCAAAACTTGTCTC 302  
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Db 303 CTTATAAAGAAATACATTTGACGCGCCAAAAAAGAAAGTGTGGAGAAAGACGAGAG 362  
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QY 423 CGGAAGTTGAGAACAAACCGGCTTATTGTAGTGGAGAT 462  
Db 423 TAGAAGTTGAGACTAAACTGTTGTTGTCAGCCAAAGAT 462

CD559536 489 bp mRNA linear EST 26-NOV-2003  
LOCUS AGENCOURT\_14496804 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971768 5', mRNA sequence.  
CD559536  
ACCESSION CD559536.2 GI:38589953  
VERSION 1  
KEYWORDS Homo sapiens (human)  
SOURCE EST  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 489)  
NTH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585604.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRBKI row: 9 column: 07  
High quality sequence start: 17  
High quality sequence stop: 489.  
Location/Qualifiers  
1. 489  
source



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QY 366 CAAAGTTCCTAGACTACCTGCAAGTATTTCTGGTGAATAAACAACCGAGTGACACCG 425
Db 107 ACCAAATTCCTAGACTACCTGCAAGAGTTTCTTGGTGTAAATGAACACCGAGTGGAATAG 48
QY 426 AAAGTTGAGAACAAACCGGCT 446
Db 47 AAAGTTGAGACTAAACTGGTT 27

CD559689 473 bp mRNA linear EST 19-NOV-2003
AGENCOURT 14496901 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971769 5', mRNA sequence.
CD559689
EST.
CD559689.2 GI:38453487
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 473)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585757.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence start: 16
High quality sequence stop: 473.
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/clone_lib="NIH MGC 195"
/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match 47.9%; Score 292.4; DB 14; Length 473;
Best Local Similarity 80.3%; Pred. No. 2.2e-61;
Matches 355; Conservative 0; Mismatches 86; Indels 1; Gaps 1;

QY 6 CAAACACTGAACATTTAGAGCTATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTG 65
Db 472 CAAACGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTG 413
QY 66 GGGCTGCGCTATGTTTCTGCTTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGA 125
Db 412 GAGCTGCGCTACGTGTATGCCATCCCAACAGAAATTTCCCAAGTGCCATTTGTAAGAGA 353
QY 126 CTTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGAACCTGATGATTC 185
Db 352 CTTTGCGCACTGCTTCTACTCATCGAATTCGGCTGATAGGCGATGGGAACCTGATGATTC 293
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Db 292 CTGTTCTCTGTACATAAAAAATCACAACCTGTCATCTGAAGAAATCTTTTCAGGGAATAGCCA 233
QY 246 CATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTTCCAAAACTTGTCTT 305
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QY 306 TAATAAAGAACACATAGAGCGCC-AAAAAAGGTTGTGAGGAGAAAGATGAGAGTG 364
Db 172 TAATAAAGAAATACATTGACGGCCAAAAAAGTGTGAGAAAGAACGAGAGTA 113
QY 365 ACAAAAGTTCTCTAGACTACTGCAAGTATTTCTTGGTGAATAAAACACCGAGTGACACCG 424
Db 112 RACCAATTCCTAGACTACTGCAAGAGTTTCTTGGTGAATGACACCGAGTGGAATAA 53
QY 425 GAAAGTTGAGAACAAACCGGCT 446
Db 52 GAAAGTTGAGACTAAACTGGTT 31

CD559690 467 bp mRNA linear EST 19-NOV-2003
AGENCOURT 14496838 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971768 5', mRNA sequence.
CD559690
EST.
CD559690.2 GI:38453490
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 467)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
On Jun 10, 2003 this sequence version replaced gi:31585758.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 07
High quality sequence stop: 467.
Location/Qualifiers
1. 467
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/mol_type="mRNA"
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FEATURES

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 /note="Vector: pNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK\_presv.dat  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 47.9%; Score 292.2; DB 14; Length 467;  
 Best Local Similarity 80.0%; Pred. No. 2.4e-61;  
 Matches 356; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 6 CAACACTGACATTTGAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTAGCTCTTG 65  
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 QY 66 GGGTGTCTATGTTTCTGCTTCTCTAGAAATCCCATGAATAGACTGGTGGCAGAGA 125  
 DB 406 GAGTGTCTAGCTGTATGCCATCCACAGANATCCCAAGTCATTTGGTGAAGAGA 347  
 QY 126 CTTTGACACTGCTCTCACTCATCGAACTTGGCTGATAGCGGATGGAACTGATGATTC 185  
 DB 346 CTTTGGCACTGCTTCTACTCATCGAACTGCTGATAGCAATGAGACTTTGAGGATTC 287  
 QY 186 CTACTCTGAAATATAAAATCACTGTCATTAAGAGTTTTCAGGGTATAGACA 245  
 DB 286 CTGTTCTGTATATAAAATCACTGTCATTAAGAGTTTTCAGGGTATAGACA 227  
 QY 246 CATTGAAGAACCAACTGCCACGGGAGGCTGTGGATAAATATTCCAAATCTTCTTT 305  
 DB 226 CACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAATCTTCTCT 167  
 QY 306 TAATAAAGACACATAGAGGCC-AAAAAAGGTGTCAGAGAGAGATGGAGTG 364  
 DB 166 TAATAAAGAAATACATTGACGGCCAAAAAAGGTGTCGGAAGAAAGACGAGAGTA 107  
 QY 365 ACAAGTTCTCTAGACTACCTGCAAGTATTTCTGGTGTATAAACACCGAGTGGACACCG 424  
 DB 106 AACCAATCTCTAGACTACCTGCAAGTATTTCTGGTGTATGAACCCGAGTGGATAATA 47  
 QY 425 GAAAGTTGAGAACAAACCGGCTTAT 449  
 DB 46 GAAAGTTGAGACTAACTGGTTGT 22

## RESULT 11

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 DEFINITION Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
 ACCESSION AY412020  
 VERSION AY412020.1 GI:39767985  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 405)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 405)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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 /db\_xref="taxon:9606"  
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 /locus\_tag="HCW4418"

ORIGIN

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 Matches 327; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 29 ATGAGAACTCTCTCAATTTGAGTTTCTAGCTCTTGGGGTGCCTATGTTTCTGCCTTT 88  
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 QY 89 GCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
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 DB 121 CGAACTTGGCTGATAGGCGAATGAGACTCTGAGGATCTCTGTTCTGTACATAAAATAC 180  
 QY 209 CAACCTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 268  
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 QY 269 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTATAAAGAACACATAGAGCGC 328  
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 QY 329 CAAAAAAGAGTGTGCAAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACTGCAA 388  
 DB 301 CAAAAAAGAGTGTGCAAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACTGCAA 360  
 QY 389 GTATTTCTTGTGTAAATAAACACCGAGTGGACACCGGAAAGTTGA 433  
 DB 361 GAGTTTCTTGTGTAAATAAACACCGAGTGGATATAAGAAAGTTGA 405

RESULT 12  
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 DEFINITION AGENCOURT\_14496997 NIH MGC 195 Homo sapiens cDNA clone IMAGE:6971867 5', mRNA sequence.  
 ACCESSION CD559608  
 VERSION CD559608.2 GI:38558942  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 477)
TITLE	NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) On Jun 10, 2003 this sequence version replaced gi:31585676. Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: <a href="mailto:egapbs-r@mail.nih.gov">egapbs-r@mail.nih.gov</a> Tissue Procurement: Narayan Bhat cDNA Library Preparation: Bhat Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: IRBK2 row: g column: 10 High quality sequence start: 107 High quality sequence stop: 353.
FEATURES	Location/Qualifiers
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	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="IMAGE:6971867"
	/tissue_type="mixed"
	/lab_host="DH5A (TI phage-resistant)"
	/clone_lib="NIH MGC 195"
	/note="vector: pDNR-Dual; Site 1: loxp-SalI; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at <a href="ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat">ftp://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat</a> a Note: this is a NIH_MGC Library."
ORIGIN	
Query Match	45.6%; Score 278.4; DB 14; Length 477;
Best Local Similarity	78.2%; Pred. No. 6e-58;
Matches	347; Conservative 0; Mismatches 96; Indels 1; Gaps 1;
QY	4 GGCAACACATGACATTTTCAGAGCTATGAGA-ATGCTTCTGAAATTTGAGTTTCTAGCTC 62
Db	15 GACTAACGCGAGACGTTTTCAGCGCTGAGAGACGCTTCTGCAATTTGAGTTTCTAGCTC 74
QY	63 TTGGGGTGCTATGTTTCTGCTTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 122
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QY	243 ACACATTGAAGAACCAACTGCCACCGGGAGGCTGTGGATAAATCTATTCAAAACCTGT 302
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QY	303 CTTTNTAATAAGAACACATAGAGCCCAAAAAAAGGTGTGCAGGAAGAAGTGGAGAG 362
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QY	423 CGGAAAGTTGAGAACAAACCGCT 446
Db	435 TATAAAGTTGAGACTAAACTGGTT 458

RESULT 13

CE331159

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CE331159

tigr-gss-dog-17000333986568 Dog Library Canis familiaris genomic,

genomic survey sequence.

CE331159

CE331159.1 GI:36147469

GSS

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 622)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

14512627

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: [ekirknes@tigr.org](mailto:ekirknes@tigr.org)

Class: shotgun.

Location/Qualifiers

1..622

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/strains="Standard Poodle"

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/clone\_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from

peripheral blood"

ORIGIN

Query Match

Best Local Similarity

Matches

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389

284

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523

570

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Db 524 CCTACTACTTATACACTTCACACAGATGAATATATTGAG 564  
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RESULT 14  
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LOCUS Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY412021  
VERSION AY412021.1 GI:39767986  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 405)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 405)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,  
Adams,M.D. and Cargill,M.  
AUTHORS Direct Submission  
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
JOURNAL Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES Location/Qualifiers  
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gene <1..>405  
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/locus\_tag="HCM4418"

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Best Local Similarity 79.8%; Pred. No. 2.1e-57;  
Matches 323; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

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Db 61 CCCACAGAAATCCCAACAGTGCATTGGTGAAGAGACCTTGGCACTGCTTTCTACTCAT 120  
QY 149 CGACTTGGCTGATAGCGGATGGGAACCTGATGTTCTTCTACTCTCTGAAATAAATATCAC 208  
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QY 209 CAATGTGCAATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268  
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QY 269 GGGGAGCTGTGGATAAATCTTCCAAAATCTGTCTTTAATAAAGAACACATAGAGCGC 328  
Db 241 GGGGGTAACTGTGGAAAGCAATTTCAAAAATCTGTCTTTAATAAAGAAATACATTTGANGC 300  
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Db 301 CAAAAAAGAGTGTGCAGAGAGAAAGATGGAGAGTGCACAAATTCCTAGACTACCTGCAA 360

QY 389 GTATTTCTTGTGTATAAAACACCGAGTGGACACCGGAAAGTTGA 433  
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RESULT 15  
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LOCUS Mus musculus IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY412022  
VERSION AY412022.1 GI:39767987  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 399)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 399)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,  
Adams,M.D. and Cargill,M.  
AUTHORS Direct Submission  
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
JOURNAL Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES Location/Qualifiers  
source 1..399  
/organism="Mus musculus"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:10090"  
gene <1..>399  
/gene="IL5"  
/locus\_tag="HCM4418"

ORIGIN  
Query Match 32.0%; Score 195; DB 29; Length 399;  
Best Local Similarity 66.7%; Pred. No. 1.9e-37;  
Matches 268; Conservative 0; Mismatches 128; Indels 6; Gaps 1;

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Db 4 AGGATGCTTCTGCACTTGAGTTTCTGACTCTAG-----CTGTGCTGGGCACCTGCC 57  
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Db 118 GCTCTGTGACAGCAATGAGNN 177  
QY 212 CTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCACGG 271  
Db 178 CTATGCAATTTGAGAAATCTTTTCAGGGGCTAGACATCTAGAAATCAAACTGCTCGTGG 237  
QY 272 GAGGCTGTGGATAAATCTTCCAAAATCTGTCTTTAATAAAGAACACATAGAGCGCAA 331  
Db 238 GGTACTGTGGAATATGCTATTCCAAAATCTGTCTTTAATAAAGAAATACATTTGACGCC 297  
QY 332 AAAAAAAGGTGTGCAGAGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAAG 391  
Db 298 AAGAGAGAGTGTGCGAGGAGAGACGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGG 357

Qy 392 TTCTTGGTGTAAACACCGAGTGGACACCGGAAAGTTGA 433  
Db 358 TTCTTGGTGTAGTACAGAGTGGCAATGGAAGGCTGA 399

Search completed: August 31, 2004, 13:00:11  
Job time : 2055.32 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 20:51:08 ; Search time 54.4245 Seconds  
(without alignments)  
6219.989 Million cell updates/sec

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Perfect score: 610  
Sequence: 1 caaggaacactgaacatt.....acagatgaatatattgag 610

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0.

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	610	100.0	610	4	US-09-322-409-82
3	610	100.0	610	4	US-09-451-527-80
4	610	100.0	610	4	US-09-451-527-82
5	402	65.9	402	4	US-09-322-409-83
6	402	65.9	402	4	US-09-322-409-84
7	402	65.9	402	4	US-09-451-527-83
8	402	65.9	402	4	US-09-451-527-84
9	401.8	65.9	405	4	US-09-371-615A-1
10	379	62.1	816	3	US-09-079-839-2
11	377.4	61.9	816	4	US-09-023-655-1236
12	345	56.6	345	4	US-09-322-409-85
13	345	56.6	345	4	US-09-322-409-87
14	345	56.6	345	4	US-09-451-527-85
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18	207.4	34.0	377	4	US-09-180-864-1
19	152.4	25.0	3230	3	US-09-280-799-78
20	152.4	25.0	3230	3	US-09-280-799-78
21	90.6	14.9	6727	3	US-08-629-643A-5
22	90.6	14.9	6727	3	US-09-280-799-1
23	90.6	14.9	6727	3	US-09-155-884-5
24	58.2	9.5	7218	1	US-08-232-463-14
25	42.2	6.9	47	1	US-08-466-852-2
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27	34.4	5.6	4843	3	US-08-986-485-1

ALIGNMENTS

RESULT 1

US-09-322-409-80  
; Sequence 80, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-CL  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-09-322-409-80

Query Match 100.0%; Score 610; DB 4; Length 610;  
Best Local Similarity 100.0%; Pred. No. 3.1e-187;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	TTTGGGGTGGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGC	120
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QY	121	AGAGACCTTGACACTGCTCTCCATCTGCAATCTGGCTGATAGCGGATGGAACTGAT	180
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QY	241	AGACACATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCT	300
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## RESULT 2

US-09-322-409-82/c  
; Sequence 82, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dretz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-82

Query Match 100.0%; Score 610; DB 4; Length 610;  
Best Local Similarity 100.0%; Pred. No. 3.1e-187;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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421 ACCGGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAAAGATGGTTT 480  
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70 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTATCATTTCACACAGATGAAA 11  
601 TATATTGAG 610  
10 TATATTGAG 1

## RESULT 3

US-09-451-527-80  
; Sequence 80, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dretz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1998-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-09-451-527-80

Query Match 100.0%; Score 610; DB 4; Length 610;  
Best Local Similarity 100.0%; Pred. No. 3.1e-187;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      541 TTCAGACAAAAGTAAATATTTCAGGCATCCTACTATTATCATTTCACACAGATGAAA 600
Qy      601 TATATTGGAG 610
Db      601 TATATTGGAG 610

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RESULT 4
US-09-451-527-82/c
; Sequence 82, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wenderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/451.527
; EARLIER FILING DATE: 1999-12-01
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-82

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Query Match      100.0%; Score 610; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 3.1e-187;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGATTTGCTAGC 60
Db      610 CAAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGATTTGCTAGC 551
Qy      61 TCTTGGGCTGCCCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGATGATGCTGGTGGC 120
Db      550 TCTTGGGCTGCCCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGATGATGCTGGTGGC 491
Qy      121 AGAGACCTTGACATGCTTCTCCACTCATCGAATCTTGCTGATAGGCGATGGGAACCTGAT 180
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Qy      181 GATTCCTACTCTCGAAATATAAAATCACCACCTGTGCAATTAAGAAAGTTTTCAGGGTAT 240
Db      430 GATTCCTACTCTCGAAATATAAAATCACCACCTGTGCAATTAAGAAAGTTTTCAGGGTAT 371
Qy      241 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAACTATTCCAAAACCTT 300
Db      370 AGACACATTTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAAACTATTCCAAAACCTT 311
Qy      301 GTCTTTAATAAAGAACACATAGAGCGCCCAAAAAGGTGTGCGAGGAGAAAGATGGAG 360
Db      310 GTCTTTAATAAAGAACACATAGAGCGCCCAAAAAGGTGTGCGAGGAGAAAGATGGAG 251
Qy      361 AGTGACAAAAGTCTCTAGACTACCTGCAAGTATTCTTGGTGTAAATAAAACACCGAGTGGAC 420
Db      250 AGTGACAAAAGTCTCTAGACTACCTGCAAGTATTCTTGGTGTAAATAAAACACCGAGTGGAC 191
Qy      421 ACCGGAAGTGTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAAGATGGTTT 480
Db      190 ACCGGAAGTGTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAAGATGGTTT 131
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Db      130 TTTGGCGATCAGATGAGGCGCCCAACCAAGTAGGACTTAAATGGCCAGTATAAATAAGC 71
Qy      541 TTCAGACAAAAGTAAATATTTCAGGCATCCTACTATTATCATTTCACACAGATGAAA 600
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Qy      601 TATATTGGAG 610
Db      10 TATATTGGAG 1

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Query Match      65.9%; Score 402; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.1e-120;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGAGATGCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60
Qy      89 GCTGTAGAAAATCCCATGATGAGCTGGTGGCAGAGACTTGACACTGCTCTCCACTCAT 148
Db      61 GCTGTAGAAAATCCCATGATGAGCTGGTGGCAGAGACTTGACACTGCTCTCCACTCAT 120
Qy      149 CGAAGCTTGCTGATAGGCGATGGGAACCTGATGATCTTCTCTGAAAATAAAATCAC 208
Db      121 CGAAGCTTGCTGATAGGCGATGGGAACCTGATGATCTTCTCTGAAAATAAAATCAC 180

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RESULT 5
US-09-322-409-83
; Sequence 83, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Yang, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wenderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/322.409
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

```

209 CAACCTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268  
Db |  
181 CAACCTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240  
QY GGGAGGCTGTGGATAAATCTTCCAAAACCTTCTTTTATATAAAGAACACATAGAGCGC 328  
Db |  
241 GGGAGGCTGTGGATAAATCTTCCAAAACCTTCTTTTATATAAAGAACACATAGAGCGC 300  
QY CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAC 388  
Db |  
301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAC 360  
QY GTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 430  
Db |  
361 GTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 402

## RESULT 6

US-03-322-409-84/c  
; Sequence 84, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-84

Query Match 65.9%; Score 402; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 4.1e-120;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGGCTGCCTATGTTCTGCCTTT 88  
Db |  
402 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGGCTGCCTATGTTCTGCCTTT 343  
QY 89 GCTGTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
Db |  
342 GCTGTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283  
QY 149 CGAATTTGGCTGATAGCGGATGGAACTTCTAGATGATTCCTCTGAAAATAAAATCAC 208  
Db |  
282 CGAATTTGGCTGATAGCGGATGGAACTTCTAGATGATTCCTCTGAAAATAAAATCAC 223  
QY 209 CAACCTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268  
Db |  
222 CAACCTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 163  
QY 269 GGGAGGCTGTGATAAATCTTCCAAAACCTTCTTTTATATAAAGAACACATAGAGCGC 328  
Db |  
162 GGGAGGCTGTGATAAATCTTCCAAAACCTTCTTTTATATAAAGAACACATAGAGCGC 103  
QY 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAC 388  
Db |  
102 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAC 43  
QY 389 GTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 430  
Db |  
42 GTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 1

## RESULT 7

US-09-451-527-83  
; Sequence 83, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-451-527-83

Query Match 65.9%; Score 402; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 4.1e-120;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGGCTGCCTATGTTCTGCCTTT 88  
Db |  
1 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGGCTGCCTATGTTCTGCCTTT 60  
QY 89 GCTGTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
Db |  
61 GCTGTAGAAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
QY 149 CGAATTTGGCTGATAGCGGATGGAACTTCTAGATGATTCCTCTGAAAATAAAATCAC 208  
Db |  
121 CGAATTTGGCTGATAGCGGATGGAACTTCTAGATGATTCCTCTGAAAATAAAATCAC 180  
QY 209 CAACCTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268  
Db |  
181 CAACCTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240  
QY 269 GGGAGGCTGTGATAAATCTTCCAAAACCTTCTTTTATATAAAGAACACATAGAGCGC 328  
Db |  
241 GGGAGGCTGTGATAAATCTTCCAAAACCTTCTTTTATATAAAGAACACATAGAGCGC 300  
QY 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAC 388  
Db |  
301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAC 360  
QY 389 GTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 430  
Db |  
361 GTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 402

## RESULT 8

US-09-451-527-84/c  
; Sequence 84, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527



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; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84

Query Match      65.9%; Score 402; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.1e-120;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 88
DB 402 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 343
QY 89 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 342 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
QY 149 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTTCTTCTCTCTCTCTCTCTCTCT 208
DB 282 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTTCTTCTCTCTCTCTCTCTCTCT 223
QY 209 CAATCTGTGCTTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACCTGCCAC 268
DB 222 CAATCTGTGCTTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACCTGCCAC 163
QY 269 GGGGAGGCTGTGATAACTATTCCAAAATTTCTTTTAAATAAAGAACACATAGAGCGC 328
DB 162 GGGGAGGCTGTGATAACTATTCCAAAATTTCTTTTAAATAAAGAACACATAGAGCGC 103
QY 329 CAAAAAAGAGTGTGAGAGAGAGTGGAGAGTGCACCAAGTTCCTAGACTACCTGCAA 388
DB 102 CAAAAAAGAGTGTGAGAGAGAGTGGAGAGTGCACCAAGTTCCTAGACTACCTGCAA 43
QY 389 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430
DB 42 GTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 9
US-09-371-615A-1
; Sequence 1, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE REFERENCE: CANINE INTERLEUKIN 5
; CURRENT APPLICATION NUMBER: US/09/371.615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1

Query Match      65.9%; Score 401.8; DB 4; Length 405;
Best Local Similarity 99.5%; Pred. No. 4.8e-120;
Matches 403; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 88
DB 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 60

; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84

Query Match      62.1%; Score 379; DB 3; Length 816;
Best Local Similarity 79.1%; Pred. No. 1.6e-112;
Matches 463; Conservative 0; Mismatches 120; Indels 2; Gaps 1;

QY 2 AAGGCAAAACACTGAAACATTTGAGAGCTATGAGAATGCTTCTGAATTTGAGTTTCTAGCT 61
DB 18 AAGGCAAAACGAGAACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTCTAGCT 77
QY 62 CTTGGGGCTGCTATGTTTCTGCTTCTGCTAGAAAATCCCATGAATAGACTGGTGCA 121
DB 78 CTTGGAGCTGCTACGTGTATGCCATCCCAAGAAATTTCCCAAGTGCATTGGTGAAA 137
QY 122 GAGACTTTGACACTGCTCTCCACTCATCGAACTTGGCTGTAGAGCGATGGGAACCTGATG 181
DB 138 GAGACTTTGGCACTGCTTTCTACTCATGCACTCTGCTGTAGCAATGAGACTCTGAGG 197
QY 182 ATTCCTACTCTGAAAAATAAAATACCAACTGTGCAATTAAGAAGTTTTTCAGGGTATA 241
DB 198 ATTCCTGTCTGTACATAAAAAATCACCACACTGTGCACTGAAGAAATCTTTTCAGGGAATA 257
QY 242 GACACTTTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAACTATTCCAAAACCTTG 301
DB 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGGTACTGTGGAAAGACTATTCAAAAACCTTG 317
QY 302 TCTTTAAATAAAGAACACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAGA 361
DB 318 TCTTTAAATAAAGAAATACATTGACGGCCAAAAAAGGTGTGGAGAGAAAGACGGAGA 377
QY 362 GTGCAAAAGTTCTAGACTACTGCAAGTATTTCTTGTGTGTAAATAAACACCGAGTGGACA 421
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Db 378 GTAACCAATCTCTAGACTACTCTCAAGAGTTCTTGTTGTAATGAACACCGAGTGGATA 437  
Qy 422 CCGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTGTTGGAAGAATG--GTT 479  
Db 438 ATAGAAAGTTGAGACTAAACTGGTTGTTGTCAGCCAAAGATTGTTGAGGAGAGGACATT 497  
Qy 480 TTTTGGGATCAGATCAGGGCCCAACCAACAGTAGGAGCTTAATGCCAGTATAAAG 539  
Db 498 TTACTGAGTGAAGTGAAGGCGCCCAAGAAAGAGTCAGGCCCTTAATTTCAATATAATTAA 557  
Qy 540 CTTGAGAGCAAGTAAATATTTTTCAGGCATCTCTACTACTTATCA 584  
Db 558 CTTGAGAGGAAAGTAAATATTTTCAGGCATCTACTGACACTTTTGCA 602

## RESULT 11

US-09-023-655-1236  
; Sequence 1236, Application US/09023655  
; Patent No. 6607879

## GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1236:

SEQUENCE CHARACTERISTICS:

LENGTH: 816 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9288309

US-09-023-655-1236

## Query Match

Best Local Similarity 61.9%; Score 377.4; DB 4; Length 816;

Matches 462; Conservative 0; Mismatches 121; Indels 2; Gaps 1;

Qy 2 AAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTTGCTAGCT 61

Db 18 AAGGCAACAGAGAGCTTTTCAGAGCAATGAGGATGCTTCTGAATTTGAGTTTGCTAGCT 77

Qy 52 CTTGGGCTGCTATGTTTCTGCTTCCATAGAAATCCCATGATAGACTGCTGGCA 121  
Db 78 CTTGGAGCTGCTACGTGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTAAA 137  
Qy 122 GAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGGATGGAACTGATG 181  
Db 138 GAGACCTTGGCACTGCTTCTTACTCATCGAACTCTGCTGATAGCAATGAGACTCTCAGG 197  
Qy 182 ATTCTACTCTGAAAATAAAAAATCAACCACTGTGCATTAAGAAGTTTTTTCAGGTTATA 241  
Db 198 ATTCTGTTCTGTACATAAAAAATCACCAACTGTGCACTGAAGAAATCTTTTCAGGGAATA 257  
Qy 242 GACACATTGAAGAACCAAACTGCCACGGGGAGGCTGTGGATAACTATTTCAAAACCTTG 301  
Db 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTTCGAAAACCTTG 317  
Qy 302 TCTTTAATAAAGAACACATAGAGCGGCCAAAAAAGGTTGTGAGGAGAAAGATGGAGA 361  
Db 318 TCCTTAATAAAGAAATACATTGACGGCCAAAAAAGGTTGTGAGAGAAAGACCGAGA 377  
Qy 362 GTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTGCTGTGTAATAAACACCGAGTGGACA 421  
Db 378 GTAACCAATCTCTAGACTACCTGCAAGGTTCTTGTGTATGAAACACCGAGTGGATA 437  
Qy 422 CCGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAATG--GTT 479  
Db 438 ATAGAAAGTTGAGACTAAACTGGTTTGTGTCAGCCAAAGATTTTGGAGGAGAGGACATT 497  
Qy 480 TTTTGGGATCAGATGAGGCGCCCAACCAAGTAGGAGCTTAATGGCCAGTAACTAAG 539  
Db 498 TTACTGAGTGAAGTGAAGGCGCCCAAGAAAGAGTCAGGCCCTTAATTTTCAATATAATTAA 557  
Qy 540 CTTGAGAGCAAGTAAATATTTTCAGGCATCTCTACTACTTTATCA 584  
Db 558 CTTGAGAGGAAAGTAAATATTTTCAGGCATCTACTGACACTTTTGCA 602

## RESULT 12

US-09-322-409-85

; Sequence 85, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

APPLICANT: Sim, Gek-kee

APPLICANT: Yang, Shumin

APPLICANT: Dreitz, Matthew J.

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

FILE REFERENCE: IM-2-C1

CURRENT APPLICATION NUMBER: US/09/322,409

CURRENT FILING DATE: 1999-05-28

EARLIER APPLICATION NUMBER: 60/087,306

EARLIER FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 154

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 85

LENGTH: 345

TYPE: DNA

ORGANISM: Canis familiaris

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(345)

US-09-322-409-85

## Query Match

Best Local Similarity 56.6%; Score 345; DB 4; Length 345;

Matches 345; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 86 TTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145

Db 1 TTTCTCTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Qy 146 CATCGAACTTGGCTGTATAGCGGAGTGGAACTGATGATTCCTCTCTGAAAAATAAAAT 205

Db 61 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAATATAAAAT 120  
Qy 206 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265  
Db 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
Qy 266 CACGGGAGGCTGTGGATAACTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 325  
Db 181 CACGGGAGGCTGTGGATAACTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 240  
Qy 326 CGCCAAAAAAGGTTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 385  
Db 241 CGCCAAAAAAGGTTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 300  
Qy 386 CAAGTATTCTTGGTGTAATAAACCACCGAGTGACACCGGAAAGT 430  
Db 301 CAAGTATTCTTGGTGTAATAAACCACCGAGTGACACCGGAAAGT 345

## RESULT 13

US-09-322-409-87/c  
; Sequence 87, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-87

Query Match 56.6%; Score 345; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 9.9e-102;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 86 TTTCGTGTAGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 145  
Db 345 TTTCGTGTAGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 286  
Qy 146 CATCGAACTTGGCTGATAGCGATGGGAACCTGATTCCTACTCTGAAATATAAAAT 205  
Db 285 CATCGAACTTGGCTGATAGCGATGGGAACCTGATTCCTACTCTGAAATATAAAAT 226  
Qy 206 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265  
Db 225 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166  
Qy 266 CACGGGAGGCTGTGGATAACTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 325  
Db 165 CACGGGAGGCTGTGGATAACTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 106  
Qy 326 CGCCAAAAAAGGTTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 385  
Db 105 CGCCAAAAAAGGTTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 46  
Qy 386 CAAGTATTCTTGGTGTAATAAACCACCGAGTGACACCGGAAAGT 430  
Db 45 CAAGTATTCTTGGTGTAATAAACCACCGAGTGACACCGGAAAGT 1

## RESULT 14

US-09-451-527-85  
; Sequence 85, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-09-451-527-85

Query Match 56.6%; Score 345; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 9.9e-102;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 TTTCGTGTAGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 145  
Db 1 TTTCGTGTAGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
Qy 146 CATCGAACTTGGCTGATAGCGATGGGAACCTGATTCCTACTCTGAAATATAAAAT 205  
Db 61 CATCGAACTTGGCTGATAGCGATGGGAACCTGATTCCTACTCTGAAATATAAAAT 120  
Qy 206 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265  
Db 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
Qy 266 CACGGGAGGCTGTGGATAACTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 325  
Db 181 CACGGGAGGCTGTGGATAACTATTCCTCAAACTGTCTTTAATAAAGAACACATAGAG 240  
Qy 326 CGCCAAAAAAGGTTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 385  
Db 241 CGCCAAAAAAGGTTGCGAGGAGAAAGATGGAGAGTGACAAAGTTCTCTAGACTACCTG 300  
Qy 386 CAAGTATTCTTGGTGTAATAAACCACCGAGTGACACCGGAAAGT 430  
Db 301 CAAGTATTCTTGGTGTAATAAACCACCGAGTGACACCGGAAAGT 345

## RESULT 15

US-09-451-527-87/c  
; Sequence 87, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409

```
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

Query Match      56.6%; Score 345; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 9.9e-102;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      86 TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCTCCACT 145
Db      345 TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCTCCACT 286

Qy      146 CATCGAACTTGGCTGTAGTAGCGGATGGGAACCTGATGATTCCTACTCCTGAAATAAAAAAT 205
Db      285 CATCGAACTTGGCTGTAGTAGCGGATGGGAACCTGATGATTCCTACTCCTGAAATAAAAAAT 226

Qy      206 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265
Db      225 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

Qy      266 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTCTTTAATAAAAGAACACATAGAG 325
Db      165 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTCTTTAATAAAAGAACACATAGAG 106

Qy      326 CGCCAAAAAAGAGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 385
Db      105 CGCCAAAAAAGAGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 46

Qy      386 CAAGTATTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 430
Db      45 CAAGTATTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 1
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Search completed: August 31, 2004, 06:34:44  
Job time : 58.4245 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:25:57 ; Search time 360.942 Seconds  
(without alignments)  
8317.320 Million cell updates/sec

Title: US-10-787-382-4

Perfect score: 610

Sequence: 1 caaggcaaacactgaacatt.....acagatgaatatatttag 610

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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2: /cgn2_6/ptodata/1/pubpna/FCI_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	610	100.0	610	9 US-09-755-633-4
2	610	100.0	610	9 US-09-755-633-6
3	610	100.0	610	15 US-10-218-654-80
4	610	100.0	610	15 US-10-218-654-82
5	610	100.0	610	15 US-10-262-439-80
6	610	100.0	610	15 US-10-262-439-82
7	402	65.9	402	9 US-09-755-633-7
8	402	65.9	402	9 US-09-755-633-8
9	402	65.9	402	15 US-10-218-654-83
10	402	65.9	402	15 US-10-218-654-84
11	402	65.9	402	15 US-10-262-439-83
12	402	65.9	402	15 US-10-262-439-84
13	379	62.1	816	16 US-10-191-997-90
14	377.4	81.6	17	US-10-641-643-1236

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15 345 56.6 345 9 US-09-755-633-9
16 345 56.6 345 9 US-09-755-633-11
17 345 56.6 345 15 US-10-218-654-85
18 345 56.6 345 15 US-10-218-654-87
19 345 56.6 345 15 US-10-262-439-85
20 345 56.6 345 15 US-10-262-439-87
21 299 49.0 671 9 US-09-755-633-21
22 276.6 45.3 858 15 US-10-295-074-8
23 275.6 45.2 858 15 US-10-295-074-10
24 232.4 38.1 864 15 US-10-295-074-14
25 231.4 37.9 864 15 US-10-295-074-12
26 171.8 28.2 1658 9 US-09-755-633-18
27 170.2 27.9 1658 9 US-09-755-633-19
28 152.4 25.0 3230 9 US-09-800-629A-78
29 152.4 25.0 3230 17 US-10-679-532-78
30 90.6 14.9 6727 9 US-09-800-629A-1
31 90.6 14.9 6727 17 US-10-679-532-1
32 81.4 13.3 5397 15 US-10-311-455-1017
33 79.8 13.1 5397 15 US-10-311-455-1018
34 42.6 7.0 65 10 US-09-908-975-2631
35 42 6.9 3673778 15 US-10-312-841-2
36 40.6 6.7 60 10 US-09-908-975-11360
37 38.8 6.4 2196 13 US-10-424-599-100905
38 38.6 6.3 1832 13 US-10-424-599-120903
39 37.2 6.1 594 13 US-10-142-426-10
40 37.2 6.1 594 15 US-10-123-155-10
41 37.2 6.1 594 15 US-10-146-731-10
42 37.2 6.1 594 15 US-10-140-472-10
43 37.2 6.1 594 15 US-10-141-761-10
44 37.2 6.1 594 15 US-10-142-855-10
45 37.2 6.1 594 15 US-10-158-790-10
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#### ALIGNMENTS

#### RESULT 1

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US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-755-633-4
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Query Match 100.0%; Score 610; DB 9; Length 610;

Best Local Similarity 100.0%; Pred. No. 4.5e-181;

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGC 60

Db 1 CAAGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGC 60

QY 61 TCTTGGGGCTGCCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGC 120

Db 61 TCCTGGGCTGCCCTATGTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGC 120  
Qy 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGGATGGGAACCTGAT 180  
Db 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGGATGGGAACCTGAT 180  
Qy 181 GATTCCTACTCTCTGAAAATATAAATACCAACTGCTGATTAAGAAGTTTTCAGGGTAT 240  
Db 181 GATTCCTACTCTCTGAAAATATAAATACCAACTGCTGATTAAGAAGTTTTCAGGGTAT 240  
Qy 241 AGACACATTGAAGAACCAAACTGCCACGGGGAGGCTGTGATAAACTATTCCAAAACCTT 300  
Db 241 AGACACATTGAAGAACCAAACTGCCACGGGGAGGCTGTGATAAACTATTCCAAAACCTT 300  
Qy 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGCGAGGAGAAAGATGGAG 360  
Db 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGCGAGGAGAAAGATGGAG 360  
Qy 361 AGTCACAAGTTCCTAGACTACCTGCAAGTATTCTTTGGTGTATAAACAACCGAGTGGAC 420  
Db 361 AGTCACAAGTTCCTAGACTACCTGCAAGTATTCTTTGGTGTATAAACAACCGAGTGGAC 420  
Qy 421 ACCGGAAGTTGAGACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAGTGGTT 480  
Db 421 ACCGGAAGTTGAGACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAGTGGTT 480  
Qy 481 TTTGGCGATGAGATGAGGCGCAACCAAGTGGGACTTAATGCGCGATATACTAAGC 540  
Db 481 TTTGGCGATGAGATGAGGCGCAACCAAGTGGGACTTAATGCGCGATATACTAAGC 540  
Qy 541 TTCAGACAAAGTAATAATTTCAGGCATCCTACTTATCATTTCACATTCACACAGATGAAA 600  
Db 541 TTCAGACAAAGTAATAATTTCAGGCATCCTACTACTTATCATTTCACATTCACACAGATGAAA 600  
Qy 601 TATATTGAG 610  
Db 601 TATATTGAG 610

## RESULT 2

US-09-755-633-6/c  
; Sequence 6, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-6

Query Match 100.0%; Score 610; DB 9; Length 610;  
Best Local Similarity 100.0%; Pred. No. 4.5e-181;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGGCAAACTGACATTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGCTAGC 60  
Db 610 CAAGGCAAACTGACATTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGCTAGC 551

Qy 61 TCCTGGGCTGCCCTATGTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGC 120  
Db 550 TCCTGGGCTGCCCTATGTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGC 491  
Qy 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGGATGGGAACCTGAT 180  
Db 490 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGGATGGGAACCTGAT 431  
Qy 181 GATTCCTACTCTCTGAAAATATAAATACCAACTGCTGATTAAGAAGTTTTCAGGGTAT 240  
Db 430 GATTCCTACTCTCTGAAAATATAAATACCAACTGCTGATTAAGAAGTTTTCAGGGTAT 371  
Qy 241 AGACACATTGAAGAACCAAACTGCCACGGGGAGGCTGTGATAAACTATTCCAAAACCTT 300  
Db 370 AGACACATTGAAGAACCAAACTGCCACGGGGAGGCTGTGATAAACTATTCCAAAACCTT 311  
Qy 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGCGAGGAGAAAGATGGAG 360  
Db 310 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGCGAGGAGAAAGATGGAG 251  
Qy 361 AGTCACAAGTTCCTAGACTACCTGCAAGTATTCTTTGGTGTATAAACAACCGAGTGGAC 420  
Db 250 AGTCACAAGTTCCTAGACTACCTGCAAGTATTCTTTGGTGTATAAACAACCGAGTGGAC 191  
Qy 421 ACCGGAAGTTGAGACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAGTGGTT 480  
Db 130 ACCGGAAGTTGAGACAAACCGGCTTATTGTAGTGAAGATTTTGGAGAGAAGTGGTT 131  
Qy 481 TTTGGCGATGAGATGAGGCGCAACCAAGTGGGACTTAATGCGCGATATACTAAGC 540  
Db 130 TTTGGCGATGAGATGAGGCGCAACCAAGTGGGACTTAATGCGCGATATACTAAGC 71  
Qy 541 TTCAGACAAAGTAATAATTTCAGGCATCCTACTTATCATTTCACATTCACACAGATGAAA 600  
Db 70 TTCAGACAAAGTAATAATTTCAGGCATCCTACTACTTATCATTTCACACAGATGAAA 11  
Qy 601 TATATTGAG 610  
Db 10 TATATTGAG 1

## RESULT 3

US-10-218-654-80  
; Sequence 80, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR FILING DATE: US/09/322,409  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-218-654-80

Query Match 100.0%; Score 610; DB 15; Length 610;  
Best Local Similarity 100.0%; Pred. No. 4.5e-181;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 US-10-218-654-82/c  
 ; Sequence 82, Application US/10218654  
 ; Publication No. US20030099609A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE: IM-2-C1  
 ; CURRENT APPLICATION NUMBER: US/10/218,654  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: US/09/322,409  
 ; PRIOR FILING DATE: 1999-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087,306  
 ; PRIOR FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 82  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-10-218-654-82

100.0%; Score 610; DB 15; Length 610;

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RESULT 5
US-10-262-439-80
; Sequence 80, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIORITY APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA

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RES001.5
US-10-262-439-80
; Sequence 80, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kea
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMM
; TITLE OF INVENTION: ACID MOLECULES, AND
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA

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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-7

Query Match 65.9%; Score 402; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTATGTTTCTGCTTTT 88
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTATGTTTCTGCTTTT 60
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTTCCACTCAT 120
QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 208
DB 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
QY 209 CAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCCAC 268
DB 181 CAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCCAC 240
QY 269 GGGAGGCTGTGATAAAGTATTTTCAAGGTATAGACACTTGAAGAACCAAACTGCCAC 328
DB 241 GGGAGGCTGTGATAAAGTATTTTCAAGGTATAGACACTTGAAGAACCAAACTGCCAC 300
QY 329 CAAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGAAGTTCCTAGACTACCTGCAA 388
DB 301 CAAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGAAGTTCCTAGACTACCTGCAA 360
QY 389 GTATTTCTTGGTGTATTAACACCGAGTGGACCGGAAAGT 430
DB 361 GTATTTCTTGGTGTATTAACACCGAGTGGACCGGAAAGT 402

RESULT 8
US-09-755-633-8/c
; Sequence 8, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-8

Query Match 65.9%; Score 402; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTATGTTTCTGCTTTT 88
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTATGTTTCTGCTTTT 60
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTTCCACTCAT 120
QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 208
DB 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
QY 209 CAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCCAC 268
DB 181 CAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCCAC 240

US-10-218-654-83
; Sequence 83, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderting, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-83

Query Match 65.9%; Score 402; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTATGTTTCTGCTTTT 88
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGTGGCTATGTTTCTGCTTTT 60
QY 89 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTTCCACTCAT 148
DB 61 GCTGTAGAAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTTCCACTCAT 120
QY 149 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 208
DB 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
QY 209 CAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCCAC 268
DB 181 CAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACTTGAAGAACCAAACTGCCAC 240

Db 181 CAACCTGTGCATTAAGAAGATTTTTCAGGGTATAGACACATTTGAAGAACCACCAACTGCCAC 240  
Qy 269 GGGGAGGCTGGGATAAATACTATTCAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 328  
Db 241 GGGGAGGCTGGGATAAATACTATTCAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300  
Qy 329 CAAAAAAGAGTGTGAGGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 388  
Db 301 CAAAAAAGAGTGTGAGGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360  
Qy 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430  
Db 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 10  
US-10-218-654-84/c  
; Sequence 84, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-84

Query Match 65.9%; Score 402; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. le-115;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 29 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCCTATGTTCTGCTTT 88  
Db 402 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCCTATGTTCTGCTTT 343  
Qy 89 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGCTTGACACTGCTCTCCACTCAT 148  
Db 342 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGCTTGACACTGCTCTCCACTCAT 283  
Qy 149 CGAACTTGGCTGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAATAATCAC 208  
Db 282 CGAACTTGGCTGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAATAATCAC 223  
Qy 209 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268  
Db 222 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 163  
Qy 269 GGGGAGGCTGGGATAAATACTATTCCAAACCTGCTTTAATAAAGAACACATAGAGCGC 328  
Db 162 GGGGAGGCTGGGATAAATACTATTCCAAACCTGCTTTAATAAAGAACACATAGAGCGC 103  
Qy 329 CAAAAAAGAGTGTGAGGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 388  
Db 102 CAAAAAAGAGTGTGAGGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 43  
Qy 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430  
Db 42 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 11  
US-10-262-439-83  
; Sequence 83, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-83

Query Match 65.9%; Score 402; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. le-115;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 29 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCCTATGTTCTGCTTT 88  
Db 1 ATGAGATGCTTCTGAAATTTGAGTTTCTAGCTTTGGGCTGCCTATGTTCTGCTTT 60  
Qy 89 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGCTTGACACTGCTCTCCACTCAT 148  
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGGAGAGCTTGACACTGCTCTCCACTCAT 120  
Qy 149 CGAACTTGGCTGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAATAATCAC 208  
Db 121 CGAACTTGGCTGTAGGCGATGGAACTGATGATTCCTACTCTGAAATAAATAATCAC 180  
Qy 209 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268  
Db 181 CAACCTGTGCATTAAGAAGTTCCTAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240  
Qy 269 GGGGAGGCTGGGATAAATACTATTCCAAACCTGCTTTAATAAAGAACACATAGAGCGC 328  
Db 241 GGGGAGGCTGGGATAAATACTATTCCAAACCTGCTTTAATAAAGAACACATAGAGCGC 300  
Qy 329 CAAAAAAGAGTGTGAGGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 388  
Db 301 CAAAAAAGAGTGTGAGGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360  
Qy 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430  
Db 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

RESULT 12  
US-10-262-439-84/c  
; Sequence 84, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-84

FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/10/262,439  
CURRENT FILING DATE: 2002-09-30  
PRIOR APPLICATION NUMBER: US/03/451,527  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 09/322,409  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/087,306  
PRIOR FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 84  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-10-262-439-84

Query Match 65.9%; Score 402; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1e-115;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGAAATGCTTCTGAAATTTGCTTGTAGCTTCTGGGGTGGCTTATGTTTCTGCTTT 88  
Db 402 ATGAGAAATGCTTCTGAAATTTGCTTGTAGCTTCTGGGGTGGCTTATGTTTCTGCTTT 343

QY 89 GCTGTAGAAATCCCATGAATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 148  
Db 342 GCTGTAGAAATCCCATGAATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 149 CGAACTGGCTGATAGCGGATGGAACTGATGATCTCTGAAATTAATAATCAC 208  
Db 282 CGAACTGGCTGATAGCGGATGGAACTGATGATCTCTGAAATTAATAATCAC 223

QY 209 CAACTGTGCAATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCCAC 268  
Db 222 CAACTGTGCAATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCCAC 163

QY 269 GGGAGGCTGTGATAAATCTTCCAAACTTCTTTTAAAGAACACATAGAGCG 328  
Db 162 GGGAGGCTGTGATAAATCTTCCAAACTTCTTTTAAAGAACACATAGAGCG 103

QY 329 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGCACAAAGTTTCTAGACTACCTGCAA 388  
Db 102 CAAAAAAGAGTGTGAGGAGAAAGATGAGAGTGCACAAAGTTTCTAGACTACCTGCAA 43

QY 389 GTATTTCTTGGTGTATATAAACACCGAGTGGACACCGGAAAGT 430  
Db 42 GTATTTCTTGGTGTATATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 13  
US-10-191-997-90  
Sequence 90, Application US/10191997  
Publication No. US20030207834A1  
GENERAL INFORMATION:  
APPLICANT: Oligos Etc., Inc.  
APPLICANT: DALE, Roderic M. K.  
APPLICANT: ARROW, Amy  
APPLICANT: THOMPSON, Terry  
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their  
FILE REFERENCE: 54800-5019  
CURRENT APPLICATION NUMBER: US/10/191,997  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US 60/303,820  
PRIOR FILING DATE: 2001-07-10  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 90  
LENGTH: 816  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-191-997-90

RESULT 14  
US-10-641-643-1236  
Sequence 1236, Application US/10641643  
Publication No. US20040077003A1  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
GENE EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1236:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 816 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: g288309  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1236 :  
 US-10-641-643-1236

Query Match 61.98; Score 377.4; DB 17; Length 816;  
 Best Local Similarity 79.08; Pred. No. 8.9e-108;  
 Matches 462; Conservative 0; Mismatches 121; Indels 2; Gaps 1;  
 QY 2 AAGCRAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCT 61  
 Db |||||  
 QY 18 AAGCRAACGAGACGTTTCAGAGCATGAGATGCTTCTGATTTGAGTTTGCTAGCT 77  
 Db |||||  
 QY 62 CTTGGGCTCCATGTTTCTGCTTGTGTAGAAATCCCATGAATAGACTGTGGCA 121  
 Db |||||  
 QY 78 CTTGGAGCTCCTACGTGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGA 137  
 Db |||||  
 QY 122 GAGACCTTGACACTGCTCTCCACTCATCGAATCTGCTGATGAGGCGATGGAACTGATG 181  
 Db |||||  
 QY 138 GAGACCTTGACACTGCTCTCTCTCTGATGAGGCTGCTGATGAGGCTGAGG 197  
 Db |||||  
 QY 182 ATTCTCTACTCCTGAATAAATACCAACTGTGCAATTAAGAAAGTTTTCAGGGTATA 241  
 Db |||||  
 QY 198 ATTCTCTCTCTGATATAAATACCAACTGTGCAATTAAGAAATCTTTCAGGGAATA 257  
 Db |||||  
 QY 242 GACACATTGAGAACCAACTGCCACGGGAGGCTGTGATTAATCTTCCAAACTTG 301  
 Db |||||  
 QY 258 GGCACACTGGAGAGTCAAACTGTGCAAGGGGCTGCTGCAAGAGACTATTGAAACTTG 317  
 Db |||||  
 QY 302 TCTTTAATAAAGAACACATAGAGCGCCAAATAAAGAGTGTGAGGAGAAAGATGGAGA 361  
 Db |||||  
 QY 318 TCCTTAATAAAGAAATACATTGACGCGCAATAAAGAGTGTGAGGAGAAAGCGAGA 377  
 Db |||||  
 QY 362 GTGACAAAGTTCTAGACTACTGGAAGTATTTCTGGTGTATTAATAACACCGAGTGGACA 421  
 Db |||||  
 QY 378 GTAAACCAATTCCTAGACTACTGCAAGAGTTTCTGGTGTATTAATAACACCGAGTGGATA 437  
 Db |||||  
 QY 422 CCGGAAAGTTGAGAACAAACCGGCTTATTTGATGGAAGATTTTGAGAGGAATG - GTT 479  
 Db |||||  
 QY 438 ATAGAAAGTTGAGACTAACTGGTTTGTGAGCCTAAAGATTTTGAGGAGAAAGACATT 497  
 Db |||||  
 QY 480 TTTTGGCGATGAGAAATGAGGGCCAAACACAGTAGGACTTAATGGCCAGTATAACTAAG 539  
 Db |||||  
 QY 498 TTAAGTCAAGTGAATGAGGGCCCAAGAAAGAGTACGGCCCTTAATTTCAATATTAATTA 557  
 Db |||||  
 QY 540 CTTTCAGAGCAAGTAATATTTTCAGGCATCTACTACTTTATCA 584  
 Db |||||  
 QY 558 CTTTCAGAGCAAGTAATATTTTCAGGCATCTACTACTTTGCCA 602  
 Db |||||

RESULT 15  
 US-09-755-633-9  
 ; Sequence 9, Application US/09755633  
 ; Patent No. US20020127200A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE: IM-2-C1-C1  
 ; CURRENT APPLICATION NUMBER: US/09/755,633  
 ; CURRENT FILING DATE: 2001-01-05  
 ; PRIOR APPLICATION NUMBER: 09/322,409  
 ; PRIOR FILING DATE: 1999-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087,306  
 ; PRIOR FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 9  
 ; LENGTH: 345  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(345)  
 ; US-09-755-633-9

Query Match 56.6%; Score 345; DB 9; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-98;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 86 TTTCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACT 145  
 Db |||||  
 QY 1 TTTCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACT 60  
 Db |||||  
 QY 146 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 205  
 Db |||||  
 QY 61 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAAT 120  
 Db |||||  
 QY 206 CACCAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATGAGAACCAACTGCC 265  
 Db |||||  
 QY 121 CACCAACTGTGCATTAAGAAAGTTTTCAGGGTATAGACACATGAGAACCAACTGCC 180  
 Db |||||  
 QY 266 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 325  
 Db |||||  
 QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAG 240  
 Db |||||  
 QY 326 CGCCAAAAAAGGTTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 385  
 Db |||||  
 QY 241 CGCCAAAAAAGGTTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG 300  
 Db |||||  
 QY 386 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430  
 Db |||||  
 QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345  
 Db |||||

Search completed: August 31, 2004, 14:03:37  
 Job time : 364.942 secs

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:21:12 ; Search time 1737.73 Seconds  
(without alignments)  
10026.797 Million cell updates/sec

Title: US-10-787-382-7  
Perfect score: 402  
Sequence: 1 atgagatgtcttgattt.....ccgagtggacaccggaagt 402

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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3: gb\_in.\*  
4: gb\_in.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: gb\_vl.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_mu.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_hhg\_hum.\*  
31: em\_hhg\_inv.\*  
32: em\_hhg\_other.\*  
33: em\_hhg\_mus.\*  
34: em\_hhg\_pln.\*  
35: em\_hhg\_rpd.\*  
36: em\_hhg\_mam.\*  
37: em\_hhg\_vrt.\*  
38: em\_sy.\*  
39: em\_hhg\_hum.\*  
40: em\_hhg\_mus.\*  
41: em\_hhg\_other.\*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	402	6	AR241538 Sequence
2	402	100.0	402	6	AR241539 Sequence
3	402	100.0	402	6	AR254494 Sequence
4	402	100.0	402	6	AR254495 Sequence
5	402	100.0	402	6	BD211560 Canine an
6	402	100.0	402	6	BD211561 Canine an
7	402	100.0	610	4	AF331919 Canis fam
8	402	100.0	610	6	AR241536 Sequence
9	402	100.0	610	6	AR241537 Sequence
10	402	100.0	610	6	AR254492 Sequence
11	402	100.0	610	6	AR254493 Sequence
12	402	100.0	610	6	BD211558 Canine an
13	402	100.0	610	6	BD211559 Canine an
14	398.8	99.2	405	6	AR300436 Sequence
15	398.8	99.2	405	6	AX083939 Sequence
16	345	85.8	345	6	AR241540 Sequence
17	345	85.8	345	6	AR241541 Sequence
18	345	85.8	345	6	AR254496 Sequence
19	345	85.8	345	6	AR254497 Sequence
20	345	85.8	345	6	BD211562 Canine an
21	345	85.8	345	6	BD211563 Canine an
22	344.4	85.7	838	4	AF025436 Felis cat
23	338.6	84.2	405	4	AF068770 Felis cat
24	335.4	83.4	405	4	ECU91947 Equus cabal
25	329.8	82.0	356	4	AF091133 Canis fam
26	326.8	81.3	405	4	BTINTLEUS Zet7872 B.taurus mr
27	326.8	81.3	529	4	SSC133452 Sus scrof
28	325.2	80.9	405	4	SSC010088 U35038 Ovis aries
29	316.2	78.7	520	4	OU35038 Ovis aries
30	281.2	70.0	354	4	AF051372 Felis cat
31	277.2	69.0	405	9	AF294756 Saimiri s
32	277.2	69.0	816	6	E01639 cDNA encodi
33	277.2	69.0	816	6	E13591 cDNA encodi
34	277.2	69.0	816	9	HSILSR X04688 Human mRNA
35	275.6	68.6	816	6	AR380691 Sequence
36	275.6	68.6	816	9	HSBCDPIA X12705 H.sapiens m
37	275.6	68.6	858	6	AX766521 Sequence
38	275.6	68.6	858	6	AX766523 Sequence
39	272.4	67.8	405	9	CEYINSA L26033 Cercopithec
40	270.8	67.4	405	9	MMU19848 U19848 Macaca mula
41	250	62.2	343	6	AX083948 Sequence
42	240.4	59.8	421	12	SVN1L5A M33949 Synthetic h
43	240.4	59.8	4946	1	PPVIRE Y07702 Plasmid pV
44	234.4	58.3	564	10	CEU34588 U34588 Cavia porce
45	231.4	57.6	864	6	AX766525 Sequence

ALIGNMENTS

RESULT 1  
AR241538  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

AR241538  
Sequence B3 from patent US 6471957.  
AR241538  
AR241538.1 GI:27287247  
Unknown.  
Unknown.  
Unclassified.  
1 (bases 1 to 402)  
Sim.G.-K., Yang,S., Dretz,M.J. and Wonderling,R.S.  
Canine IL-4 immunoregulatory proteins and uses thereof  
Patent: US 6471957-A 83 29-OCT-2002;  
Location/Qualifiers

linear PAT 20-DEC-2002

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source
1. .402
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 402; DB 6; Length 402;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTTGGGCTGCCCTATGTTTCTGCTTT 60

Qy 61 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 61 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

Qy 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAAATAAAAATCAC 180
Db 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAAATAAAAATCAC 180

Qy 301 CAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGAAGTTTCCTAGACTACCTGCAA 360
Db 301 CAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGAAGTTTCCTAGACTACCTGCAA 360

Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
Db 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402

RESULT 2
AR241539/c
LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6471957.
ACCESSION AR241539
VERSION AR241539.1 GI:27287248
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 84 29-OCT-2002;
FEATURES
Location/Qualifiers
source
1. .402
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 402; DB 6; Length 402;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTTGGGCTGCCCTATGTTTCTGCTTT 60
Db 402 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTTGGGCTGCCCTATGTTTCTGCTTT 343

Qy 61 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Db 342 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

Qy 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAAATAAAAATCAC 180
Db 282 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAAATAAAAATCAC 223
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Qy 181 CAACGTGTCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
Db 222 CAACGTGTCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 163

Qy 241 GGGAGAGGCTGTGGATAAATACTATTCCTGCTTTTAAATAAAGAACACATAGAGCGC 300
Db 162 GGGAGAGGCTGTGGATAAATACTATTCCTGCTTTTAAATAAAGAACACATAGAGCGC 103

Qy 301 CAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGAAGTTTCCTAGACTACCTGCAA 360
Db 102 CAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGAAGTTTCCTAGACTACCTGCAA 43

Qy 361 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 402
Db 42 GTATTTCTTGGTGTAAATAAACACCGAGTGGACCCGGAAGT 1

RESULT 3
AR254494
LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 83 from patent US 6482403.
ACCESSION AR254494
VERSION AR254494.1 GI:27303382
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;
FEATURES
Location/Qualifiers
source
1. .402
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 402; DB 6; Length 402;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAAATGCTTCGAAATTTGAGTTTCTAGCTCTTTGGGCTGCCCTATGTTTCTGCTTT 60

Qy 61 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
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Qy 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAAATAAAAATCAC 180
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Qy 181 CAACGTGTCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240
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Qy 241 GGGAGAGGCTGTGAGGAGAAAGATGGAGAGTGAAGTTTCCTAGACTACCTGCAA 360
Db 301 CAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGAAGTTTCCTAGACTACCTGCAA 360

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RESULT 4
AR254495/c
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LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002  
 DEFINITION Sequence 84 from patent US 6482403.  
 ACCESSION AR254495  
 VERSION AR254495.1 GI:27303383  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6482403-A 84 19-NOV-2002;  
 FEATURES  
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 BD211560 402 bp DNA linear PAT 17-JUL-2003  
 LOCUS  
 DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.  
 ACCESSION BD211560.1 GI:33021330  
 VERSION JP 2002516104-A/66.  
 KEYWORDS Canis familiaris (dog)  
 SOURCE Canis familiaris  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same  
 JOURNAL Patent: JP 2002516104-A 66 04-JUN-2002;  
 HESKA CORP  
 COMMENT OS Canis familiaris (dog)  
 PN JP 2002516104-A/66  
 PD 04-JUN-2002  
 PF 28-MAY-1999 JP 2000551002

PR 29-MAY-1998 US 60/087306  
 PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC  
 C12N15/00,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,  
 PC A61K39/395,  
 PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/535,  
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 PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC  
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 molecules and  
 CC method of using the same  
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 LOCUS  
 DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.  
 ACCESSION BD211561.1 GI:33021331  
 VERSION JP 2002516104-A/67.  
 KEYWORDS Canis familiaris (dog)  
 SOURCE Canis familiaris  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same  
 JOURNAL Patent: JP 2002516104-A 67 04-JUN-2002;  
 HESKA CORP

COMMENT OS Canis familiaris (dog)  
 PN JP 2002516104-A/67  
 PD 04-JUN-2002  
 PF 28-MAY-1999 JP 2000551002  
 PR 29-MAY-1998 US 60/087306  
 PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC  
 C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395,  
 PC A61K39/395,  
 PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,  
 PC C07K14/54,  
 PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
 G01N33/15  
 PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
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 molecules and  
 CC method of using the same  
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 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAAATTTGAGTTTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60  
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QY 61 GCTGTAGAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCCATCAT 120  
 DB 342 GCTGTAGAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCCATCAT 283

QY 121 CGAATCTGGCTGATAGCGGATGGGAACTGATGATCTCTCTGAAATATAATATCAC 180  
 DB 282 CGAATCTGGCTGATAGCGGATGGGAACTGATGATCTCTCTGAAATATAATATCAC 223

QY 181 CAATGTGCTATTAAGAAGTTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
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QY 241 GGGGAGCTGTGGTAAACTATTCCTGAACTGCTTTTAAAGAACACATAGAGCG 300  
 DB 162 GGGGAGCTGTGGTAAACTATTCCTGAACTGCTTTTAAAGAACACATAGAGCG 103

QY 301 CAAAAAAGAGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360  
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RESULT 7  
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 LOCUS AF331919 610 bp mRNA linear MAM 04-OCT-2001  
 DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.  
 ACCESSION AF331919  
 VERSION AF331919.1 GI:15919180  
 KEYWORDS  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 610)  
 Yang, S., Sellins, K.S., Weber, E. and McCall, C.  
 Canine interleukin-5: molecular characterization of the gene and  
 TITLE

expression of biologically active recombinant protein  
 J. Interferon Cytokine Res. 21 (6), 361-367 (2001)  
 MEDLINE 21334408  
 PUBMED 11440633  
 REFERENCE 2 (bases 1 to 610)  
 AUTHORS Yang, S.  
 Direct Submission  
 TITLE Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613  
 JOURNAL Prospect Parkway, Ft Collins, CO 80525, USA  
 FEATURES Location/Qualifiers  
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3'UTR  
 ORIGIN

Query Match 100.0%; Score 402; DB 4; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-101;  
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 DB 89 GCTGTAGAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTCCATCAT 148

QY 121 CGAATCTGGCTGATAGCGGATGGGAACTGATGATCTCTCTGAAATATAATATCAC 180  
 DB 149 CGAATCTGGCTGATAGCGGATGGGAACTGATGATCTCTCTGAAATATAATATCAC 208

QY 181 CAATGTGCTATTAAGAAGTTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
 DB 209 CAATGTGCTATTAAGAAGTTTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 268

QY 241 GGGGAGCTGTGGTAAACTATTCCTGAACTGCTTTTAAAGAACACATAGAGCG 300  
 DB 269 GGGGAGCTGTGGTAAACTATTCCTGAACTGCTTTTAAAGAACACATAGAGCG 328

QY 301 CAAAAAAGAGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360  
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QY 361 GTATTTCTGGTGTAAATAAACCGAGTGGACACCGGAAAGT 402  
 DB 389 GTATTTCTGGTGTAAATAAACCGAGTGGACACCGGAAAGT 430

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 AR241536  
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 DEFINITION Sequence 80 from patent US 6471957.  
 ACCESSION AR241536  
 VERSION AR241536.1 GI:27287245  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 1 (bases 1 to 610)  
 Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.  
 Canine IL-4 immunoregulatory proteins and uses thereof  
 TITLE



JOURNAL Patent: US 6471957-A 80 29-OCT-2002;  
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Query Match 100.0%; Score 402; DB 6; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-101;  
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 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
 QY 121 CGAACTTGGCTGATAGCGCATGGAACTCGATGATTCCCTACCTCGAAAAATAAAAAATCAC 180  
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 209 CAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 268  
 QY 241 GGGGAGGCTGGGATTAACATTCCAAAACCTGCTCTTTAATAAAAGAACACATAGAGCGC 300  
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 QY 361 GTATTCTTGGTGTAAATAAACCGAGTGGACACCGGAAAGT 402  
 Ddb | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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 ACCESSION AR241537  
 VERSION AR241537.1 GI:27287246  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 610)  
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6471957-A 82 29-OCT-2002;  
 FEATURES Location/Qualifiers  
 1. 610  
 /organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-101;  
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 522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463  
 QY 121 CGAACTTGGCTGATAGCGCATGGAACTCGATGATTCCCTACTCCTGAAAAATAAAAAATCAC 180

RESULT 11  
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 Sequence 82 from patent US 6482403.  
 AR254493  
 ACCESSION  
 AR254493.1 GI:27303381  
 VERSION  
 AR254493.1  
 KEYWORDS  
 Unknown.  
 SOURCE  
 ORGANISM  
 Unclassified.  
 REFERENCE  
 1 (bases 1 to 610)  
 AUTHORS  
 Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE  
 Canine IL-13 immunoregulatory proteins and uses thereof  
 JOURNAL  
 Patent: US 6482403-A 82 19-NOV-2002;  
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 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 QY 181 CAATCTGCATTAAAGAAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCCAC 240  
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 BD211558  
 LOCUS  
 DEFINITION  
 Canine and feline immunoregulatory proteins, nucleic acid molecules  
 and method of using the same.  
 BD211558  
 ACCESSION  
 BD211558.1 GI:33021328  
 VERSION  
 JP 2002516104-A/64.  
 KEYWORDS  
 Canis familiaris (dog)  
 SOURCE  
 ORGANISM  
 Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 610)  
 REFERENCE  
 Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 AUTHORS  
 Canine and feline immunoregulatory proteins, nucleic acid molecules  
 and method of using the same  
 TITLE  
 Patent: JP 2002516104-A 64 04-JUN-2002;  
 JOURNAL  
 HESKA CORP  
 COMMENT  
 OS Canis familiaris (dog)  
 PN IP 2002516104 A/64

PD 04-JUN-2002  
 PF 28-MAY-1999 JP 2000551002  
 PR 29-MAY-1998 US 60/087306  
 PI GERKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC  
 C12N15/09, A61K31/7088, A61K38/00, A61K38/21, A61K39/00, A61K39/395,  
 PC A61K39/395,  
 PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,  
 PC C07K14/54,  
 PC C07K14/56, C07K14/705, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC  
 G01N33/15,  
 PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine  
 and feline immunoregulatory proteins, nucleic acid CC  
 molecules and  
 CC method of using the same  
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 FT CDS (29)..(430).  
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 Query Match 100.0%; Score 402; DB 6; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-101;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGGAATGCTTCGAATTGAGTTGCTAGCTTCTGGGCTGCTATGTTCTGCCTTT 60  
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 QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACCTGCTCCACATCAT 120  
 Db 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACCTGCTCCACATCAT 148  
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 Db 329 CAAAAAAGGCTGGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 388  
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 BD211559/c  
 LOCUS  
 DEFINITION  
 Canine and feline immunoregulatory proteins, nucleic acid molecules  
 and method of using the same.  
 BD211559  
 ACCESSION  
 BD211559.1 GI:33021329  
 VERSION  
 JP 2002516104-A/65.  
 KEYWORDS  
 Canis familiaris (dog)  
 SOURCE  
 ORGANISM  
 Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 610)  
 REFERENCE  
 Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 AUTHORS  
 Canine and feline immunoregulatory proteins, nucleic acid molecules  
 and method of using the same  
 TITLE  
 Patent: JP 2002516104-A 65 04-JUN-2002;  
 JOURNAL  
 HESKA CORP  
 COMMENT  
 OS Canis familiaris (dog)  
 PN IP 2002516104 A/65

JOURNAL	Patent: US 6537781-A 1 25-MAR-2003;
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	ACCESSION	AX083939.2	GI:14532940	
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	KEYWORDS			
	SOURCE	Canis familiaris (dog)		
	ORGANISM	Canis familiaris		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Carnivora; fissipedia; Canidae; Canis.		
	REFERENCE	1		
	AUTHORS	Guo,H., Lawton,R., Wermer,B. and Aiyappa,A.P.		
	TITLE	Methods and compositions concerning canine interleukin 5		
	JOURNAL	Patent: WO 0111049-A 1 15-FEB-2001;		
		IDEXX LABORATORIES, INC (US)		
	COMMENT	On Jun 24, 2001 this sequence version replaced gi:13185501.		
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ORIGIN
Query Match          99.2%;   Score 398.8;   DB 6;   Length 405;
Best Local Similarity 99.5%;   Pred. No. 4.6e-100;
Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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XX AAZ55548;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-5 (IL-5) cDNA coding region.  
XX  
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
XX Canis familiaris.  
OS  
XX  
XX WO9961618-A2.  
XX  
XX  
PD 02-DEC-1999.  
XX  
XX  
PF 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-0087306P.  
XX  
XX (HESK-) HESKA CORP.  
XX  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
PI  
XX  
DR WPI; 2000-072623/06.  
XX  
XX P-PSDB; AAY58219.  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
XX Claim 1b; Page 225; 264pp; English.  
XX  
XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
XX feline IL-5 (IL-5), canine or feline CD40, canine or feline CD154 (CD40  
XX feline Flt-3 ligand, canine or feline IL-13, feline interferon-alpha (IFN-alpha)  
XX ligand), canine IL-5, canine IL-13, feline colony-stimulating factor (GM-CSF), and  
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
XX nucleotides which encode these immunoregulatory proteins. The proteins,  
XX their associated nucleic acids, specific antibodies and inhibitors may be  
XX used as vaccines for therapeutic or prophylactic regulation of an immune  
XX response in animals (particularly cats, dogs, horses and humans). They  
XX may be used to treat autoimmune or infectious diseases including  
XX allergies, tumours, inflammation and graft rejection, and to increase the

AAZ55548 standard; cDNA; 402 BP.  
AAZ55548;  
14-MAR-2000 (first entry)  
Canine interleukin-5 (IL-5) cDNA coding region.  
Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
Canis familiaris.  
WO9961618-A2.  
02-DEC-1999.  
28-MAY-1999; 99WO-US011942.  
29-MAY-1998; 98US-0087306P.  
(HESK-) HESKA CORP.  
Sim G, Yang S, Dreitz MJ, Wonderling RS;  
WPI; 2000-072623/06.  
P-PSDB; AAY58219.  
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useful for treating or preventing e.g. tumors or autoimmune disease.  
Claim 1b; Page 225; 264pp; English.  
Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
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feline IL-5 (IL-5), canine or feline CD40, canine or feline CD154 (CD40  
feline Flt-3 ligand, canine or feline IL-13, feline interferon-alpha (IFN-alpha)  
ligand), canine IL-5, canine IL-13, feline colony-stimulating factor (GM-CSF), and  
and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
nucleotides which encode these immunoregulatory proteins. The proteins,  
their associated nucleic acids, specific antibodies and inhibitors may be  
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allergies, tumours, inflammation and graft rejection, and to increase the

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	344.4	85.7	838	3	AAZ44265 Porcine I
9	316.2	78.7	520	2	AAZ50755 Ovine IL-
10	311.8	77.6	399	2	AAZ50756 Ovine IL-
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12	277.2	69.0	816	3	AAZ44857 Human ade
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14	277.2	69.0	816	3	AAZ20979 Human low
15	277.2	69.0	816	7	AAZ296673 Human nuc
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CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

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 XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX  
 OS Canis familiaris.

XX WO9961618-A2.  
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 XX 02-DEC-1999.  
 XX  
 XX 28-MAY-1999; 99WO-US011942.  
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 XX 29-MAY-1998; 98US-0087306P.  
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 XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX  
 XX WPI; 2000-072623/06.  
 DR P-PSDB; AAY58219.  
 XX  
 XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 PS Claim 1h; Page 226; 264pp; English.

XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 3; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-110;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX AAZ55546;  
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 DT 14-MAR-2000 (first entry)  
 XX Canine interleukin-5 (IL-5) cDNA.  
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 XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX  
 OS Canis familiaris.

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XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US011942.
XX PR 29-MAY-1998; 98US-0087306P.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX DR WPI: 2000-072623/06.
XX DR P-PSDB; AAY58219.
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX PS Claim 1h; Page 223-224; 264pp; English.
XX CC Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40
XX CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX CC nucleotides which encode these immunoregulatory proteins. The proteins,
XX CC their associated nucleic acids, specific antibodies and inhibitors may be
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XX CC response in animals (particularly cats, dogs, horses and humans). They
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XX CC allergies, tumours, inflammation and graft rejection, and to increase the
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XX CC also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for modulators
XX CC of activity, while the antibodies may be used in detection, and in drug
XX CC targeting
XX SQ Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX DT 14-MAR-2000 (first entry)
XX DE Canine interleukin-5 (IL-5) cDNA complement.
XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX OS Canis familiaris.
XX FH Key Location/Qualifiers
XX FT CDS complement(178..582)
XX FT /*tag= a
XX FT /product= "Canine IL-5"
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US011942.
XX PR 29-MAY-1998; 98US-0087306P.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX DR WPI: 2000-072623/06.
XX DR P-PSDB; AAY58219.
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XX CC also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for modulators
XX CC of activity, while the antibodies may be used in detection, and in drug
XX CC targeting
XX SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTTGGGGCTGCTATGTTCTGCTTT 60
```

```

Db 582 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTGGGCTGCCTATGTTTCTGCGCTTT 523
QY 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACTCAT 120
Db 522 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACTCAT 463
QY 121 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
Db 462 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 403
QY 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 240
Db 402 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 343
QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db 342 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 283
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 282 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 223
QY 361 GTATTTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 402
Db 222 GTATTTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 181

```

## RESULT 5

AAF74300 standard; DNA; 405 BP.

AC AAF74300;

DT 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #1.

KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;

KW inflammatory reaction; ds.

OS Canis sp.

FN WO20011049-A2.

PD 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021651.

PF 10-AUG-1999; 99US-00371615.

XX (INDEX-) IDEXX LAB INC.

XX Guo H, Lawton R, Mermer B, Aliyappa AP;

XX WPI; 2001-191542/19.

DR P-PSDB; AAB72615.

XX Novel canine interleukin 5 polynucleotide and polypeptides are used for

PT generating antibodies which are useful in treating allergies in dogs.

XX Claim 31; Page 46; 48pp; English.

PS The present invention provides the protein and coding sequences of the

CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,

CC cancer and inflammatory reactions in dogs. The present sequence is one

CC version of the IL-5 coding sequence shown in the specification

XX Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

XX Query Match 99.2%; Score 398.8; DB 4; Length 405;

XX Best Local Similarity 99.5%; Pred. No. 2.1e-109;

XX Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTGGGCTGCCTATGTTTCTGCGCTTT 60
Db 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTGGGCTGCCTATGTTTCTGCGCTTT 60
QY 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACTCAT 120
Db 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCCACTCAT 120
QY 121 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
Db 121 CGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTCTCTGAAAAATAAAATCAC 180
QY 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 240
Db 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACATTAAGAACCAAACTGCCAC 240
QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
Db 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCGC 300
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
QY 361 GTATTTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 402
Db 361 GTATTTCTTGTGTAATAAACCAGAGTGGACACCGGAAAGT 402

```

## RESULT 6

AZ55550 standard; cDNA; 345 BP.

AC AZ55550;

DT 14-MAR-2000 (first entry)

DE Canine mature interleukin-5 (IL-5) cDNA.

KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

FN WO9961618-A2.

PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX P-PSDB; AAY58220.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease.

XX Claim 1h; Page 226-227; 264pp; English.

CC Sequences AA255546-255551 represent cDNA sequences encoding canine

CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or

CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40

CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)

CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and

CC nucleotides which encode these immunoregulatory proteins. The proteins,

CC their associated nucleic acids, specific antibodies and inhibitors may be

CC used as vaccines for therapeutic or prophylactic regulation of an immune



CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;  
  
Query Match 85.8%; Score 345; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 58 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 117  
Db 1 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 60  
  
QY 118 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 177  
Db 61 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120  
  
QY 178 CACCACTGTGCATTAAGAGATTTTTCAGGGTATAGACATGTGAGACCAAACTGCC 237  
Db 121 CACCACTGTGCATTAAGAGATTTTTCAGGGTATAGACATGTGAGACCAAACTGCC 180  
  
QY 238 CACGGGAGGCTGTGGATAAACTATTCCTGATGATTCCTACTCTGAAAAATAAAAT 297  
Db 181 CACGGGAGGCTGTGGATAAACTATTCCTGATGATTCCTACTCTGAAAAATAAAAT 240  
  
QY 298 CGCCAAAAAAGGTGTGAGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 357  
Db 241 CGCCAAAAAAGGTGTGAGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 300  
  
QY 358 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 402  
Db 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 345  
  
RESULT 7  
AAZ5551/C  
ID AAZ5551 standard; cDNA; 345 BP.  
AC AAZ5551;  
XX  
XX 14-MAR-2000 (first entry)  
DT Canine mature interleukin-5 (IL-5) cDNA complement.  
DE Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
XX Canis familiaris.  
XX WO961618-A2.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-0087306P.  
XX (HESK-) HESKA CORP.  
XX  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
FI WPI; 2000-072623/06.  
XX P-PSDB; AAY58220.  
DR  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
PT

PT useful for treating or preventing e.g. tumors or autoimmune disease.  
XX Claim 1h; Page 228; 264pp; English.  
XX  
XX Sequences AAZ5551-25551 represent cDNA sequences encoding canine  
CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
CC nucleotides which encode these immunoregulatory proteins. The proteins,  
CC their associated nucleic acids, specific antibodies and inhibitors may be  
CC used as vaccines for therapeutic or prophylactic regulation of an immune  
CC response in animals (particularly cats, dogs, horses and humans). They  
CC may be used to treat autoimmune or infectious diseases including  
CC allergies, tumours, inflammation and graft rejection, and to increase the  
CC response from a co-administered antigen. The nucleotide sequences can  
CC also be used for the recombinant production of a protein, while  
CC nucleotide fragments are useful as probes, as amplification primers and  
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
CC The proteins may be used to raise antibodies and to screen for modulators  
CC of activity, while the antibodies may be used in detection, and in drug  
CC targeting  
XX  
SQ Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;  
  
Query Match 85.8%; Score 345; DB 3; Length 345;  
Best Local Similarity 100.0%; Pred. No. 2.7e-93;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 58 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 117  
Db 345 TTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACCTGCTCTCCACT 286  
  
QY 118 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 177  
Db 285 CATCGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 226  
  
QY 178 CACCACTGTGCATTAAGAGATTTTTCAGGGTATAGACATGTGAGACCAAACTGCC 237  
Db 225 CACCACTGTGCATTAAGAGATTTTTCAGGGTATAGACATGTGAGACCAAACTGCC 166  
  
QY 238 CACGGGAGGCTGTGGATAAACTATTCCTGATGATTCCTACTCTGAAAAATAAAAT 297  
Db 165 CACGGGAGGCTGTGGATAAACTATTCCTGATGATTCCTACTCTGAAAAATAAAAT 106  
  
QY 298 CGCCAAAAAAGGTGTGAGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 357  
Db 105 CGCCAAAAAAGGTGTGAGAGAAAGATGAGAGTGACAAAGTTCCTAGACTACCTG 46  
  
QY 358 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 402  
Db 45 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 1  
  
RESULT 8  
AAZ44265  
ID AAZ44265 standard; DNA; 838 BP.  
XX  
XX AAZ44265;  
XX  
XX 31-MAR-2000 (first entry)  
DT  
DE Porcine IL-5 DNA.  
XX  
XX Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4;  
KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.  
XX  
XX Sus scrofa.  
XX  
XX CN1231339-A.  
XX  
XX 13-OCT-1999.  
XX

PF 29-JAN-1999; 99CN-00113447.  
 XX  
 PR 29-JAN-1999; 99CN-00113447.  
 XX  
 XX (UVTW-) UNIV NO 2 MILITARY MEDICAL PLA.  
 XX  
 XX Sun S, Dai J;  
 XX  
 DR WPI; 2000-087904/08.  
 XX  
 PT Nucleic acid vaccine for cysticercosis co-contracted by human and pig.  
 XX  
 PS Claim 3; Page 9; 21pp; Chinese.  
 XX  
 CC This invention describes a novel nucleic acid vaccine for preventing and  
 CC curing human and pork cysticercosis. The invention involves the formation  
 CC of a eukaryotic expression plasmid from fusion transcript expression unit  
 CC consisting of three protective antigen genes (cCl, cC3 and cC4) of pig  
 CC tenial cysticercus and coexpression unit of related cell factor gamma  
 CC interferon (IFN-gamma) and pork interleukin 5 (IL-5)) genes. The  
 CC production and purification process of said nucleic acid vaccine is  
 CC simple and convenient, the physical and chemical properties of the  
 CC vaccine are stable, and the vaccine is easy to store and transport, and  
 CC possesses effective immunological protective function for human and pig  
 CC cysticercosis. This sequence represents the pig IL-5 gene used in the  
 CC method of the invention  
 XX  
 SQ Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;  
 Query Match 85.7%; Score 344.4; DB 3; Length 838;  
 Best Local Similarity 91.0%; Pred. No. 5.8e-93;  
 Matches 366; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
 QY 1 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCTTT 60  
 DB 45 ATGGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCCTATGTTCTGCTTT 104  
 QY 61 GCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
 DB 105 GCTGTACAACTCCATGAATAGCTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 164  
 QY 121 CGAATCTGGCTGATAGCGGATGGGAACTGATGATTCCTTCTGAAATATAAATAC 180  
 DB 165 CGAATCTGATGATAGCGGAACTGATGATTCCTTCTGAAATATAAATAC 224  
 QY 181 CAATGTGCAATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240  
 DB 225 CAATGTGCAATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAAAGTTGCCG 284  
 QY 241 GGGAGGCTGTGGATAAATATTCCTGCTTTTAAATAAAGAACACATAGAGCGC 300  
 DB 285 GGGGATGCTGTGGAAGAGCTTTCCGAACTGCTTTTAAATAAAGAACACATAGAGCGC 344  
 QY 301 CAAATAAAGGCTGTGAGGAGAAAGTGGAGAGTGCAGAAAGTTCCTAGACTACCTGCA 360  
 DB 345 CAAATAAAGGCTGTGAGGAGAAAGTGGAGAGTGCAGAAAGTTCCTAGACTACCTGCA 404  
 QY 361 GTATTTCTGCTGTAATAAATACCGAGTGGACCCGGAAGT 402  
 DB 405 GTGTTCTGCTGTAATAAATACCGAGTGGACCAATGGAAGT 446  
 RESULT 9  
 AAT50755  
 ID AAT50755 standard; DNA; 520 BP.  
 XX  
 AC AAT50755;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 24-SEP-1997 (first entry)  
 XX  
 DE Ovine IL-5 gene.  
 XX

KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
 KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
 KW immunosuppression; allergy; reproductive system; growth; early maturity;  
 KW antibody; diagnosis; immunopotentiator;  
 KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
 KW secretion; IGM; IGA; bacterial endotoxin; gamma-interferon; ss.  
 XX  
 OS Ovis aries.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 46..444  
 FT /\*tag= a  
 FT /product= "Ovine\_IL-5"  
 FT exon 46..183  
 FT /\*tag= b  
 FT exon 184..216  
 FT /\*tag= c  
 FT exon 217..345  
 FT /\*tag= d  
 FT exon 346..480  
 FT /\*tag= e  
 FT exon 481..520  
 PN WO9700321-A1.  
 XX  
 PD 03-JAN-1997.  
 XX  
 PF 14-JUN-1996; 96WO-AU000360.  
 PR 14-JUN-1995; 95AU-00003502.  
 PR 27-OCT-1995; 95AU-00006244.  
 XX  
 PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX  
 PI Seow H, Wood P;  
 XX  
 DR WPI; 1997-077528/07.  
 DR P-FSDB; AAW08479.  
 XX  
 PT Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine  
 PT adjuvants and to treat or prevent microbial infections in livestock.  
 XX  
 PS Claim 6; Page 39-40; 78pp; English.  
 XX  
 CC The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).  
 CC Ovine IL-5 or IL-12 are used to treat and/or prevent infections in  
 CC livestock (esp. cows and sheep), particularly where the animals are  
 CC stressed, e.g. during transport. IL-5 and IL-12 can also be used as  
 CC adjuvants in vaccines for veterinary use (partic. weakly immunogenic  
 CC subunit or synthetic peptide vaccines). They may also be used to treat  
 CC cancer, immunosuppression and allergy, to enhance/suppress the  
 CC reproductive system and to promote growth or early maturity. Optionally  
 CC interleukin can be delivered from constructs or delivery cells and  
 CC antibodies are useful in enzyme immunoassays for rapid diagnosis of  
 CC infection. The interleukins are immunopotentiators, especially IL-5  
 CC promotes growth of early haematopoietic progenitor cells and generation  
 CC of cytotoxic cells from thymocytes, also it stimulates production and  
 CC secretion of IGM and IGA (in synergism with bacterial endotoxin). IL-12  
 CC induces production of gamma-interferon by, and proliferation of, T and NK  
 CC cells and increases the (non-)specific cytolytic lymphocyte response. The  
 CC genetic constructs can also be used for in vitro production of IL-5 or -  
 CC 12. (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 520 BP; 166 A; 99 C; 124 G; 131 T; 0 U; 0 Other;  
 Query Match 78.7%; Score 316.2; DB 2; Length 520;  
 Best Local Similarity 86.8%; Pred. No. 1.4e-84;  
 Matches 348; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
 QY 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTGGGGCTGCCTATGTTCTGCTTT 60



PA (IDEX-) IDEXX LAB INC.  
 XX Guo H, Lawton R, Mermer B, Aiyappa AP;  
 XX WPI; 2001-191542/19.  
 XX Novel canine interleukin 5 polynucleotide and polypeptides are used for  
 PT generating antibodies which are useful in treating allergies in dogs.  
 XX Claim 1; Page 35; 48pp; English.  
 XX The present invention provides the protein and coding sequences of the  
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
 CC cancer and inflammatory reactions in dogs. The present sequence is one  
 CC version of the IL-5 coding sequence shown in the specification  
 XX  
 XX Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;  
 Query Match 71.5%; Score 287.4; DB 4; Length 393;  
 Best Local Similarity 99.7%; Pred. No. 5.5e-76;  
 Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 103 ACATGCTCTCCACTCATCGAAGCTTGGCTGATAGGCGATGGAACTGATGATTCCTACT 162  
 Db 1 ACATGCTCTCCACTCATCGAAGCTTGGCTGATAGGCGATGGAACTGATGATTCCTACT 60  
 QY 163 CCTGAAATAAATAATACCAACTGTGCAATTAAGAAAGTTTTTCAGGGTATAGACACATTG 222  
 Db 61 CCTGAAATAAATAATACCAACTGTGCAATTAAGAAAGTTTTTCAGGGTATAGACACATTG 120  
 QY 223 AAGAACCAACTGCGGCGGAGGCTGTGATAAATACTTCCAAACTGCTTTTAATA 282  
 Db 121 AAGAACCAACTGCGGCGGAGGCTGTGATAAATACTTCCAAACTGCTTTTAATA 180  
 QY 283 AAAGAACACATAGAGCGCCCAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAG 342  
 Db 181 AAAGAACACATAGAGCGCCCAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAG 240  
 QY 343 TTCTAGACTACCTGCAAGTATTTCTTGGTGTATATAAACACCGAGTGA 391  
 Db 241 TTCTAGACTACCTGCAAGTATTTCTTGGTGTATATAAACACCGAGTGA 289  
 RESULT 12  
 ID AAA34857 standard; DNA; 816 BP.  
 XX AAA34857;  
 AC AAA34857;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2546.  
 XX  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;  
 KW antiallergic; antiasthmatic; cytoskeletal; analgesic; impaired airway;  
 KW lung disease; ischemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200009525-A2.  
 PN  
 XX 24-FEB-2000.  
 PD  
 XX 03-AUG-1999; 99WO-US017712.  
 XX  
 XX 03-AUG-1998; 98US-0095212P.  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW.  
 XX WPI; 2000-205971/18.  
 XX  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Disclosure; Page 716; 1343pp; English.  
 XX  
 XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytoskeletal and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impaired respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;  
 Query Match 69.0%; Score 277.2; DB 3; Length 816;  
 Best Local Similarity 80.6%; Pred. No. 8.4e-73;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
 QY 1 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTTCTGGGGCTGCTATGTTCTGCCTTT 60  
 Db 45 ATGAGGATGCTTCTGCATTTGAGTTTCTAGCTTCTGGAGCTGCTATGCTATGCCATC 104  
 QY 61 GCTGTAGAAAATCCCATGATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
 Db 105 CCCACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT 164  
 QY 121 CGAACTGGCTGATAGCGGATGGAACTGATGATTTCTACTCTGAAAATAAAATACAC 180  
 Db 165 CGAACTCTGCTGATAGCAATGAGACTCTGAGGATTCCTGTTCTGTACATAAAATCAC 224  
 QY 181 CAACCTGTCATTAAGAAGTTTTCAGGGTATAGACACTTGAAGACCAACCTGCCAC 240  
 Db 225 CACTGTGCTGCTGAAGAAATCTTTCAGGGAATAGGCACCTGGAGAGTCAACTGTGCAA 284  
 QY 241 GGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAGCGC 300  
 Db 285 GGGGCTACTGTGGAAGACTATTCAAAAACCTGTCTTTAATAAAGAACATACATTGCGGC 344  
 QY 301 CAAAAAAGGCTGTGCGAGGAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 360  
 Db 345 CAAAAAAGGCTGTGCGAGGAAGATGGAGAGTGACAAAGTTCTAGACTACCTGCAA 404  
 QY 361 GTATTTCTTGGTGTAAATAAAACACCGAGTGACACCGGAAAGT 402  
 Db 405 GAGTTTCTTGGTGTAAATAAAACACCGAGTGATATAGAAAGT 446

301	CAAAAAAAAAAGGTGTGCAGGAGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGC	360
QY		
345	CAAAAAAAAAAGTGTGGAGAGAGAAAGACCGAGAGTAAACCAATTCCTAGACTACCTGC	404
Db		
361	GTATTTCTTGGTGTAAATAAACCCGAGTGCACCCGAAAGT	402
QY		
405	GAGTTCTTGGTGTAAATGAACACCGAGTGGATATGAAAGT	446
Db		

RESULT 14  
AAF20979  
ID AAF20979 standard: DNA: 816 BP.

xx	
AC	AAF20979;
XX	
DT	14-MAR-2001
	(first entry)

Human	low adenosine antisense oligonucleotide related sequence #2546.
DE	
XX	
XX	
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allelxy;

KW human; urinary urobilinogen; erythrocytes; bilirubin; hemoglobin  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW  
KW  
KW  
KW  
KW  
KW

sulfonamide hypoglycaemia; pulmonary infection;  
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
chronic obstructive pulmonary disease; pulmonary infection bronchitis;

XX  
OS  
XX

Homo sapiens.

EN 00200002730 REL:  
 XX  
 XX  
 PD 26-OCT-2000.  
 XX

XX  
PR 06-APR-1999; 99US-0127958P.  
XX

PA (NYCE/) NYCE J W.  
XX  
PT NYCE JW:

WPI; 2000-679539/66.  
Low adenosine (A) content antisense oligonucleotides which do not trigger

PT and respiratory obstructions.  
XX  
PS Disclosure: Page 788: 1592pp: English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base.

(I) can have respiratory, bronchodilatory, anasthmatic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antitense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with

transcription factors, transcription factors, activating peptide factors and transmitters, antibody receptors, cytokines and immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenous produced specific and non-specific enzymes,

CC binding proteins),  $\alpha$ -adrenergic receptors, central  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors. CNS and peripheral nervous and non-nervous system peptide  
CC receptors. CNS and peripheral nervous and non-nervous system peptide

transmembrane) receptors, growth factors, and malignancy associated proteins. The receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction

CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impaired respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 69.0%; Score 277.2; DB 3; Length 816;  
 Best Local Similarity 80.6%; Pred. No. 8.4e-73;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
 QY 1 ATGAGATGCTTCTGAATTGAGTTGCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60  
 Db 45 ATGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGGAGCTGCTACGTATGCCATC 104  
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGCGAGAGACCTTGACACTCTCCATCAT 120  
 Db 105 CCCACAGAAATCCCAAGTGCAATTTGGTGAAGAGACCTTGGACGCTCTTCTACTCAT 164  
 QY 121 CGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAATAAAATCAC 180  
 Db 165 CGAACTCTGCTGATAGCAATGAGACTCTGAGGATTCCTGCTGTACATAAAATCAC 224  
 QY 181 CAACTGTGCATTAAGAAGTTTTCAGGTATAGACATTTGAAGAACCAATGCCAC 240  
 Db 225 CAACTGTGCATTAAGAAGTTTTCAGGGAATAGGACATGAGAGTCAAACTGTGCAA 284  
 QY 241 GGGGAGCTGTGGATAAATATTCACAAATCTTGTCTTAAATAAAGAACACATAGAGCG 300  
 Db 285 GGGGAGCTGTGGATAAATATTCACAAATCTTGTCTTAAATAAAGAACACATAGAGCG 344  
 QY 361 GTATTTCTTGGTGTAAATAAACCGAGTGGACACCGGAAAGT 402  
 Db 405 GAGTTTCTTGGTGTAAATAAACCGAGTGGATTAATAGAAAGT 446

RESULT 15  
 ABZ96673  
 ID ABZ96673 standard; DNA; 816 BP.

AC ABZ96673;

XX 17-OCT-2003 (first entry)

XX Human nucleic acid sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

PA (EPITG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasegna A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

DR Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

XX Disclosure; SEQ ID NO 11915; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 69.0%; Score 277.2; DB 7; Length 816;  
 Best Local Similarity 80.6%; Pred. No. 8.4e-73;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCTGAATTGAGTTTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60  
 Db 45 ATGAGATGCTTCTGCAATTTGAGTTTCTAGCTCTTGGAGCTGCTACGTATGCCATC 104  
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGCGAGAGACCTTGACACTCTCTCCATCAT 120  
 Db 105 CCCACAGAAATCCCAAGTGCAATTTGGTGAAGAGACCTTGGACGCTCTTCTACTCAT 164  
 QY 121 CGAACTTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCTGAAATAAAATCAC 180  
 Db 165 CGAACTCTGCTGATAGCAATGAGACTCTGAGGATTCCTGCTGTACATAAAATCAC 224  
 QY 181 CAACTGTGCATTAAGAAGTTTTCAGGGAATAGACATTTGAAGAACCAATGCCAC 240  
 Db 225 CAACTGTGCATTAAGAAGTTTTCAGGGAATAGGACATGAGAGTCAAACTGTGCAA 284  
 QY 241 GGGGAGCTGTGGATAAATATTCACAAATCTTGTCTTAAATAAAGAACACATAGAGCG 300  
 Db 285 GGGGAGCTGTGGATAAATATTCACAAATCTTGTCTTAAATAAAGAACACATAGAGCG 344  
 QY 301 CAAAAAAGGCTGTGCGAGGAAGATGGAGAGTGCAGAAAGTTCCTAGACTACCTGCAA 360  
 Db 345 CAAAAAAGGCTGTGCGAGGAAGATGGAGAGTGCAGAAAGTTCCTAGACTACCTGCAA 404  
 QY 361 GTATTTCTTGGTGTAAATAAACCGAGTGGACACCGGAAAGT 402  
 Db 405 GAGTTTCTTGGTGTAAATAAACCGAGTGGATTAATAGAAAGT 446

Search completed: August 30, 2004, 21:48:18  
 Job time : 192.733 secs

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 20:51:08 ; Search time 35.8667 Seconds  
(without alignments)  
6219.989 Million cell updates/sec

Title: US-10-787-382-7  
Perfect score: 402  
Sequence: 1 atgagaatgtttctgaattt.....ccgagtgacacggaaagt 402

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/pCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	402	4	US-09-322-409-83
2	402	100.0	402	4	US-09-322-409-84
3	402	100.0	402	4	US-09-451-527-83
4	402	100.0	402	4	US-09-451-527-84
5	402	100.0	610	4	US-03-322-409-80
6	402	100.0	610	4	US-03-322-409-82
7	402	100.0	610	4	US-09-451-527-80
8	402	100.0	610	4	US-09-451-527-82
9	398.8	99.2	405	4	US-09-371-615A-1
10	345	85.8	345	4	US-09-322-409-85
11	345	85.8	345	4	US-09-322-409-87
12	345	85.8	345	4	US-09-451-527-85
13	345	85.8	345	4	US-09-451-527-87
14	277.2	69.0	816	3	US-09-079-839-2
15	275.6	68.6	816	4	US-09-023-655-1236
16	206.4	51.3	1534	3	US-09-629-643A-4
17	206.4	51.3	1534	3	US-09-155-884-4
18	206.2	51.3	377	4	US-09-180-854-1
19	99.4	24.7	3230	3	US-09-280-799-78
20	99.4	24.7	3230	6	5324640-1
21	90.6	22.5	6727	3	US-08-629-643A-5
22	90.6	22.5	6727	3	US-09-280-799-1
23	90.6	22.5	6727	3	US-09-155-884-5
24	40.2	10.0	47	1	US-08-466-852-2
25	38	9.5	7218	1	US-08-232-453-14
26	34.4	8.6	4843	3	US-08-986-485-1
27	33.4	8.3	22846	2	US-08-469-461-3

28 33.4 8.3 22846 3 US-07-890-609-3 Sequence 3, Appli  
c 29 32.4 8.1 2797 4 US-09-453-702B-244 Sequence 244, App  
c 30 31.8 7.9 832 4 US-09-621-976-2813 Sequence 2813, Ap  
c 31 31.8 7.9 1902 4 US-09-220-132-74 Sequence 74, Appl  
c 32 31.6 7.9 927 4 US-09-134-001C-150 Sequence 150, App  
33 31.6 7.9 1642 4 US-03-737-698B-24 Sequence 24, Appl  
34 31.6 7.9 1642 4 US-09-737-626A-24 Sequence 24, Appl  
35 31.6 7.9 9626 4 US-09-150-867-2 Sequence 2, Appli  
c 36 31.6 7.9 174493 4 US-09-804-471A-3 Sequence 3, Appli  
c 37 31.6 7.9 174493 4 US-10-238-709-3 Sequence 3, Appli  
c 38 31.6 7.9 1664976 4 US-08-916-421B-1 Sequence 1, Appli  
c 39 31.4 7.8 1497 4 US-09-220-132-94 Sequence 94, Appl  
c 40 31.4 7.8 21338 4 US-08-961-527-20 Sequence 20, Appl  
c 41 31.2 7.8 505 4 US-09-621-976-15639 Sequence 15639, A  
c 42 31.2 7.8 1664976 4 US-08-916-421B-1 Sequence 1, Appli  
c 43 31 7.7 222 4 US-09-543-681A-1166 Sequence 1166, Ap  
c 44 31 7.7 3434 4 US-09-388-743-9 Sequence 9, Appli  
45 30.8 7.7 1842 4 US-09-328-352-2806 Sequence 2806, Ap

ALIGNMENTS

RESULT 1  
US-09-322-409-83  
; Sequence B3, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-83

Query Match 100.0%; Score 402; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5.9e-123;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 60  
Db 1 ATGAGAAATCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTT 60  
QY 61 GCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
Db 61 GCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
QY 121 CGAACTTGCTGATAGGCGATGGGAACCTGATGATCTTCTCTGAAATAAATCAAC 180  
Db 121 CGAACTTGCTGATAGGCGATGGGAACCTGATGATCTTCTCTGAAATAAATCAAC 180  
QY 181 CCAACTGTGATTAAGAAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240  
Db 181 CCAACTGTGATTAAGAAAGTTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCCAC 240  
QY 241 GGGAGGCTGTGATTAACCTATTCGAAATCTTCTTAAATAAGAACACATAGAGCGC 300  
Db 241 GGGAGGCTGTGATTAACCTATTCGAAATCTTCTTAAATAAGAACACATAGAGCGC 300  
QY 301 CAAATAAAGGTGTGTCAGGAGAAAGATGAGAGTGCACAAAGTCTCTAGACTACCTGCAA 360

Db 301 CAAAAAAGGTGTGCGAGGAAGATGGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
Qy 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402  
Db 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402

## RESULT 2

US-09-322-409-84/c  
; Sequence 84, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-84

Query Match 100.0%; Score 402; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5,9e-123;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTTGGGCGCTGCCTATGTTTCTGCTTT 60  
Db 402 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTTGGGCGCTGCCTATGTTTCTGCTTT 343  
Qy 61 GCTGTAGAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
Db 342 GCTGTAGAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283  
Qy 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTCTCTCTCTCTCTCTCTCT 180  
Db 282 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTCTCTCTCTCTCTCTCTCT 223  
Qy 181 CAATGTGCAATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
Db 222 CAATGTGCAATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 163  
Qy 241 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
Db 162 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 103  
Qy 301 CAAAAAAGGTGTGCGAGGAAGATGGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
Db 102 CAAAAAAGGTGTGCGAGGAAGATGGAGTGCACAAAGTTCCTAGACTACCTGCAA 43  
Qy 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402  
Db 42 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 1

## RESULT 3

US-09-451-527-83  
; Sequence 83, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; EARLIER FILING DATE: 1999-12-01  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-451-527-83

Query Match 100.0%; Score 402; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5,9e-123;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTTGGGCGCTGCCTATGTTTCTGCTTT 60  
Db 1 ATGAGATGCTTCGAAATTTGAGTTTGCTAGCTCTTGGGCGCTGCCTATGTTTCTGCTTT 60  
Qy 61 GCTGTAGAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
Db 61 GCTGTAGAAATCCCATGAATAGACTGCTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
Qy 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTCTCTCTCTCTCTCTCTCT 180  
Db 121 CGAATCTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTCTCTCTCTCTCTCTCTCT 180  
Qy 181 CAATGTGCAATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
Db 181 CAATGTGCAATTAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
Qy 241 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
Db 241 GGGAGGCTGTGGATAAATATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
Qy 301 CAAAAAAGGTGTGCGAGGAAGATGGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
Db 301 CAAAAAAGGTGTGCGAGGAAGATGGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
Qy 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402  
Db 361 GTATTTCTTGTTGTAATAAACACCGAGTGGACACCGGAAAGT 402

## RESULT 4

US-09-451-527-84/c  
; Sequence 84, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; EARLIER FILING DATE: 1999-12-01  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA



Db 89 GCTGTGAAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGCACACTGCTCTCCACTCAT 141  
 Qy 121 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTTACTCCTCGAAATATAAAATCAC 180  
 Db 149 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTTACTCCTCGAAATATAAAATCAC 208  
 Qy 181 CAACCTGTGCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240  
 Db 209 CNACTGTGCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268  
 Qy 241 GGGGAGGCTGTGGATAAATCTATTCCAAAACCTGTCTTTTAATAAAGAACACATAGAGCGC 300  
 Db 269 GGGGAGGCTGTGGATAAATCTATTCCAAAACCTGTCTTTTAATAAAGAACACATAGAGCGC 328  
 Qy 301 CAAAAAATAAGGCTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
 Db 329 CAAAAAATAAGGCTGTGAGGAGAAAGTGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388  
 Qy 361 GTATTCTTCTGTGTAATAAACCCGAGTGGACACCGGAAAGT 402  
 Db 389 GTATTCTTCTGTGTAATAAACCCGAGTGGACACCGGAAAGT 430

RESULT 6  
 US-09-322-409-82/c  
 ; Sequence 82, Application US/09322409  
 ; Patent No. 6471957  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Drezitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE: IM-2-C1  
 ; CURRENT APPLICATION NUMBER: US/09/322,409  
 ; CURRENT FILING DATE: 1999-05-28  
 ; EARLIER APPLICATION NUMBER: 60/087,306  
 ; EARLIER FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 82  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-322-409-82

Query Match 100.0%; Score 402; DB 4; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-123;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 ATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTGGGCTGCCTATGTTTCTGCTTT 60  
 Db 582 ATGAGAAATGCTTCTGAAATTTGAGTTTGTCTAGCTCTTGGGCTGCCTATGTTTCTGCTTT 523  
 Qy 61 GCTGTAGAAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCACTCAT 120  
 Db 522 GCTGTAGAAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCACTCAT 463  
 Qy 121 CGAACTTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAATCAC 180  
 Db 462 CGAACTTGGCTGATAGGGGATGGGAACCTGATGATTCCTACTCCTGAAAAATAAAATCAC 403  
 Qy 181 CAACCTGTGCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240  
 Db 402 CAACCTGTGCATTAAAGAAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 343  
 Qy 241 GGGGAGGCTGTGGATAAATCTATTCCAAAACCTGTCTTTTAATAAAGAACACATAGAGCGC 300  
 Db 342 GGGGAGGCTGTGGATAAATCTATTCCAAAACCTGTCTTTTAATAAAGAACACATAGAGCGC 283  
 Qy 301 CAAAAAATAAGGCTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360

Db 282 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA 223  
 QY 361 GTATTTCTGGTGAATAAAACACCGAGTGGACACCGGAAAGT 402  
 Db 222 GTATTTCTGGTGAATAAAACACCGAGTGGACACCGGAAAGT 181

## RESULT 7

US-09-451-527-80  
 ; Sequence 80, Application US/09451527  
 ; Patent No. 6482403  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; FILE REFERENCE: IM-2-C2  
 ; CURRENT APPLICATION NUMBER: US/09/451,527  
 ; EARLIER FILING DATE: 1999-12-01  
 ; EARLIER APPLICATION NUMBER: 09/322,409  
 ; EARLIER FILING DATE: 1999-05-28  
 ; EARLIER APPLICATION NUMBER: 60/087,306  
 ; EARLIER FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 174  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 80  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 ; NAME/KEY: CDS  
 ; LOCATION: (29)...(430)  
 US-09-451-527-80

Query Match 100.0%; Score 402; DB 4; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-123;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGATGCTTCGAATTTGAGTTTGGCTTCTAGCTCTGGGCTGCTATGTTTCTGCTTT 60  
 Db 29 ATGAGATGCTTCGAATTTGAGTTTGGCTTCTAGCTCTGGGCTGCTATGTTTCTGCTTT 68  
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
 Db 89 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148  
 QY 121 CGAATTTGGCTGATAGCGGATGGACCTGATGATTCCTACTCTGAAATAAAATATCAC 180  
 Db 149 CGAATTTGGCTGATAGCGGATGGACCTGATGATTCCTACTCTGAAATAAAATATCAC 208  
 QY 181 CAATGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
 Db 209 CAATGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 268  
 QY 241 GGGAGGCTGTGATAAACTATTCCAAACTTCTCTTTAATAAAGAACACATAGAGCGC 300  
 Db 269 GGGAGGCTGTGATAAACTATTCCAAACTTCTCTTTAATAAAGAACACATAGAGCGC 328  
 QY 301 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
 Db 329 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 388  
 QY 361 GTATTTCTGGTGAATAAAACACCGAGTGGACACCGGAAAGT 402  
 Db 389 GTATTTCTGGTGAATAAAACACCGAGTGGACACCGGAAAGT 430

## RESULT 8

US-09-451-527-82/c  
 ; Sequence 82, Application US/09451527  
 ; Patent No. 6482403

; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; FILE REFERENCE: IM-2-C2  
 ; CURRENT APPLICATION NUMBER: US/09/451,527  
 ; EARLIER FILING DATE: 1999-12-01  
 ; EARLIER APPLICATION NUMBER: 09/322,409  
 ; EARLIER FILING DATE: 1999-05-28  
 ; EARLIER APPLICATION NUMBER: 60/087,306  
 ; EARLIER FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 174  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 82  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-451-527-82

Query Match 100.0%; Score 402; DB 4; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-123;  
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGATGCTTCGAATTTGAGTTTGGCTTCTAGCTCTGGGCTGCTATGTTTCTGCTTT 60  
 Db 582 ATGAGATGCTTCGAATTTGAGTTTGGCTTCTAGCTCTGGGCTGCTATGTTTCTGCTTT 523  
 QY 61 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
 Db 522 GCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463  
 QY 421 CGAATTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 180  
 Db 462 CGAATTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTGAAATAAAATATCAC 403  
 QY 181 CAATGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
 Db 402 CAATGTGCATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 343  
 QY 241 GGGAGGCTGTGATAAACTATTCCAAACTTCTCTTTAATAAAGAACACATAGAGCGC 300  
 Db 342 GGGAGGCTGTGATAAACTATTCCAAACTTCTCTTTAATAAAGAACACATAGAGCGC 283  
 QY 301 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 360  
 Db 282 CAAAAAAGGTGTGCGAGGAAGATGGAGAGTGCACAAAGTTCCTAGACTACCTGCAA 223  
 QY 361 GTATTTCTGGTGAATAAAACACCGAGTGGACACCGGAAAGT 402  
 Db 222 GTATTTCTGGTGAATAAAACACCGAGTGGACACCGGAAAGT 181

## RESULT 9

US-09-371-615A-1  
 ; Sequence 1, Application US/09371615A  
 ; Patent No. 6537781  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IDEXX LABORATORIES  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
 ; FILE REFERENCE: 03604001700US00  
 ; CURRENT APPLICATION NUMBER: US/09/371,615A  
 ; CURRENT FILING DATE: 1999-08-10  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 405  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-371-615A-1

Query Match 99.2%; Score 398.8; DB 4; Length 405;  
Best Local Similarity 99.5%; Pred. No. 6.7e-122;  
Matches 400; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGAAATGCTTGAATTTGAGTTTGTAGCTCTTGGGCTGCCATCTTCTGCTTT 60  
DB 1 ATGAGAAATGCTTGAATTTGAGTTTGTAGCTCTTGGGCTGCCATCTTCTGCTTT 60

QY 61 GCTGTAGAAATCCCATGATAGCTGTTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120  
DB 61 GCTGTAGAAATCCCATGATAGCTGTTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 121 CGAACTTGGCTGATAGGCGATGGAACTGATGATTTCTTCTCTGAAATATAAATAC 180  
DB 121 CGAACTTGGCTGATAGGCGATGGAACTGATGATTTCTTCTCTGAAATATAAATAC 180

QY 181 CAACCTGCTGATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240  
DB 181 CAACCTGCTGATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCCAC 240

QY 241 GGGGAGCTGCTGATAAATCTTCCAAACTTCTTTTAAATAAAGAACACATAGAGCGC 300  
DB 241 GGGGAGCTGCTGATAAATCTTCCAAACTTCTTTTAAATAAAGAACACATAGAGCGC 300

QY 301 CAAAAAAGGCTGCGAGAGAAAGATGGAGAGTGCACAAAGTTCTAGACTACCTGCAA 360  
DB 301 CAAAAAAGGCTGCGAGAGAAAGATGGAGAGTGCACAAAGTTCTAGACTACCTGCAA 360

QY 361 GTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402  
DB 361 GTATTTCTTGGTGTATTAACACCGAGTGGACATGGAAAGT 402

RESULT 10  
US-09-322-409-85  
; Sequence 85, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-CL  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris

Query Match 85.8%; Score 345; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.5e-104;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117  
DB 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

QY 118 CATCGAACTTGGCTGATAGGCGATGGAACTGTATCTTCTTCTTAAATAAATAAATAA 177  
DB 61 CATCGAACTTGGCTGATAGGCGATGGAACTGTATCTTCTTCTTAAATAAATAAATAA 120

QY 178 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 237  
DB 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 180

QY 238 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 297  
DB 191 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 240

QY 298 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 357  
DB 241 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 300

QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402  
DB 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345

RESULT 11  
US-09-322-409-87/c  
; Sequence 87, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-CL  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris

Query Match 85.8%; Score 345; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.5e-104;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117  
DB 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

QY 118 CATCGAACTTGGCTGATAGGCGATGGAACTGTATCTTCTTCTTAAATAAATAAATAA 177  
DB 285 CATCGAACTTGGCTGATAGGCGATGGAACTGTATCTTCTTCTTAAATAAATAAATAA 226

QY 178 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 237  
DB 225 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAAACTGCC 166

QY 238 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 297  
DB 165 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAG 106

QY 298 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 357  
DB 105 CGCCAAAAAAGGCTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 46

QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402  
DB 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 1

RESULT 12  
US-09-451-527-85  
; Sequence 85, Application US/09451527

Patent No. 6482403  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Dreitz, Matthew J.  
 APPLICANT: Wonderling, Ramani S.  
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 FILE REFERENCE: IM-2-C2  
 CURRENT APPLICATION NUMBER: US/09/451,527  
 CURRENT FILING DATE: 1999-12-01  
 EARLIER APPLICATION NUMBER: 09/322,409  
 EARLIER FILING DATE: 1999-05-28  
 EARLIER APPLICATION NUMBER: 60/087,306  
 EARLIER FILING DATE: 1998-05-29  
 NUMBER OF SEQ ID NOS: 174  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 85  
 LENGTH: 345  
 TYPE: DNA  
 ORGANISM: Canis familiaris  
 NAME/KEY: CDS  
 LOCATION: (1)..(345)  
 US-09-451-527-85

Query Match 85.8%; Score 345; DB 4; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-104;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 58 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCACT 117  
 DB 1 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCACT 60  
 QY 118 CATGCACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 177  
 DB 61 CATCAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 120  
 QY 178 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 237  
 DB 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180  
 QY 238 CACGGGAGGCTGTGGATAAATCTTCCAAAATTTGCTTTAATAAAGAACACATAGAG 297  
 DB 181 CACGGGAGGCTGTGGATAAATCTTCCAAAATTTGCTTTAATAAAGAACACATAGAG 240  
 QY 298 CGCCAAAAAAGGTGTGCAGAGAAAGATGGAGATGACAAAGTTCCTAGACTACCTG 357  
 DB 241 CGCCAAAAAAGGTGTGCAGAGAAAGATGGAGATGACAAAGTTCCTAGACTACCTG 300  
 QY 358 CAAGTATTTCTTGGTGTATAAACCAGGTGACACCGGAAAGT 402  
 DB 301 CAAGTATTTCTTGGTGTATAAACCAGGTGACACCGGAAAGT 345

RESULT 13  
 US-09-451-527-87/c  
 Sequence 87, Application US/09451527  
 Patent No. 6482403  
 GENERAL INFORMATION:  
 APPLICANT: Sim, Gek-Kee  
 APPLICANT: Yang, Shumin  
 APPLICANT: Dreitz, Matthew J.  
 APPLICANT: Wonderling, Ramani S.  
 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 FILE REFERENCE: IM-2-C2  
 CURRENT APPLICATION NUMBER: US/09/451,527  
 CURRENT FILING DATE: 1999-12-01  
 EARLIER APPLICATION NUMBER: 09/322,409  
 EARLIER FILING DATE: 1999-05-28  
 EARLIER APPLICATION NUMBER: 60/087,306  
 EARLIER FILING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 174  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 87  
 LENGTH: 345  
 TYPE: DNA  
 ORGANISM: Canis familiaris  
 US-09-451-527-87

Query Match 85.8%; Score 345; DB 4; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-104;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 58 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCACT 117  
 DB 345 TTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCACT 286  
 QY 118 CATCAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 177  
 DB 285 CATCAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTCTGAAAATAAAAAT 226  
 QY 178 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 237  
 DB 225 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 166  
 QY 238 CACGGGAGGCTGTGGATAAATCTTCCAAAATTTGCTTTAATAAAGAACACATAGAG 297  
 DB 165 CACGGGAGGCTGTGGATAAATCTTCCAAAATTTGCTTTAATAAAGAACACATAGAG 106  
 QY 298 CGCCAAAAAAGGTGTGCAGAGAAAGATGGAGATGACAAAGTTCCTAGACTACCTG 357  
 DB 105 CGCCAAAAAAGGTGTGCAGAGAAAGATGGAGATGACAAAGTTCCTAGACTACCTG 46  
 QY 358 CAAGTATTTCTTGGTGTATAAACCAGGTGACACCGGAAAGT 402  
 DB 45 CAAGTATTTCTTGGTGTATAAACCAGGTGACACCGGAAAGT 1

RESULT 14  
 US-09-079-839-2  
 Sequence 2, Application US/09079839  
 Patent No. 6048726  
 GENERAL INFORMATION:  
 APPLICANT: Wellman, Joel K.  
 APPLICANT: Karim, Aftab S.  
 TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION  
 FILE REFERENCE: 09998/002001  
 CURRENT APPLICATION NUMBER: US/09/079,839  
 CURRENT FILING DATE: 1998-05-15  
 NUMBER OF SEQ ID NOS: 2  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 816  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-079-839-2

Query Match 69.0%; Score 277.2; DB 3; Length 816;  
 Best Local Similarity 80.6%; Pred. No. 1.3e-81;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
 QY 1 ATGAGATGCTTCTGGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 60  
 DB 45 ATGAGATGCTTCTGCAATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCCATC 104  
 QY 61 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCACTCAT 120  
 DB 105 CCCACAGAAATCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTCTACTCAT 164  
 QY 121 CGAACTTGGCTGTAGCGGATGGAACTGATGATTCCTACTCTCTGAAAATAAAAATCAC 180  
 DB 165 CGAACTTGGCTGTAGCGCAATGAGACTCTGAGGATTCCTGTTCTCTGTACATAAATCAC 224  
 QY 181 CAAGTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCCAC 240

Db 225 CAACCTGTGACTGAAGAAATCTTTAGGGAATAGGCACACTGGAGTCAAACTGTGCAA 284  
Qy 241 GGGAGGCTGTGGATAAACTATTCAAAACCTGTCTTTTAAATAAAGAACACATAGAGCGC 300  
Db 285 GGGGTACTGTGGAAAGACTATTCAAAAACTTGTCTTAAATAAAGAAATACATTGACGCGC 344  
Qy 301 CAATAAAAGAGTGTCCAGAGAAAGATGGAGAGTGCACAAAGTCTCTAGACTACCTGCAA 360  
Db 345 CAATAAAAGAGTGTGGAGAAAGAACGGAGAGTAAACCAATCTCTAGACTACCTGCAA 404  
Qy 361 GTATTTCTTGGTGTATAAACAACCGAGTGGACACCGGAAAGT 402  
Db 405 GAGTTTCTTGGTGTATGAACACCGAGTGGATAATAGAAAGT 446

## RESULT 15

US-09-023-655-1236  
; Sequence 1236, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: FA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1236:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 816 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: G288309  
US-09-023-655-1236

Query Match 68.6%; Score 275.6; DB 4; Length 816;  
Best Local Similarity 80.3%; Pred. NO. 4.4e-81;  
Matches 323; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 1 ATGAGATGCTTCTGAATTCAGTTGCTAGCTCTTGGGCTGCCTATGTTCTGCCTTT 60  
Db 45 ATGAGGATGCTTCTGCATTGAGTTGCTAGCTCTTGGAGCTGCCTATGCTATGCCATC 104

Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGTGACACTGTCTTCCACTCAT 120  
Db 105 CCCACAGAAATTCACCAAGTGCATTGGTGAAGAGAGACCTTGGCACTTCTTACTCAT 164  
Qy 121 CGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTCTGAAATATAAAATCAC 180  
Db 165 CGAACTCTGTCTGATAGCAATGAGACTCTGAGGATTCCTGTCTGTATATAAAATCAC 224  
Qy 181 CAACCTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAAC 240  
Db 225 CAACCTGTGCATTGAAGAAATCTTTTCAGGGAATAGGCACACTGGAGAGTCAAACTGTGCAA 284  
Qy 241 GGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTTAAATAAAGAACACATAGAGCGC 300  
Db 285 GGGGTACTGTGGAAAGACTATTGAAAACCTTGTCTTAAATAAAGAAATACATTGACGCGC 344  
Qy 301 CAATAAAAGAGTGTGCAGAGAAAGATGGAGAGTGCACAAAGTCTCTAGACTACCTGCAA 360  
Db 345 CAATAAAAGAGTGTGGAGAAAGAACGGAGAGTAAACCAATCTCTAGACTACCTGCAA 404  
Qy 361 GTATTTCTTGGTGTATAAACAACCGAGTGGACACCGGAAAGT 402  
Db 405 GAGTTTCTTGGTGTATGAACACCGAGTGGATAATAGAAAGT 446

Search completed: August 31, 2004, 06:34:46  
Job time : 37.8667 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 21:24:28 ; Search time 1350.53 Seconds  
(without alignments)  
8888.782 Million cell updates/sec

Title: US-10-787-382-7  
Perfect score: 402  
Sequence: 1 atgagaaatctcttgaattt.....ccgagtggaacaccggaagt 402

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

BST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_lam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vri:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277.2	69.0	405	29	AY412020 Homo sapi
2	277.2	69.0	456	14	CD559532
C 3	277.2	69.0	456	14	CD559686
C 4	277.2	69.0	470	14	CD559687

5	277.2	69.0	492	14	CD559533
6	273.2	68.0	405	29	AY412021
7	266.8	66.4	467	14	CD559688
C 8	266.8	66.4	478	14	CD559534
9	266.2	66.2	463	14	CD559535
C 10	266.2	66.2	473	14	CD559689
11	266.2	66.2	489	14	CD559536
C 12	264.6	65.8	467	14	CD559690
C 13	261.6	65.1	477	14	CD559608
14	192.6	47.9	399	29	AY412022
15	131.8	32.8	622	29	CE311159
C 16	78	19.4	503	13	BQ598873
17	42.4	10.5	1025	13	EX441235
18	40.6	10.1	522	12	BI670794
19	40	10.0	317	14	CD087271
20	39.8	9.9	535	28	AZ370501
21	39.2	9.8	603	12	BJ328562
22	39.2	9.8	619	12	BJ328648
23	39.2	9.8	905	29	CNS00D59
24	38.8	9.7	1201	13	EX397166
25	38.6	9.6	1359	12	BG543026
26	38.2	9.5	667	29	CE510121
27	38.2	9.5	797	29	CC567321
28	38	9.5	432	9	AA560540
29	38	9.5	494	14	CE094467
30	38	9.5	623	28	AQ576964
31	38	9.5	666	28	AQ326668
C 32	38	9.5	1011	29	CNS00JRI
33	37.8	9.4	584	13	BQ526053
34	37.8	9.4	671	13	EX707130
35	37.8	9.4	684	13	EX758408
36	37.8	9.4	715	13	EX773473
37	37.8	9.4	724	13	EX773491
38	37.8	9.4	783	14	CF343019
39	37.8	9.4	892	13	EX776535
C 40	37.6	9.4	699	28	AQ781738
41	37.6	9.4	964	14	CD048643
C 42	37.6	9.4	1026	13	EX461051
43	37.6	9.4	1201	9	AL550373
44	37.4	9.3	457	12	BI379332
45	37.4	9.3	695	28	BZ019774

#### ALIGNMENTS

RESULT 1	AV412020	405 bp	DNA	linear	GSS 16-DEC-2003
LOCUS	Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	Genomic survey sequence.				
ACCESSION	AY412020				
VERSION	AY412020.1	GI:39767985			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
	1 (bases 1 to 405)				
	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,				
	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,				
	Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous				
	Gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 405)				
AUTHORS	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,				
	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,				
	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,				
	Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

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## ORIGIN

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 Best Local Similarity 80.6%; Pred. No. 2.3e-59;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 1 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60  
 Db 1 ATGAGATGCTTCTGAATTTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTTCTGCTTT 60

Qy 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTGACACTGCTCTCCACTCAT 120  
 Db 61 CCCACAGAAATCCCATGATAGACTGGTGGCAGACCTTGACACTGCTCTCCACTCAT 120

Qy 121 CGAACTTGGCTGTAGCGGATGGAACTGATGATTCCTACTCTCTGAATAAATAATCAC 180  
 Db 121 CGAACTTGGCTGTAGCGGATGGAACTGATGATTCCTACTCTCTGAATAAATAATCAC 180

Qy 181 CAATGTGCAATTAAGAAGTTTTCAGGATATGACACATTTGAAGAACCAATTCGCCAC 240  
 Db 181 CAATGTGCAATTAAGAAGTTTTCAGGATATGACACATTTGAAGAACCAATTCGCCAC 240

Qy 241 GGGGAGCTGGGATTAACATTTCCAAACTTCTTAAATAAAGACACATAGAGCG 300  
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Qy 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 360  
 Db 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 360

Qy 361 GTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 402  
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RESULT 2  
 CD559532 456 bp mRNA linear EST 11-JUN-2003  
 LOCUS  
 DEFINITION AGENCOURT\_14497057 NIH\_MGC\_195 Homo sapiens cDNA clone  
 IMAGE:6971772 5', mRNA sequence.

ACCESSION CD559532  
 VERSION CD559532.1 GI:31585600  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 456)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: gcgabs-t@mail.nih.gov

Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: IRBK1 row: g column: 11

High quality sequence stop: 456.

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Location/Qualifiers

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/db\_xref="taxon:9606"

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/note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is CDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 456;  
 Best Local Similarity 80.6%; Pred. No. 2.3e-59;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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Qy 61 GCTGTAGAAATCCCATGATAGACTGGTGGCAGACCTTGACACTGCTCTCCACTCAT 120  
 Db 82 CCCACAGAAATCCCATGATAGACTGGTGGCAGACCTTGACACTGCTCTCTACTCAT 141

Qy 121 CGAACTTGGCTGTAGCGGATGGAACTGATGATTCCTACTCTCTGAAAAATAAATCAC 180  
 Db 142 CGAACTTGGCTGTAGCGGATGGAACTGATGATTCCTACTCTCTGAAAAATAAATCAC 201

Qy 181 CAATGTGCAATTAAGAAGTTTTCAGGATATGACACATTTGAAGAACCAATTCGCCAC 240  
 Db 202 CAATGTGCAATTAAGAAGTTTTCAGGATATGACACATTTGAAGAACCAATTCGCCAC 261

Qy 241 GGGGAGCTGGGATTAACATTTCCAAACTTCTTAAATAAAGACACATAGAGCGC 300  
 Db 262 GGGGAGCTGGGATTAACATTTCCAAACTTCTTAAATAAAGACACATAGAGCGC 321

Qy 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 360  
 Db 322 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCAAAAGTTCTCTAGACTACCTGCAA 381

Qy 361 GTATTTCTTGGTGTAAATAACACCGAGTGGACCCGGAAGT 402  
 Db 382 GAGTTTCTTGGTGTAAATAACACCGAGTGGATAATAAGAAAGT 423

## RESULT 3

CD559686/c

LOCUS

DEFINITION AGENCOURT\_14497093 NIH\_MGC\_195 Homo sapiens linear

IMAGE:6971772 3', mRNA sequence.

ACCESSION CD559686

VERSION CD559686.1 GI:31585754

KEYWORDS EST.



SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 456)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 VERSION K559687  
 KEYWORDS MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: IRBK1 row: g column: 11  
 High quality sequence stop: 456.  
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 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 456;  
 Best Local Similarity 80.6%; Pred. No. 2.3e-58;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
 Qy 1 ATGAGATGCTTCTGAATTGAGTTTGTCTAGCTCTTGGGCTGCTATGTTCTGCTTT 60  
 Db 433 ATGAGGATGCTTCTGCAATTTGAGTTTGTCTAGCTCTTGGAGTCTGCTATGCCATC 374  
 Qy 61 GCTGTAGAAATCCCATGATAGACTGTGGCAGACCTTGACACTGCTCTCCACTCAT 120  
 Db 373 CCCACAGAAATCCCAAGTGCATTTGTGMAAGAGACCTTGGACACTGCTTCTACTCAT 314  
 Qy 121 CGAACTTGGCTGATAGGCGATGGGAACCTGATGATTTCTACTCTGTAATAAATAATCAC 180  
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 Qy 181 CAACGTGTCATTAAGAAGTTTTCAGGGTATAGACATGTAGAGACCAACCTGCCAC 240  
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Qy 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACTGCAA 360  
 Db 133 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGCACAAAGTTCCTAGACTACTGCAA 74  
 Qy 361 GTATTTCTGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402  
 Db 73 GAGTTTCTGTGTAAATAAACACCGAGTGGATATAGAAAGT 32  
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 LOCUS AGENCOURT 14497029 NIH MGC 195 Homo sapiens cDNA clone  
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 ACCESSION CD559687  
 VERSION CD559687.2 GI:38453484  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 470)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 69.0%; Score 277.2; DB 14; Length 470;  
 Best Local Similarity 80.6%; Pred. No. 2.3e-58;  
 Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY	1	ATGAGAA	TGCTTCT	CAATTTG	AGTTT	GAGTTT	GCTAG	CTCTT	GGGCT	GCCTAT	GTTTCT	GCCTTT	60
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QY	61	GCTGTAG	AAAAAT	CCCATGA	ATAGACT	GGTGG	CAGAG	ACCTT	GACACT	GTGCT	TCCACT	CAT	120
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QY	121	CGAACTT	GGCTG	ATAGGG	CGATGG	GAACT	GTATGA	TTC	TCTACT	CCTG	AAAAAT	TAAAT	180
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Db	266	CAACTGT	GCAC	TGAAG	AATCTTT	CAGGGA	TAGGC	ACACT	CGAGAG	TCA	ACTGTG	CA	207
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Db	206	GGGGGTA	CTGTG	GGAAG	ACTATTC	CAAAAC	CTTG	CTCTTA	TATAA	AGAAAT	TACAT	TGACGC	147
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Db	146	CAAAAAA	AAAGTGT	GGNAG	AAAGAC	GGAGAG	TAA	CCATTC	TCTAG	ACTAC	TGCA	87	
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LOCUS	CD559533				
DEFINITION	AGENCOURT 14496993 NIH MGC 195 Homo sapiens cDNA clone				
ACCESSION	IMAGE:697771 5', mRNA sequence.				
VERSION	CD559533				
KEYWORDS	CD559533.2	GI:38558947			
FEATURES	EST.				
ORGANISM	Homo sapiens (human)				
SOURCE	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 492)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585601.				

```

0rice or Cancer Genomics / NIH
National Cancer Institute / NIH
BLDg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-x@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 10
High quality sequence start: 14
High quality sequence stop: 492.
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FEATURES
source
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PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pMR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
A Note: this is a NIH MGC Library."

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a Note: This is a NIH_MCC Library.

ORIGIN

Query Match          69.0%; Score 277.2; DB 14; Length 492;
Best Local Similarity 80.6%; Pred. No. 2.3e-58;
Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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Db       56  ATGAGATGCTTCTGCAATTGAGTTTGCTAGCTCTTTGGAGCTGCCTACGTTGATGCATC 115
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QY      121  CGAATCTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAATAAAAAATCAC 180
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QY      181  CAACTGTGCATTAAAGAAGCTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240
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      |||
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QY      301  CAAAAAANAAGGTGTGCAGGAGAAAGATGCGAGAGTGACAAAGTTCCTAGACTACCTGCAA 360
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AY412021.1	GI:39767986		
GSS.			
Pan troglodytes (chimpanzee)			
Pan troglodytes			
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.			
1 (bases 1 to 405)			
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejaraiwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
Science 302 (5652), 1960-1963 (2003)			
14671302			
2 (bases 1 to 405)			

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.

FEATURES	Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="IL5"
/locus_tag="HCN4418"

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Best Local Similarity	79.6%;	Pred. NO.	2.3e-57;		
Matches 300. Conservative	0;	Mismatches	82;	Indels	0;
Gaps	0;				

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100  
 121  
 100

[illegible]

181 CAACCTGTGTCATTAAGGAGATGTTTTCAGGGTATAGACACATTTGGAGAAACCTTTATCTGCCCCAC 240

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Db 241 GGGGGTACTGTGGAAAGACTATTCCAAAACTTGTCCCTAAATAAAGAAAATACATTGGANGC 300

301 CAAAAAAGTGTGCAGAGAAAAGATGGAGAGTGCACAAAGTTCTAGACTACCTGCAT 360

Db 301 CAAAAAAAAGTGTGGAGAGAAAGACGGAGAGTAACCAATTCCTAGACTACCTGCAA 360

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Db 361 GACTTTCTTGGTGTAAATGACACCGAGTGGATAATAGAAAGT 402

## RESULT 7

CD559688/c	CD559688	467 bp	mRNA	linear	EST 19-NOV-2003
LOCUS					

DEFINITION AGENCOURT\_14496964 NIH\_MGC\_195 Homo sapiens cDNA clone IMAGE:6971770 5', mRNA sequence.

CD559688  
ACCESSION  
CD559688.2  
VERSION  
GI:38453486

KEYWORDS  
SOURCE  
EST.  
Homo sapiens (human)

ORGANISM	Homo sapiens	Craniata	Vertebrata	Euteleostomi
Source	Ensembl	Ensembl	Ensembl	Ensembl

DIFFERENCE 1 (bases 1 to 457)

REFERENCE	AUTHORS	TITLE
1 (Pages 1 to 107)	NIH-MGC	http://mgc.nci.nih.gov/.
	National Institutes of Health.	Mammalian Gene Collection (MGC)

JOURNAL  
UNPUBLISHED (1999)  
ON THE 10 2003 THIS SEQUENCE REPLACED AT:31585756.

COMMENT  
On Jan 10, 2003 this sequence version replaced gars000001.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics

Office of Cancer Genomics  
National Cancer Institute / NIH  
Building 31, Room 1007 Bethesda, MD 20892

Bldg. 31 KML0A07 Bethesda, MD 20832  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)



ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 66.2%; Score 266.2; DB 14; Length 463;  
Best Local Similarity 80.4%; Pred. No. 1.2e-55;  
Matches 324; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
  
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DB 28 ATGAGGATGCTTCTGATTTGAGTTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 87  
  
QY 61 GCTGTAGAAATCCCATGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 120  
DB 88 CCACAGAAATCCCATGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 147  
  
QY 121 CGAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 180  
DB 148 CGAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 207  
  
QY 181 CAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 240  
DB 208 CAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 267  
  
QY 241 GGGGAGCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 300  
DB 268 GGGGAGCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 327  
  
QY 301 C-AAAAAAGGCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 359  
DB 328 C-AAAAAAGGCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 387  
  
QY 360 AGTATTTCTTGTGCTGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 402  
DB 388 AGTATTTCTTGTGCTGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 430

RESULT 10  
CD559689/c

LOCUS CD559689 473 bp mRNA linear EST 19-NOV-2003  
DEFINITION AGENCOURT\_14496801 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971769 5', mRNA sequence.  
CD559689  
VERSION CD559689.2 GI:38453487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 473)  
NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585757.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NCI  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: Bhat Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
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FEATURES  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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/clone="IMAGE:6971769"  
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PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
cells lines or pooled total RNA from 10 different tissues  
from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Fredrick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 66.2%; Score 266.2; DB 14; Length 473;  
Best Local Similarity 80.4%; Pred. No. 1.2e-55;  
Matches 324; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
  
QY 1 ATGAGATGCTTCTGATTTGAGTTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 60  
DB 449 ATGAGATGCTTCTGATTTGAGTTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 390  
  
QY 61 GCTGTAGAAATCCCATGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 120  
DB 389 CCACAGAAATCCCATGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 330  
  
QY 121 CGAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 180  
DB 329 CGAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 270  
  
QY 181 CAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 240  
DB 269 CAATCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 210  
  
QY 241 GGGGAGCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 300  
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DB 149 C-AAAAAAGGCTGCTGATGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 90  
  
QY 360 AGTATTTCTTGTGCTGCTGCTAGCTTCTGGGGCTGCTATGTTCTGCTTT 402  
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RESULT 11  
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LOCUS CD559536 489 bp mRNA linear EST 26-NOV-2003  
DEFINITION AGENCOURT\_14496804 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971768 5', mRNA sequence.  
CD559536  
VERSION CD559536.2 GI:38558953  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 489)  
NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31565604.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: dcgaps-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: Bhat Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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High quality sequence start: 17  
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PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxP sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
a Note: this is a NIH MGC Library."

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a Note: this is a NIH_MGC Library."

ORIGIN
Query Match      66.2%; Score 266.2; DB 14; Length 489;
Best Local Similarity 80.4%; Pred. No. 1.2e-55;
Matches 324; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY      1  ATGAGAAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 60
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Db      54  ATGAGATGCTTCTGCAATTTGAGTTTGCTAGCTCTTGGAGCTGCCTACGTGTATGCATC 113
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QY      61  GCTGTAGAAATCCCATGAATACACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
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Db     114  CCCACAGAAATCCCACAGTGCATTGGTGAAGAGACCTTGGCACTGCTTTCTACTCAT 173
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RESULT 12  
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DEFINITION ACENGCOURT\_14496838 NIH\_MGC\_195 Homo sapiens cDNA clone IMAGE:6971768 5', mRNA sequence.  
ACCESSION CD559690  
VERSION CD559690.2 GI:38453490  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 467)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999).  
JOURNAL On Jun 10, 2003 this sequence version replaced gi:31585758.  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: Bhat Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

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FEATURES  
source

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ORIGIN
a Note: this is a NIH_MGC Library."

Query Match      65.8%; Score 264.6; DB 14; Length 467;
Best Local Similarity 80.1%; Pred. No. 3.1e-55;
Matches 323; Conservative 0; Mismatches 79; Indels 1; Gaps 1;

QY      1  ATGGAATGCTTCTGAATTTGAGTTTGCTAGCTCTTGGGGCTGCTATGTTTTCGCCTTT 60
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QY      61  GCTGTAGAAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

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 AGENCOURT\_14496997 NIH\_MGC\_195 Homo sapiens cDNA clone  
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 CD559608  
 CD559608.2 GI:38558942  
 EST.  
 Homo sapiens (human)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 NIH-MGC http://mgi.nci.nih.gov/  
 1 (bases 1 to 477)  
 TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 JOURNAL  
 On Jun 10, 2003 this sequence version replaced gi:31585676.  
 COMMENT  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-@email.nih.gov  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: IRBK2 row: 9 column: 10  
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 High quality sequence stop: 353.  
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 /note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites

## FEATURES

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 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites

of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 65.1%; Score 261.6; DB 14; Length 477;  
 Best Local Similarity 78.8%; Pred. No. 1.7e-54;  
 Matches 312; Conservative 0; Mismatches 84; Indels 0; Gaps 0;  
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## RESULT 14

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 LOCUS  
 DEFINITION  
 Mus musculus IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 AY412022  
 AY412022.1 GI:39767987

## ACCESSION

AY412022

## VERSION

AY412022.1

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 399)

## AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

## TITLE

Inferred nonneutral evolution from human-chimp-mouse orthologous  
 gene trios

Science 302 (5652), 1960-1963 (2003)

## JOURNAL

Science 302 (5652), 1960-1963 (2003)

## PUBMED

14671302

## REFERENCE

2 (bases 1 to 399)

## AUTHORS

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

## TITLE

Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

## JOURNAL

This sequence was made by sequencing genomic exons and ordering

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FEATURES
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  Best Local Similarity 66.6%; Pred. No. 2.3e-37;
  Matches 265; Conservative 0; Mismatches 127; Indels 6; Gaps 1;

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Qy  124 ACTTGGCTGATAGCGGATGGAACTTGATGATTTCTTACTCTCGAAATAAAATCACCAA 183
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Qy  184 CTGTGCAATTAAGAAGTTTTCAGGTATAGACACATTCAGAACCAACTGCCACGGG 243
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Qy  244 GAGGCTGTGGATAAATATTCCTTCTTTAATAAAGAACACATAGAGCGCCAA 303
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Qy  304 AAAAAAGGTGTGAGAGAGAAAGATGGAGAGTGCACAAAGTTCTAGACTACCTGCAAGTA 363
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Qy  364 TTCTTGTGCTGTAATAAACCGAGTGGACACCGGAAAG 401
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RESULT 15
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DEFINITION genomic survey sequence.
ACCESSION CE331159
VERSION    CE331159.1 GI:36147469
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 622)
            Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
            Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and
            Venter,J.C.
            The dog genome: survey sequencing and comparative analysis
            Science 301 (5641), 1898-1903 (2003)
            22875432
            PUBMED
            14512627
            COMMENT
            Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
            Location/Qualifiers

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  Best Local Similarity 95.1%; Pred. No. 2.7e-22;
  Matches 136; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy  231 AACTGCCACCGGAGGCTGTGATAACTATTCCTTCTTTAATAAAGAACCA 290
Db  95  AACTGCCACCGGAGGCTGTGATAACTATTCCTTCTTTAATAAAGAACCA 154

Qy  291 CATAGAGCGCCAAAAAAGGT 313
Db  155 CATAGAGCGCCAAAAAAGTAAAGT 177

Search completed: August 31, 2004, 13:00:13
Job time : 1352.53 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:25:57 ; Search time 237.867 Seconds  
(without alignments)  
8317.320 Million cell updates/sec

Title: US-10-787-382-7  
Perfect score: 402  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 246071050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications NA:\*
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
  - 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
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  - 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
  - 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	402	100.0	402	15	US-10-218-654-83
4	402	100.0	402	15	US-10-218-654-84
5	402	100.0	402	15	US-10-262-439-83
6	402	100.0	402	15	US-10-262-439-84
7	402	100.0	610	9	US-09-755-633-4
8	402	100.0	610	9	US-09-755-633-6
9	402	100.0	610	15	US-10-218-654-80
10	402	100.0	610	15	US-10-218-654-82
11	402	100.0	610	15	US-10-262-439-80
12	402	100.0	610	15	US-10-262-439-82
13	345	85.8	345	9	US-09-755-633-9
14	345	85.8	345	9	US-09-755-633-11

15	345	85.8	345	15	US-10-218-654-85	Sequence 85, Appl
16	345	85.8	345	15	US-10-218-654-87	Sequence 87, Appl
17	345	85.8	345	15	US-10-262-439-85	Sequence 85, Appl
18	345	85.8	345	15	US-10-262-439-87	Sequence 87, Appl
19	277.2	69.0	816	16	US-10-191-997-90	Sequence 90, Appl
20	275.6	68.6	816	17	US-10-641-643-1236	Sequence 1236, Ap
21	275.6	68.6	858	15	US-10-295-074-8	Sequence 8, Appl
22	275.6	68.6	858	15	US-10-295-074-10	Sequence 10, Appl
23	259	64.4	671	9	US-09-755-633-21	Sequence 21, Appl
24	231.4	57.6	864	15	US-10-235-074-12	Sequence 12, Appl
25	231.4	57.6	864	15	US-10-235-074-14	Sequence 14, Appl
26	145.8	36.3	1658	9	US-09-755-633-18	Sequence 18, Appl
27	144.2	35.9	1658	9	US-09-755-633-19	Sequence 19, Appl
28	99.4	24.7	3230	9	US-09-800-629A-78	Sequence 78, Appl
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33	65.6	16.3	5397	15	US-10-311-455-1017	Sequence 1017, Ap
34	42.6	10.6	65	10	US-09-908-975-2631	Sequence 2631, Ap
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37	37.2	9.3	694	13	US-10-424-599-27005	Sequence 27005, A
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39	35.8	8.9	1049	13	US-10-424-599-41750	Sequence 41750, A
40	35.8	8.9	6129	15	US-10-240-485-136	Sequence 136, App
41	35.6	8.9	17280	13	US-10-221-714A-498	Sequence 498, App
42	35.4	8.8	530	13	US-10-424-599-3699	Sequence 3699, Ap
43	35.4	8.8	710	17	US-10-437-963-69757	Sequence 69757, A
44	35.4	8.8	175077	13	US-10-087-192-1168	Sequence 1168, Ap
45	35.2	8.8	488	13	US-10-027-632-39049	Sequence 39049, A

ALIGNMENTS

RESULT 1  
US-09-755-633-7  
; Sequence 7, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IN-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-7

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QY	61	GCTGTAGAAATCCCATGATGATGCTGTCAGAGACTTGCACACTCTCTCCACTCAT	120	
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; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 84  
; TYPE: DNA  
; LENGTH: 402  
; ORGANISM: Canis familiaris  
US-10-218-654-84  
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Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 121 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTTCTGAAATAAAATAC 180  
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RESULT 5  
US-10-262-439-83  
; Sequence 83, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-84  
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Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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; Sequence 84, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
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; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
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; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-84  
Query Match 100.0%; Score 402; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTCGCTATGTTCTGCTTT 60  
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QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 120  
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 283  
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; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 84  
; TYPE: DNA  
; LENGTH: 402  
; ORGANISM: Canis familiaris  
US-10-218-654-84  
Query Match 100.0%; Score 402; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTCGCTATGTTCTGCTTT 60  
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTCGCTATGTTCTGCTTT 343  
QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 120  
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QY 121 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTTCTGAAATAAAATAC 180  
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QY 181 CAACCTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240  
Db 222 CAACCTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 163  
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Db 162 GGGAGGCTGTGATAAATCTATTCCAAAACCTTGTCTTTAATAAAGAACACATAGAGCG 103  
QY 301 CAAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360  
Db 102 CAAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43  
QY 361 GTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 402  
Db 42 GTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 1  
RESULT 5  
US-10-262-439-83  
; Sequence 83, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-84  
Query Match 100.0%; Score 402; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTCGCTATGTTCTGCTTT 60  
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTCGCTATGTTCTGCTTT 343  
QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 120  
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTTCCACTCAT 283  
QY 121 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTTCTGAAATAAAATAC 180  
Db 282 CGAATCTGGCTGATAGCGATGGAACTGATGATCTTCTTCTGAAATAAAATAC 223  
QY 181 CAACCTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240  
Db 222 CAACCTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 163  
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QY 301 CAAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360  
Db 102 CAAAAAAAAGGTGTGCAGAGAAAGATGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43  
QY 361 GTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 402  
Db 42 GTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT 1

Db 402 ATGAGATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 343  
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120  
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Qy 121 CGAATCTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATATAAATAC 180  
Db 282 CGAATCTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATATAAATAC 223  
Qy 181 CAATCTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240  
Db 222 CAATCTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 163  
Qy 241 GGGAGGCTGTGATTAACACTTCCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 300  
Db 162 GGGAGGCTGTGATTAACACTTCCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 103  
Qy 301 CAAAAAAAAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360  
Db 102 CAAAAAAAAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 43  
Qy 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402  
Db 42 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

## RESULT 7

US-09-755-633-4  
; Sequence 4, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-09-755-633-4

Query Match 100.0%; Score 402; DB 9; Length 610;  
Best Local Similarity 100.0%; Pred. No. 7.2e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60  
Db 29 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 88  
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120  
Db 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 148  
Qy 121 CGAATCTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATATAAATAC 180  
Db 149 CGAATCTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATATAAATAC 208  
Qy 181 CAATCTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240

Db 209 CAATCTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 268  
Qy 241 GGGAGGCTGTGGATAAATACTATTCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 300  
Db 269 GGGAGGCTGTGGATAAATACTATTCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 328  
Qy 301 CAAAAAAAAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360  
Db 329 CAAAAAAAAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 388  
Qy 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402  
Db 389 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 430

## RESULT 8

US-09-755-633-6/c  
; Sequence 6, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-6

Query Match 100.0%; Score 402; DB 9; Length 610;  
Best Local Similarity 100.0%; Pred. No. 7.2e-117;  
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60  
Db 582 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 523  
Qy 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120  
Db 522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 463  
Qy 121 CGAATCTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATATAAATAC 180  
Db 462 CGAATCTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATATAAATAC 403  
Qy 181 CAATCTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 240  
Db 402 CAATCTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCAC 343  
Qy 241 GGGAGGCTGTGGATAAATACTATTCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 300  
Db 342 GGGAGGCTGTGGATAAATACTATTCAAAACCTTGTCTTTTAAATAAGAACACATAGAGCG 283  
Qy 301 CAAAAAAAAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360  
Db 282 CAAAAAAAAGGTGTGCAGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 223  
Qy 361 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402  
Db 222 GTATTTCTTGTGTAATAAACACCGAGTGGACACCGGAAAGT 181

US-10-218-654-80  
Sequence 80 Application US/10218654  
Publication No. US2003009609A1  
GENERAL INFORMATION:  
APPLICANT: Sim. Gek-Ke  
APPLICANT: Yang, Shumin  
APPLICANT: Dreitz, Matthew J.  
APPLICANT: Wonderling, Ramani S.  
TITLE OF INVENTION: CANINE AND FELINE  
TITLE OF INVENTION: ACID MOLECULES

```

1  APPLICANT: Dreitz, Matthew J.
2  APPLICANT: Wonderling, Ramani S.
3  TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
4  TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
5  FILE REFERENCE: IM-2-C1
6  CURRENT APPLICATION NUMBER: US/10/218,654
7  CURRENT FILING DATE: 2002-08-13
8  PRIOR APPLICATION NUMBER: US/09/322,409
9  PRIOR FILING DATE: 1999-05-28
10 PRIOR APPLICATION NUMBER: 60/087,306
11 PRIOR FILING DATE: 1998-05-29
12 NUMBER OF SEQ ID NOS: 154
13 SOFTWARE: PatentIn Ver. 2.0
14 SEQ ID NO 80
15 LENGTH: 610
16 TYPE: DNA
17 ORGANISM: Canis familiaris
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: (29)..(430)
21 US-10-218-654-80

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Query Match	100.0%;	Score	402;	DB	15;	Length	610;
Best Local Similarity	100.0%;	Pred. No.	7.2e-117;				
Matches	402;	Conservative	0;	Mismatches	0;	Gaps	0;

  

QY	1	ATCAGAAATGCTTCTGTAATTGAGTTTGCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT	60
Db	29	ATCAGAAATGCTTCTGTAATTGAGTTTGCTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT	88
QY	61	GCTGTGAAAAATCCCATGAATAGACTGGTGGCGAGAGACCTTGCACACTGCTCTCCACTCAT	120
Db	89	GCTGTGAAAAATCCCATGAATAGACTGGTGGCGAGAGACCTTGCACACTGCTCTCCACTCAT	148
QY	121	CGAACTTGGCTGATAGCGGATGGAACTCATGATTCCTACTCTGTAATAATAAAATCAC	180
Db	149	CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTGTAATAATAAAATCAC	208
QY	181	CAACTGTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTGGAAGACCACAACTGCCAC	240
Db	209	CAACTGTGCATTAAAGAAGTTTTTTCAGGGTATAGACACATTGGAAGACCACAACTGCCAC	268
QY	241	GGGAGCGCTGTGGATAAACCTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAGGC	300
Db	269	GGGAGCGCTGTGGATAAACCTATTCCAAAACTTGTCTTTAATAAAGAACACATAGAGGC	328
QY	301	CAAAAAAAGGCTGTCAGAGGAAGATGGAGAGTGACAAAGTTCCTTAGACTACTCTGCAA	360
Db	329	CAAAAAAAGGCTGTCAGAGGAAGATGGAGAGTGACAAAGTTCCTTAGACTACTCTGCAA	368
QY	361	GTATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT	402
Db	389	GTAATTTCTTGGTGTAAATAAACCCGAGTGGACACCGGAAAGT	430

US-100-218-654-82/c  
 ; Sequence 82, Application US/10218654  
 ; Publication No. US2003009609A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Keo  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE  
 ; TITLE OF INVENTION: ACID MOLECULES

```

, FILE REFERENCE: IM-2-C1
,
, CURRENT APPLICATION NUMBER: US/10/218,654
,
, CURRENT FILING DATE: 2002-08-13
,
, PRIOR APPLICATION NUMBER: US/09/322,409
,
, PRIOR FILING DATE: 1999-05-28
,
, PRIOR APPLICATION NUMBER: 60/087,306
,
, PRIOR FILING DATE: 1998-05-29
,
, NUMBER OF SEQ ID NOS: 154
,
, SOFTWARE: Patentin Ver. 2.0
,
, SEQ ID NO 82
,
, LENGTH: 610
,
, TYPE: DNA
,
, ORGANISM: Canis familiaris
,
, US-10-218-654-82

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Query Match	100.0%;	Score 402;	DB 15;	Length 610;
Best Local Similarity	100.0%;	Pred. No. 7.2e-117;		
Matches 402;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAGAACTCTCTCGAATTGAGTTTGCTAGCTCTTTGGGGCTGCCCTATCTTTTCTGCGCTTT	60	
Db	582	ATGAGAACTCTCTGNAATTGAGTTTGCTAGCTCTTTGGGGCTGCCCTATCTTTTCTGCGCTTT	523	
QY	61	GCTGTAGAAAATCCCATGAAATAGACTGTTGGCAGAGACCTTGACACTGCTCTCCACTCAT	120	
Db	522	GCTGTAGAAAATCCCATGAAATAGACTGTTGGCAGAGACCTTGACACTGCTCTCCACTCAT	463	
QY	121	CGAACTTTGGCTGATAGGGCGATGGGAACCTGATGATTCTCTACTCTCTGAAAATAAAAAATCAC	180	
Db	462	CGAACTTTGGCTGATAGGGCGATGGGAACCTGATGATTCTCTACTCTCTGAAAATAAAAAATCAC	403	
QY	181	CAACTGTGCATTAAAGAAAGTTTTTTCAGGATATAGACACATTGGAAGAACCAAACTGCCAC	240	
Db	402	CAACTGTGCATTAAAGAAAGTTTTTTCAGGATATAGACACATTGGAAGAACCAAACTGCCAC	343	
QY	241	GGGGAGGCTGTGATATAAATACTATTCAAAACTTGTCTTTTAATAAAGAAACACATAGAGCGC	300	
Db	342	GGGGAGGCTGTGATATAAATACTATTCAAAACTTGTCTTTTAATAAAGAAACACATAGAGCGC	283	
QY	301	CAAAAAAAAAGGTGTGCAGGAGAAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA	360	
Db	282	CAAAAAAAAAGGTGTGCAGGAGBAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAA	223	
QY	361	GTATTTCTTGGTGTAATAAACACCCGAGTGGACACCCGAAAAGT	402	
Db	222	GTATTTCTTGGTGTAATAAACACCCGAGTGGACACCCGAAAAGT	181	

US-10-262-439-80  
; Sequence 80, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:

1 APPLICANT: Sim, Gek-Keo  
 2 APPLICANT: Yang, Shumin  
 3 APPLICANT: Dreitz, Matthew J.  
 4 APPLICANT: Wonderling, Ramani S.  
 5 TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 6 TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 7 FILE REFERENCE: IM-2-C2  
 8 CURRENT APPLICATION NUMBER: US/10/262,439  
 9 CURRENT FILING DATE: 2002-09-30  
 10 PRIOR APPLICATION NUMBER: US/09/451,527  
 11 PRIOR FILING DATE: 1999-12-01  
 12 PRIOR APPLICATION NUMBER: 09/322,409  
 13 PRIOR FILING DATE: 1999-05-28  
 14 PRIOR APPLICATION NUMBER: 60/087,306  
 15 PRIOR FILING DATE: 1998-05-29  
 16 NUMBER OF SEQ ID NOS: 174  
 17 SOFTWARE: PatentIn Ver. 2.0  
 18 SEQ ID NO 80  
 19 LENGTH: 610  
 20 TYPE: DNA

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; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)...(430)
US-10-262-439-80

Query Match      100.0%; Score 402; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAATTTGAGTTTGTCTCTTGGGGCTGCTATGTTCTGCTTT 523
DB 29 ATGAGATGCTTCGAATTTGAGTTTGTCTCTTGGGGCTGCTATGTTCTGCTTT 120
QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
DB 89 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 148
QY 121 CGAATCTGGCTGATAGGCGATGGGAACCTGATGATTCCTCTCTGAAAATAAAAAATCAC 180
DB 149 CGAATCTGGCTGATAGGCGATGGGAACCTGATGATTCCTCTCTGAAAATAAAAAATCAC 208
QY 181 CAATCTGTCANTAAAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
DB 209 CAATCTGTCANTAAAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 268
QY 241 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
DB 269 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 328
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
DB 329 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 388
QY 361 GTATTCTTGTGTAAATAACACCGAGTGGACACCGGAAAGT 402
DB 389 GTATTCTTGTGTAAATAACACCGAGTGGACACCGGAAAGT 430

RESULT 12
US-10-262-439-82/c
; Sequence 82, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-82

Query Match      100.0%; Score 402; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATGCTTCGAATTTGAGTTTGTCTCTTGGGGCTGCTATGTTCTGCTTT 60

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DB 582 ATGAGATGCTTCGAATTTGAGTTTGTCTCTTGGGGCTGCTATGTTCTGCTTT 523
QY 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
DB 522 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 463
QY 121 CGAATCTGGCTGATAGGCGATGGGAACCTGATGATTCCTCTGAAAATAAAAAATCAC 180
DB 462 CGAATCTGGCTGATAGGCGATGGGAACCTGATGATTCCTCTGAAAATAAAAAATCAC 403
QY 181 CAATCTGTCANTAAAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 240
DB 402 CAATCTGTCANTAAAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCCAC 343
QY 241 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 300
DB 342 GGGGAGGCTGTGGATAAATCTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAGAGCGC 283
QY 301 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 360
DB 282 CAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAA 223
QY 361 GTATTCTTGTGTAAATAACACCGAGTGGACACCGGAAAGT 402
DB 222 GTATTCTTGTGTAAATAACACCGAGTGGACACCGGAAAGT 181

RESULT 13
US-09-755-633-9
; Sequence 9, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McGill, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(345)
US-09-755-633-9

Query Match      85.8%; Score 345; DB 9; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.6e-99;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
DB 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
QY 118 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTCTGAAAATAAAAAAT 177
DB 61 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTCTGAAAATAAAAAAT 120
QY 178 CACCAACTGTGCATTAAGAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 237
DB 121 CACCAACTGTGCATTAAGAGAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 180
QY 238 CACGGGAGGCTGTGATTAACACTATTTCCAAAACCTTGTCTTTTAAATAAAGAACACATAG 297

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Db 181 CACGGGAGGCTGTGATTAACCTATTCCTCAAACTTCTTTTAAATAAAGAACACATAGAG 240  
QY 298 CGCCAAAAAAGGCTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 357  
Db 241 CGCCAAAAAAGGCTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 300  
QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402  
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345

## RESULT 14

US-09-755-633-11/c  
; Sequence 11, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-CI-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-11

Query Match 85.8%; Score 345; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.6e-99;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117  
Db 345 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286  
QY 118 CATCGAACTTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 177  
Db 285 CATCGAACTTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 226  
QY 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTGGAAGAACCAAACTGCC 237  
Db 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTGGAAGAACCAAACTGCC 166  
QY 238 CACGGGAGGCTGTGGATAAAGTATTCCTCAAACTTGTCTTTTAAATAAAGAACACATAGAG 297  
Db 165 CACGGGAGGCTGTGGATAAAGTATTCCTCAAACTTGTCTTTTAAATAAAGAACACATAGAG 106  
QY 298 CGCCAAAAAAGGCTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 357  
Db 105 CGCCAAAAAAGGCTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 46  
QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402  
Db 45 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 1

## RESULT 15

US-10-218-654-85  
; Sequence 85, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-10-218-654-85

Query Match 85.8%; Score 345; DB 15; Length 345;  
Best Local Similarity 100.0%; Pred. No. 6.6e-99;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117  
Db 1 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
QY 118 CATCGAACTTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 177  
Db 61 CATCGAACTTGGCTGTAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120  
QY 178 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTGGAAGAACCAAACTGCC 237  
Db 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTGGAAGAACCAAACTGCC 180  
QY 238 CACGGGAGGCTGTGGATAAAGTATTCCTCAAACTTGTCTTTTAAATAAAGAACACATAGAG 297  
Db 181 CACGGGAGGCTGTGGATAAAGTATTCCTCAAACTTGTCTTTTAAATAAAGAACACATAGAG 240  
QY 298 CGCCAAAAAAGGCTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 357  
Db 241 CGCCAAAAAAGGCTGTGAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG 300  
QY 358 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 402  
Db 301 CAAGTATTTCTTGGTGTATTAACACCGAGTGGACACCGGAAAGT 345

Search completed: August 31, 2004, 14:03:39  
Job time : 239.867 secs

Blank Sheet



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:21:12 ; Search time 2636.86 Seconds  
(without alignments)  
10026.797 Million cell updates/sec

Title: US-10-787-382-4

Perfect score: 610

Sequence: 1 caaggaacactgaacatt.....acagatgaataatttgag 610

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
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36: em.htg.mam.\*  
37: em.htg.vrt.\*  
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39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	610	100.0	610	6	AR241536 Sequence
3	610	100.0	610	6	AR241537 Sequence
4	610	100.0	610	6	AR254492 Sequence
5	610	100.0	610	6	AR254493 Sequence
6	610	100.0	610	6	BD211558 Canine an
7	610	100.0	610	6	BD211559 Canine an
8	405.8	66.5	838	4	AF025436 Felis cat
9	402	65.9	402	6	AR241538 Sequence
10	402	65.9	402	6	AR241539 Sequence
11	402	65.9	402	6	AR254494 Sequence
12	402	65.9	402	6	AR254495 Sequence
13	402	65.9	402	6	BD211560 Canine an
14	402	65.9	402	6	BD211561 Canine an
15	401.8	65.9	405	6	AR300436 Sequence
16	401.8	65.9	405	6	AX083939 Sequence
17	379	62.1	816	6	E01639 cdna encodi
18	379	62.1	816	6	E13591 cdna encodi
19	379	62.1	816	9	X04668 Human mRNA
20	377.4	61.9	816	6	AR380891 Sequence
21	377.4	61.9	816	9	HSBCDFIA
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23	357.4	58.6	529	4	SSC133452
24	345	56.6	345	6	AR241540 Sequence
25	345	56.6	345	6	AR241541 Sequence
26	345	56.6	345	6	AR254496 Sequence
27	345	56.6	345	6	AR254497 Sequence
28	345	56.6	345	6	BD211562 Canine an
29	345	56.6	345	6	BD211563 Canine an
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31	337.8	55.4	405	4	ECU91947 Equus cabal
32	329.8	54.1	356	4	AF091133 Canis fam
33	329.8	54.1	405	4	BTINILEUS
34	326.6	53.5	405	4	SSC010088 Sus scrof
35	281.2	46.1	354	4	AF051372 Felis cat
36	280.2	45.9	405	9	AF294756 Salmir's
37	276.6	45.3	858	6	AX766521 Sequence
38	275.6	45.2	858	6	AX766523 Sequence
39	275.4	45.1	405	9	CSYINSA
40	273.8	44.9	405	9	MMU19848
41	267.4	43.8	564	10	CPU34588
42	250	41.0	343	6	AX083948
43	244.2	40.0	4946	1	PPVIRE
44	243.4	39.9	421	12	SYNLSA
45	232.4	38.1	864	6	AX766527 Sequence

## ALIGNMENTS

RESULT 1  
AF331919  
LOCUS AF331919  
DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.  
ACCESSION AF331919  
VERSION AF331919.1 GI:15919180  
KEYWORDS  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE  
1 (bases 1 to 610)  
Yang, S., Sellins, K.S., Weber, E. and McCall, C.  
AUTHORS Canine interleukin-5: molecular characterization of the gene and  
TITLE expression of biologically active recombinant protein

J. Interferon Cytokine Res. 21 (6), 361-367 (2001)  
 21334408  
 MEDLINE  
 PUBMED  
 11440633  
 REFERENCE  
 2 (bases 1 to 610)  
 Yarg, S.  
 Direct Submission  
 Submitted (22-DEC-2000) Immunology, Heeska Corporation, 1613  
 Prospect Parkway, Ft Collins, CO 80525, USA  
 JOURNAL  
 TITLE  
 FEATURES  
 location/Qualifiers  
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 433..610

3'UTR  
 ORIGIN

Query Match 100.0%; Score 610; DB 4; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;  
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGCAAACTGAACTTCAGAGCTATGAGAACTGCTTCTGAATTTGAGTTGCTAGC 60  
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 DB 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGGCGATGGAACTGAT 180

QY 181 GATTCCTACTCTGAAATTAATAATCAACAACTGTCATTAAGAGAGTTTTCAGGGTAT 240  
 DB 181 GATTCCTACTCTGAAATTAATAATCAACAACTGTCATTAAGAGAGTTTTCAGGGTAT 240

QY 241 AGACACATTGAAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCAAAACCTT 300  
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QY 301 GTCTTTTAATAAAGAACACATAGAGCGCCAAAAGAGGTGTCAGAGAAAGATGGAG 360  
 DB 301 GTCTTTTAATAAAGAACACATAGAGCGCCAAAAGAGGTGTCAGAGAAAGATGGAG 360

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QY 601 TATATTGAG 610  
 DB 601 TATATTGAG 610

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 LOCUS  
 DEFINITION  
 Sequence 80 from patent US 6471957.  
 AR241536  
 ACCESSION  
 AR241536.1 GI:27287245  
 VERSION  
 KEYWORDS  
 location/Qualifiers  
 SOURCE  
 Unknown.  
 ORGANISM  
 Unclassified.  
 REFERENCE  
 1 (bases 1 to 610)  
 AUTHORS  
 Sim, G.-K., Yang, S., Dreitz, M. J. and Wonderling, R. S.  
 TITLE  
 Canine IL-4 immunoregulatory proteins and uses thereof  
 JOURNAL  
 Patent: US 6471957-A 80 29-OCT-2002;  
 FEATURES  
 Location/Qualifiers  
 source  
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 /mol\_type="genomic DNA"

Query Match 100.0%; Score 610; DB 6; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-154;  
 Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 CAAGGCAAACTGAACTTCAGAGCTATGAGAACTGCTTCTGAATTTGAGTTGCTAGC 60

QY 61 TCTTGGGCTGCTATGTTCTTCCCTTGTGCTAGAAATCCCATCAATAGACTGGTGGC 120  
 DB 61 TCTTGGGCTGCTATGTTCTTCCCTTGTGCTAGAAATCCCATCAATAGACTGGTGGC 120

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QY 361 AGTGACAAAAGTTCTAGACTACCTGCAAGTATTTCTTGGTGAATAAACCAGAGTGGAC 420  
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QY 601 TATATTGAG 610  
 DB 601 TATATTGAG 610

RESULT 3  
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LOCUS AR241537 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 82 from patent US 6471957.  
ACCESSION AR241537  
VERSION AR241537.1 GI:27287246  
KEYWORDS  
ORGANISM Unknown.  
SOURCE Unclassified.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 82 29-OCT-2002;  
FEATURES  
Location/Qualifiers  
source 1..610  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 100.0%; Score 610; DB 6; Length 610;  
Best Local Similarity 100.0%; Pred. No. 4.4e-154;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 TCTTGGGGCTGCCATGATTTCTGCTTGTGCTAGAAATCCCATGAATAGACTGCTGGC 120  
DB 550 TCTTGGGGCTGCCATGATTTCTGCTTGTGCTAGAAATCCCATGAATAGACTGCTGGC 491  
QY 121 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGGGATGGGAACCTGAT 180  
DB 490 AGAGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGGGATGGGAACCTGAT 431  
QY 181 GATTCCTACTCCTGAAATAAATAATCAACCACTGTGCATTAAGAAAGTTTTCAGGGTAT 240  
DB 430 GATTCCTACTCCTGAAATAAATAATCAACCACTGTGCATTAAGAAAGTTTTCAGGGTAT 371  
QY 241 AGACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCACAAACTT 300  
DB 370 AGACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCACAAACTT 311  
QY 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGAGGAAAGATGGAG 251  
DB 310 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGAGGAAAGATGGAG 251  
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DB 190 ACCGGAAAGTTGAGAACCAACCGGCTTATTTAGTGGAGATTTTGGAGAGAAATGGTTT 131  
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QY 541 TTGAGACAAAGTAAATATTTGAGGATCCTACTACTTTATCATCTTCACAGATGAAA 600  
DB 70 TTGAGACAAAGTAAATATTTGAGGATCCTACTACTTTATCATCTTCACAGATGAAA 11  
QY 601 TATATTTGAG 610  
DB 10 TATATTTGAG 1

RESULT 4  
AR254492  
LOCUS AR254492 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 80 from patent US 6482403.  
ACCESSION AR254492  
VERSION AR254492.1 GI:27303380

LOCUS AR254493 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 82 from patent US 6482403.  
ACCESSION AR254493  
VERSION AR254493.1 GI:27303381  
KEYWORDS  
ORGANISM Unknown.  
SOURCE Unclassified.

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 80 19-NOV-2002;  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 4.4e-154;  
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 CAAGGCAACACATGACATTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTTGCTAGC 60  
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QY 241 AGACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCACAAACTT 300  
DB 241 AGACATTTGAAGAACCAAACTGCCACCGGGAGGCTGTGGATAAACTATTCACAAACTT 300  
QY 301 GTCTTTAATAAAGAACACATAGAGCGCCAAAAGAGTGTGAGGAAAGATGGAG 360  
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DB 601 TATATTTGAG 610

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DEFINITION Sequence 82 from patent US 6482403.  
ACCESSION AR254493  
VERSION AR254493.1 GI:27303381  
KEYWORDS  
ORGANISM Unknown.  
SOURCE Unclassified.

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REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins and uses thereof
JOURNAL Caniney IL-13 immunoregulatory proteins and uses thereof
PATENT Patent: US 6482403-A 82 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..610
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Best Local Similarity 100.0%; Pred. No. 4,4e-154;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 250 AGTGACAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACAACCGAGTGGAC 191
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Db 190 ACCGAAAGTTGAGAACAAACCGGCTTATGTAGTGAAGATTTTGGAGAAAGATGGTT 131
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Qy 541 TTCAGAGACAAAGTAAATATTTTCAGGCATCCTACTACTTTATCATTCAACAGATGAAA 600
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Db 10 TATATTTGAG 1

RESULT 6
BD211558 610 bp DNA linear PAT 17-JUL-2003
LOCUS Canine and feline immunoregulatory proteins, nucleic acid molecules
DEFINITION Canine and method of using the same.
ACCESSION BD211558
VERSION BD211558.1 GI:33021328
KEYWORDS JP 2002516104-A/64.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

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TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
JOURNAL and method of using the same
PATENT Patent: JP 2002516104-A 64 04-JUN-2002;
COMMENT HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/64
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PI 29-MAY-1998 US 60/087306
PC 12N15/09,A61K31/7088,A61K38/21,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
FT CDS (29)..(430).

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/mol_type="genomic DNA"
/db_xref="taxon:9615"

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Best Local Similarity 100.0%; Pred. No. 4,4e-154;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CAAGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGAGTTGCTAGC 60
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Db 121 AGAGACCTTGACACTGCTTCCACTCATCGAACTTGGCTGATAGGCGATGGAACTGTAT 180
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QY	601	TATATTTCAG 610
DB	601	TATATTTCAG 610
RESULT 7 BD211559/c		
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DEFINITION	Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same.	
ACCESSION	BD211559	
VERSION	BD211559.1	GI:33021329
KEYWORDS	JP 2002516104-A/65.	
SOURCE	Canis familiaris (dog)	
ORGANISM	Canis familiaris	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
1 (bases 1 to 610)		
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.		
Canine and feline immunoregulatory proteins, nucleic acid molecules and method of using the same		
Patent: JP 2002516104-A 65 04-JUN-2002;		
HESKA CORP		
OS	Canis familiaris (dog)	
PN	JP 2002516104-A/65	
PD	04-JUN-2002	
PR	28-MAY-1999 JP 2000551002	
PF	29-MAY-1998 US 60/087306	
PI	GSKKEE SIM SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC C12N15/09,A61K31/7088,A61K38/00,A61K39/21,A61K39/395,	
PC	A61K39/395	
PC	A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,	
PC	C07K14/54,	
PC	C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC G01N33/15,	
PC	G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine and feline immunoregulatory proteins, nucleic acid CC molecules and	
CC	method of using the same	
FH	Key Location/Qualifiers	
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FT	/organism='Canis familiaris (dog)'	
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Best Local Similarity	100.0%; Pred. No. 4.4e-154;	
Matches 610; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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DB	610	CAAGCAAACACTGAACTTTCAGAGCTATGAGAATGCTTGTAATTTGAGTTGTTCAGC 551
QY	61	TCCTGGCGCTGCCTATGTTCTTCGCTTGTAGAAAATCCCATAATGAATAGCATGGTGGC 120
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QY	121	AGAGACCTTGACACTGCTCTCCATCATGCACTTGGCTGATAGCGATGGGAACCTGAT 180
DB	490	AGAGACCTTGACACTGCTCTCCATCATGCACTTGGCTGATAGCGATGGGAACCTGAT 431
QY	181	GATTCCTACTCTCTGAAAAATAAATCACCACTGTGCATTAAAGAGTTTTTCAGGGTAT 240
DB	430	GATTCCTACTCTCTGAAAAATAAATCACCACTGTGCATTAAAGAGTTTTTCAGGGTAT 371
QY	241	AGACACATTGAAGAACCAAACTGCCACCGGGAGCTGTGATAACTATTCCAAAACCTT 300
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 ACCESSION AR241538  
 VERSION AR241538.1 GI:27287247  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM  
 Unclassified.  
 REFERENCE 1 (bases 1 to 402)  
 AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
 TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
 JOURNAL Patent: US 6471957-A 83 29-OCT-2002;  
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ACCESSION AR254494
VERSION AR254494.1
KEYWORDS GI:27303382
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim G.-K., Yang S., Dretz M.J. and Wonderling R.S.
TITLE Caniney IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;
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QY	149	CGAACCTGGCTGATAGCGATGGAACTGATGATCTCTACTCCTGAAATAAAAAATCAC	208		
DB	121	CGAACCTGGCTGATAGCGATGGAACTGATGATCTCTACTCCTGAAATAAAAAATCAC	180		
QY	209	CAACTGTGCATTAAGAAGTTTTTCAGGGGTATAGACACATTGAAGAACCAAACTGCCAC	268		
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JOURNAL
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Sequence 84 from patent US 6482403.
AR254495
AR254495.1 GI:27303383
Unknown.
Source
Unclassified.
1 (bases 1 to 402)
Sim, G.-K., Yang, S., Dreitz, M. J. and Wonderling, R. S.
Caney IL-13 immunoregulatory proteins and uses thereof
Patent: US 6482403-A 84,19-NOV-2002;
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Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same.  
BD211.560  
BD211.560.1 GI:33021330  
JP 2002516104-A/66.  
Canis familiaris (dog)  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1. (bases 1 to 402)  
S1m,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
Patent: JP 2002516104-A 66 04-JUN-2002;  
HESKA CORP  
OS  
Canis familiaris (dog)  
JP 2002516104-A/66  
BN

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PD	04-JUN-2002	JP	2000551002		
PP	28-MAY-1999	JP	2000551002		
PPR	29-MAY-1998	US	60/087306		
PPI	GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC				
	C12N15/09, A61K31/7088, A61K38/00, A61K39/00, A61K39/395,				
PC	A61K39/395,				
PC	A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,				
PC	C07K14/54,				
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QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGCTGCTATGTTTCTGCCTTT 88
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QY 149 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTTCTACTCTCTGAAAATAAAAATCAC 208
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Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION
BD211561
VERSION
BD211561.1 GI:33021331
KEYWORDS
JP 2002516104-A/67.
SOURCE
Canis familiaris (dog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 402)
Sim, G., Yang, S., Dreitz, M.J. and Wonderling, R.S.
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP
COMMENT
OS Canis familiaris (dog)
PN JP 2002516104-A/67
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09 A61K31/7088 A61K38/00 A61K38/21 A61K39/00 A61K39/395,
PC A61K39/395,
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molecules and method of using the same
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Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGCTGCTATGTTTCTGCCTTT 88
DB 402 ATGAGATGCTTCTGAATTTGAGTTTGTAGTCTTTGGGGCTGCTATGTTTCTGCCTTT 343

QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 148
DB 342 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 149 CGAACTTGGCTGATAGCGGATGGGAACCTGATGATTTCTACTCTCTGAAAATAAAAATCAC 208
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VERSION
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ORGANISM
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REFERENCE
1 (bases 1 to 405)
AUTHORS
Guo, H., Lawton, R., Mermer, B. and Aiyappa, A. P.
TITLE
Methods and compositions concerning canine interleukin 5
JOURNAL
Patent: US 6537781-A 1 25-MAR-2003;
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QY 89 GCTGTAGAAAATCCCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCACTCAT 148
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QY	149	CGAACTGGCTGATAGCGATGGGAACCTGATGATTCCTACTCCTGAAATTAATCAAC	208
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QY	209	CAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTCAGAAACCAACTGCCAC	268
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QY	269	GGGAGGCTGTGATAAACTATTCCTGCTTTTAAATAAAGAACACATAGAGCC	328
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QY	329	CAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCA	388
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Copyright (c) 1993 - 2004 CompuGen Ltd.

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- 29: gb\_gss2:\*\*

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42	37.4	10.8	457	12	B3737332	B3737332 BFLG1_000
43	37.4	10.8	695	28	BZ019774	BZ019774 ced85f04.
C 44	37.4	10.8	965	29	CNS03PGL	AL207966 Tetraodon
C 45	37.2	10.8	330	10	BF091941	BF091941 RC6-TN007

ALIGNMENTS

RESULT 1

AY412020

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AV412020 Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 16-DEC-2003

Genomic survey sequence.

AY412020

AY412020.1 GI:39767985

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 405)

Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

Direct Submission



LOCUS	CD559687	470 bp	mRNA	linear	EST 19-NOV-2000
DEFINITION	AGENCOURT14497029 NIH_MGC_195 Homo sapiens cDNA clone IMAGE:6971771 5', mRNA_sequence.				
ACCESSION	CD559687				
VERSION	CD559687.2	GI:38453484			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 470)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585755.				

Contact: Daniela S. Gerhardt, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Narayan Bhat  
CDNA Library Preparation: Bhat Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: IRBKI row: 9 column: 10  
High quality sequence start: 14

High quality sequence stop: 470.

FEATURES

Location/Qualifiers
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source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971771"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
loxP-HindIII; Clones from this library have been to contain the
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearayed_plates/IRBK_presV.dat
a Note: this is a NIH MGC Library."

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ORIGIN	Query Match	Score	231 4:	DB 14:	Length	470:
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	Query: M01001.1; Length: 271; GC: 46.1%;	Best Local Similarity: 80.4%;	Pred. No.: 9.9e-46;	Mismatches: 66;	Indels: 0;	Gaps: 0;
	Matches: 271;	Conservative:				
Qy	9	AGAAAAATCCCATGATAGACTGTGGCGAGAGACCTTGGACACTGCTCTCCACTCATCGAAC	68			
Db	381	AGAAATTCCTCCCAAGTGCATTTGGTGAAGAGACCTTGGCACTGCTTTCTACTCATCGAAC	322			
Qy	69	TTGCGCTGATAGGCGATGGGAACTCGATGATTTCTACTCTCTGAAAAATAAAAAATCACCAACT	128			
Db	321	TCTGCTGATAGCAATGAGACTCTGAGGATTCCTGCTGTGATATAAAAAATCACCAACT	252			
Qy	129	GTGCATTAAAGAAGTATTTTCAGGGTATAGACACATTGAAGAACAAACTGCCACGGGGA	188			
Db	261	GTGCACCTGAAGAAATCTTTTCAGGGATPAGCACTGAGAGATCAAACTGTGAAGGGGG	202			

Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRBK1 row: 9 column: 11  
 High quality sequence stop: 456.  
 Location/Qualifiers

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1. .456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971772"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
loxP-HindIII. Clones from this_library have been _:
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30

```

cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University).

```

of the pDNR-dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, MCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK_presv.dat
a Note: this is a NIH_MGC Library."

IRGIN
Query Match          67.1%;   Score 231.4;   DB 14;   Length 456;
Best Local Similarity 80.4%;   Pred. No. 9.9e-46;
Matches 271;   Conservative 0;   Mismatches 66;   Indels 0;   Gaps 0;

y          9  AGAAATCCCATGAATAGACTGGTGGCAGAGACTTGCACACTGCTCTCCACTCATCGAAC 68
b          368 AGAAATTTCCCAAGTCATTTGGTGAAGAGACTTGGCACTGGCTTTCTACTCATCGAAC 309

y          69  TTGGCTGATAGGCGATGGGAACTGTGATGTTCTCTACTCTCTGAAAAATAAAATACCCAACT 128
b          308 TCTGCTGATAGCCAAATAGACTCTGAGGATTCCTGTTCTCTGTACATAAAAATACCCAACT 249

y          129 GTGCATTAAAGAAGTTTTTTCAGGGTATAGACATTTGAAGAAACCAAACTGCCACGGGGA 188

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248 GTGCAC TGAAGAAAATCTTTTCAGGGATATGGCACACTGGAGAGCTCAAACTGTGCAGGGGG 189

189	GGGCTGGGATTAACATATTCAGAACTTGTCTTAATAAGAAACATACATTGACGGCCCAAA	248
b	188 TACTGTGGAAGACTATTCAAAACCTGTCTTAATAAGAAATACATTGACGGCCCAAA	129
y	249 AAAAAAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTTGCAAAGTATT	308
b	128 AAAAAAGTGTGGAGAAAGACGGAGAGTAAACCAATTCTTAGACTACCTTGCAAAGAGTT	69
y	309 TCTTGTGTATAAACAACCGAGTGACACCGGAAAGT	345
b	68 TCTTGTGTATAACACCGAGTGGATAATAGAAAGT	32

RESULT 4  
559657/C

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QY 189 GGCTGTGGATAAATCCAAACTTGTCTTTAATAAAGAACACATAGAGCGCCAAA 248
Db 201 TACTGTGGGAAGACTATTCCAAACTTGTCTTTAATAAAGAAATACATTGACGCGCAAA 142
QY 249 AAAAAGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT 308
Db 141 AAAAAGTGTGGAGAGAAAGACGGAGAGTAACCAATTCCTAGACTACCTGCAAGATT 82
QY 309 TCTTGGTGTATAAACCAGGAGTGACACCGGAAAGT 345
Db 81 TCTTGGTGTATAAACCAGGAGTGATATAAGAAAGT 45

RESULT 5
CD559533
LOCUS
DEFINITION
AGENCOURT 14496993 NIH MGC 195 Homo sapiens cDNA clone
IMAGE:6971771 5', mRNA sequence.
ACCESSION
CD559533
VERSION
CD559533.2 GI:38558947
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 492)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
On Jun 10, 2003 this sequence version replaced gi:31585601.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaeps-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRBK1 row: 9 column: 10
High quality sequence start: 14
High quality sequence stop: 492.
Location/Qualifiers
1..492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971771"
/tissue_type="mixed"
/lab_hosts="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971771"
/tissue_type="mixed"
/lab_hosts="DH5A (T1 phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
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(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxp sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 65.9%; Score 227.4; DB 29; Length 405;
Best Local Similarity 79.2%; Fred. No. 9.3e-45;

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Query Match 67.1%; Score 231.4; DB 14; Length 492;
Best Local Similarity 80.4%; Fred. No. 9.9e-46;
Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 9 AGAAATCCCATGATGACCTGGTGGCAGAGACCTTGACACTGTCTCCCACTCATCGAAC 68
Db 121 AGAAATCCCATGATGACCTGGTGGCAGAGACCTTGACACTGTCTCTACTCATCGAAC 180
QY 69 TTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCTCTGAAATAAATACCAACT 128
Db 181 TCTGCTGATAGCCAACTGAGACTCTGAGGATTCCTGTTCTGTATACATAAAATACCAACT 240
QY 129 GTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCACGGGGA 188
Db 241 GTGCACTGAAGAATCTTTTCAGGAAATAGGCACACTGGAGAGTCAAACCTGCAAGGGG 300
QY 189 GGCTGTGATAAATATTCCAAAATCTTGTCTTTAATAAAGAACACATAGAGCCCAAAA 248
Db 301 TACTGTGGAAGACTATTTCAAAATCTTGTCTTTAATAAAGAAATACATTGACGCGCCAAA 360
QY 249 AAAAAGTGTGCAGGAGAAAGATGAGAGTGACAAAGTTCTCTAGACTACCTGCAAGTATT 308
Db 361 AAAAAGTGTGGAAGAAAGACGAGAGTAAACCAATTCCTAGACTACCTGCAAGATT 420
QY 309 TCTTGGTGTATAAACCAGGAGTGACACCGGAAAGT 345
Db 421 TCTTGGTGTATAAACCAGGAGTGATATAAGAAAGT 457

RESULT 6
AY412021
LOCUS
DEFINITION
Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY412021
VERSION
AY412021.1 GI:39767986
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 405)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
JOURNAL
PUBMED
2 (bases 1 to 405)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..405
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>405
/clone="IL5"
/locus_tag="HCM4418"

ORIGIN
Query Match 65.9%; Score 227.4; DB 29; Length 405;
Best Local Similarity 79.2%; Fred. No. 9.3e-45;

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Matches 267; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 9 AGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACATCATCGAAC 68

Db 66 AGAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACATCATCGAAC 125

Qy 69 TTGCTGATAGGCGATGGGAACCTGATGATCTCTCTGAGAAATATAAAATCACCAACT 128

Db 126 TCTGCTAATAGCAATGAGACTCTGAGGATCTCTCTGATACATAAAATCACCAACN 185

Qy 129 GTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTAAGAAACCAACTGCCACGGGGA 188

Db 186 NNGCACTGAAGAATCTTTTCAGGGAATAGCACTGGAGAGTCAACTGTGCAAGGGGG 245

Qy 189 GGTGTGGAATAACTATTCACAACTGTCTTTTAATAAAGAAACACATGAGCGCCAAA 248

Db 246 TACTGTGGAAGACTATTCAAAACTGTCTTTTAATAAAGAAATACATTGANGGCCAAA 305

Qy 249 AAAAGGTGCGAGGAGAGATGGAGATGACAAAGTTCTCTAGACTACTGCAAGTATT 308

Db 306 AAAAAGTGGGAGAGAAAGACGGAGGTAACCAATCTCTAGACTACTGCAAGATT 365

Qy 309 TCTGTGTGTAATAAACACCGAGTGGACCCGGAAAGT 345

Db 366 TCTGTGTGTAATAAACACCGAGTGGATATAGAAAGT 402

RESULT 7

CD559608

LOCUS

DEFINITION

AGENCOURT 1449697 NIH MGC 195 Homo sapiens cDNA clone

IMAGE:6971867 5', mRNA sequence.

CD559608.2 GI:38558942

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

EST.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 477)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585756.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

High quality sequence start: 107

High quality sequence stop: 353.

Location/Qualifiers

1..477

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6971867"

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/clone\_lib="NIH\_MGC\_195"

/note="vector: pNR-Dual; Site 1: loxP-Sali; Site 2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [http://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)

a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 64.5%; Score 222.4; DB 14; Length 477;

Best Local Similarity 78.9%; Pred. No. 1.5e-43;

Matches 265; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy 70 TGGCTGATAGGCGATGGGAACCTGATGATCTCTCTGAAATATAAAATCACCAACTG 129

Db 167 CTGCTGATAGCAATGAGACTCTGAGGATCTCTGTTCTGTACATAAAATCACCAACTG 226

Qy 130 TGCATTAAAGAAAGTTTTCAGGGTATAGACACATTAAGAAACCAACTGCCACGGGAG 189

Db 227 TGCACTGAAGAAATCTTTTCAGGGAATATGCACCTGGAGAGTCAACTGTGCAAGGGGT 286

Qy 190 GGTGTGGAATAACTATTCACAACTGTCTTTTAATAAAGAAACACATAGACGCCAAA 249

Db 287 ACTGTGGAAGACTATTCAAAACTGTCTTTTAATAAAGAAATACATTGACGGCCAAA 346

Qy 250 AAAAGTGTGAGGAGAAAGATGGAGTGGACAAAGTTCTCTAGACTACTGCAAGTATT 309

Db 347 AAAAAGCTGTAGAAAGAAAGACGGAGAGTAAACCAATCTCTTAAACTACTCTGCAAGATT 406

Qy 310 CTGTGTGTAATAAACACCGAGTGGACCCGGAAAGT 345

Db 407 CTGTGTGTAATAAACACCGAGTGGATATATAGT 442

RESULT 8

CD559688/c

LOCUS

DEFINITION

AGENCOURT 1449694 NIH MGC 195 Homo sapiens cDNA clone

IMAGE:6971770 5', mRNA sequence.

CD559688

CD559688.2 GI:38453486

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

EST.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 467)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585756.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: IRBK1 row: g column: 09

High quality sequence start: 11  
High quality sequence stop: 467.  
Location/Qualifiers  
1. 467

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6971770"  
/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_195"  
/note="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 64.1%; Score 221; DB 14; Length 467;  
Best Local Similarity 80.4%; Pred. No. 3.3e-43;  
Matches 271; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTCTCTCCACTCATCGAAC 68  
DB |||||  
QY 69 TTGCTGATAGCGGATGGGAACCTGATGATCTCTCTGAAATATAAAATCACCAC 128  
DB |||||  
QY 318 TCTGCTATGACCAATGAGACTCTGAGATCTCTGTTCTCTGTAATAAAATCACCAC 259  
DB |||||  
QY 129 GTGCATTAAAGAGAGTCTTTTCAGGGTATAGACACATTGAAGAACCAACTGCCACGGGA 188  
DB |||||  
QY 258 GTGCACCTGAAGAAATCTTTTCAGGGATAGGCACACTGGAGAGTCAAACTGTGCAAGGGG 199  
DB |||||  
QY 189 GGCTGTGGATAAATACTATTCAAAACCTGCTTTTAATAAAGACACATAGAGCGCCAAA 248  
DB |||||  
QY 198 TACTGTGGAAGACTATTCAAAACCTGCTTTTAATAAAGAAATACATAGTCGGCCAAA 139  
DB |||||  
QY 249 AAAAAAGTGTCCAGGAGAAAGATGGAGAGTGACAAAAGTCTCTAGACTACTGCAAGTATT 308  
DB |||||  
QY 138 AAAAA-GTGTGGAGAGAAAGACGGAGAGTAACCAATCTCTAGACTACTGCAAGATT 80  
DB |||||  
QY 309 TCTTGTGTATAAACAACCGAGTGGACACCGGAAAGT 345  
DB |||||  
QY 79 TCTTGTGTATAAACAACCGAGTGGATATAAGAAAGT 43  
DB |||||

RESULT 9  
CD559534  
LOCUS  
DEFINITION AGENCOURT\_14496928 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971770 5', mRNA sequence.  
ACCESSION CD559534  
VERSION CD559534.2 GI:38558949  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Jun 10, 2003 this sequence version replaced gi:31585602.  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRBK1 row: g column: 09  
High quality sequence start: 3  
High quality sequence stop: 478.  
Location/Qualifiers  
1. 478

## FEATURES

source

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/clone="IMAGE:6971770"  
/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_195"  
/note="vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 64.1%; Score 221; DB 14; Length 478;  
Best Local Similarity 80.4%; Pred. No. 3.3e-43;  
Matches 271; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

QY 9 AGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTCTCTCCACTCATCGAAC 68  
DB |||||  
QY 69 TTGCTGATAGCGGATGGGAACCTGATGATCTCTCTGAAATATAAAATCACCAC 128  
DB |||||  
QY 170 TCTGCTATGACCAATGAGACTCTGAGGATTCCTGTTCTGTATATAAAATCACCAC 229  
DB |||||  
QY 129 GTGCATTAAAGAGTCTTTTCAGGGTATAGACACATTGAAGAACCAACTGCCACGGGA 188  
DB |||||  
QY 230 GTGCACCTGAGAAATCTTTTCAGGGATAGGCACACTGGAGAGTCAAACTGTGCAAGGGG 289  
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QY 189 GGCTGTGGATAAATACTATTCAAAACCTGCTTTTAATAAAGAAACACATAGAGCGCCAAA 248  
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QY 350 AAAAA-GTGTGGAGAGAAAGACGGAGAGTAACCAATCTCTAGACTACTGCAAGATT 408  
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QY 309 TCTTGTGTATAAACAACCGAGTGGACACCGGAAAGT 345  
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QY 409 TCTTGTGTATAAACAACCGAGTGGATATAAGAAAGT 445  
DB |||||



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RESULT 10
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LOCUS      AGENCOURT 14496865 NIH MGC 195 Homo sapiens cDNA clone
DEFINITION      IMAGE:6971769 5', mRNA sequence.
ACCESSION      CD559535
VERSION      CD559535.2 GI:38558950
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 463)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      On Jun 10, 2003 this sequence version replaced gi:31595603.
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBK1 row: g column: 08
High quality sequence stop: 463.
Location/Qualifiers
1. 463
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/clone="IMAGE:6971769"
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/lab_host="DH5A (TI phage-resistant)"
/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxP-Salt; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH MGC Library."

ORIGIN
Query Match      63.9%; Score 220.4; DB 14; Length 463;
Best Local Similarity 80.2%; Pred No. 4,6e-43;
Matches 271; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY      9      AGAAATCCCATGATAGACGTGGTGGCAGACCTTGACACTGCTTCCATCATCGAAC 68
DB      93      AGAAATCCCAAGTCATGTTGGTGAAGAGACCTTGGCACTGCTTTCTACTCATCGAAC 152
QY      69      TTGGCTGTAGCGGATGGACCTGATGATTCCTACTCCTGAATAAATACCAACT 128
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RESULT 11
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LOCUS      AGENCOURT 14496901 NIH MGC 195 Homo sapiens cDNA clone
DEFINITION      IMAGE:6971769 5', mRNA sequence.
ACCESSION      CD559689
VERSION      CD559689.2 GI:38453487
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 473)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      On Jun 10, 2003 this sequence version replaced gi:31595757.
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 473.
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/clone_lib="NIH MGC 195"
/notes="Vector: pDNR-Dual; Site 1: loxP-Salt; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
http://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH MGC Library."

FEATURES
source
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cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxp sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearranged\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat)  
 a Note: this is a NIH\_MGC Library."

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 VERSION  
 AY412022.1 GI:39767987  
 KEYWORDS  
 GSS.  
 SOURCE  
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ORGANISM  
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 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 399)  
 REFERENCE  
 AUTHORS  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 Science 302 (5652), 1960-1963 (2003)  
 14671302  
 2 (bases 1 to 399)  
 REFERENCE  
 AUTHORS  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
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 Matches 230; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
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 genomic survey sequence.  
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 VERSION  
 CE331159.1 GI:36147469  
 KEYWORDS  
 GSS.  
 SOURCE  
 Canis familiaris (dog)  
 Canis familiaris  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE  
AUTHORS

REFERENCE	1 (bases 1 to 622)
AUTHORS	Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
TITLE	The dog genome: survey sequencing and comparative analysis
JOURNAL	Science 301 (5641), 1898-1903 (2003)
MEDLINE	22875432
PUBMED	14512627
COMMENT	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirknes@tigr.org Class: shotgun.

## FEATURES

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## ORIGIN

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Search completed: August 31, 2004, 13:00:14  
Job time : 1160.04 secs

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US-10-027-632-39049  
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ALIGNMENTS

RESULT 1

US-09-755-633-9 Application US/09755633  
; Sequence 9, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-CL-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-09-755-633-9

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Matches 345; Conservative 0; Mismatches 0;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	345	100.0	345	9	US-09-755-633-9	Sequence 9, Appli
2	345	100.0	345	9	US-09-755-633-11	Sequence 11, Appl
3	345	100.0	345	15	US-10-218-654-85	Sequence 85, Appl
4	345	100.0	345	15	US-10-218-654-87	Sequence 87, Appl
5	345	100.0	345	15	US-10-262-439-85	Sequence 85, Appl
6	345	100.0	345	15	US-10-262-439-87	Sequence 87, Appl
7	345	100.0	402	9	US-09-755-633-7	Sequence 7, Appli
8	345	100.0	402	9	US-09-755-633-8	Sequence 8, Appli
9	345	100.0	402	15	US-10-218-654-83	Sequence 83, Appl
10	345	100.0	402	15	US-10-218-654-84	Sequence 84, Appl
11	345	100.0	402	15	US-10-262-439-83	Sequence 83, Appl
12	345	100.0	402	15	US-10-262-439-84	Sequence 84, Appl
13	345	100.0	610	9	US-09-755-633-4	Sequence 4, Appli
14	345	100.0	610	9	US-09-755-633-6	Sequence 6, Appli

Db 61 CATCGAACTTGGCTGATGGGATGGAACTGATGATTCCTCTGAAAAATAAAAAAT 120  
QY 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
Db 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
QY 181 CACGGGGAGGCTGGGATTAACATTTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 240  
Db 181 CACGGGGAGGCTGGGATTAACATTTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 240  
QY 241 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300  
Db 241 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300  
QY 301 CAAGTATTTCTTGGTGTATTAATAACACCGAGTGGACACCGGAAAGT 345  
Db 301 CAAGTATTTCTTGGTGTATTAATAACACCGAGTGGACACCGGAAAGT 345

RESULT 2  
US-09-755-633-11/c  
; Sequence 11, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McGill, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-11

Query Match 100.0%; Score 345; DB 9; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286  
QY 61 CATCGAACTTGGCTGATGGGATGGAACTGATGATTCCTCTGAAAAATAAAAAAT 120  
285 CATCGAACTTGGCTGATGGGATGGAACTGATGATTCCTCTGAAAAATAAAAAAT 226  
QY 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
225 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 166  
QY 181 CACGGGGAGGCTGGGATTAACATTTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 240  
165 CACGGGGAGGCTGGGATTAACATTTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 106  
QY 241 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300  
105 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 46  
QY 301 CAAGTATTTCTTGGTGTATTAATAACACCGAGTGGACACCGGAAAGT 345  
45 CAAGTATTTCTTGGTGTATTAATAACACCGAGTGGACACCGGAAAGT 1

RESULT 3  
US-10-218-654-85  
; Sequence 85, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-10-218-654-85

Query Match 100.0%; Score 345; DB 15; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
Db 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
QY 61 CATCGAACTTGGCTGATGGGATGGAACTGATGATTCCTCTGAAAAATAAAAAAT 120  
Db 61 CATCGAACTTGGCTGATGGGATGGAACTGATGATTCCTCTGAAAAATAAAAAAT 120  
QY 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
Db 121 CACCAACTGTGCTATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
QY 181 CACGGGGAGGCTGGGATTAACATTTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 240  
Db 181 CACGGGGAGGCTGGGATTAACATTTCCAAAACTTGTCTTTAATAAAGAACACATAGAG 240  
QY 241 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300  
Db 241 CGCCAAAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300  
QY 301 CAAGTATTTCTTGGTGTATTAATAACACCGAGTGGACACCGGAAAGT 345  
Db 301 CAAGTATTTCTTGGTGTATTAATAACACCGAGTGGACACCGGAAAGT 345

RESULT 4  
US-10-218-654-87/c  
; Sequence 87, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13

Best Local Similarity 100.0%; Pred. No. 1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
Db 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAAT 120  
Db 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAAT 120  
QY 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
Db 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
QY 181 CACGGGGAGGCTGGGATATAACTATCCAAAACCTTGCTTTAATAAAGAAACACATAGAG 240  
Db 181 CACGGGGAGGCTGGGATATAACTATCCAAAACCTTGCTTTAATAAAGAAACACATAGAG 240  
QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300  
Db 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300  
QY 301 CAAGTATTTCTTGGTGTATAAACCAGAGTGGACACCGGAAAGT 345  
Db 301 CAAGTATTTCTTGGTGTATAAACCAGAGTGGACACCGGAAAGT 345  
RESULT 5  
US-10-262-439-87/c  
; Sequence 87, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-87  
Query Match 100.0%; Score 345; DB 15; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286  
QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAAT 120  
Db 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAAT 226  
QY 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
Db 225 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166  
QY 181 CACGGGGAGGCTGGGATATAACTATCCAAAACCTTGCTTTAATAAAGAAACACATAGAG 240

PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-87  
Query Match 100.0%; Score 345; DB 15; Length 345;  
Best Local Similarity 100.0%; Pred. No. 1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286  
QY 61 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAAT 120  
Db 285 CATCGAACTTGGCTGTAGAGCGATGGGAACCTGATGATTTCTTACTCTCTGAAAAATAAAAT 226  
QY 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
Db 225 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166  
QY 181 CACGGGGAGGCTGGGATATAACTATCCAAAACCTTGCTTTAATAAAGAAACACATAGAG 240  
Db 165 CACGGGGAGGCTGGGATATAACTATCCAAAACCTTGCTTTAATAAAGAAACACATAGAG 106  
QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 300  
Db 105 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTTAGACTACCTG 46  
QY 301 CAAGTATTTCTTGGTGTATAAACCAGAGTGGACACCGGAAAGT 345  
Db 45 CAAGTATTTCTTGGTGTATAAACCAGAGTGGACACCGGAAAGT 1  
RESULT 5  
US-10-262-439-85  
; Sequence 85, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-10-262-439-85  
Query Match 100.0%; Score 345; DB 15; Length 345;

Db 165 CACGGGAGGCTGTGATAAATCCAAACCTGCTTTAATAAAGACACATAG 106  
 Qy 241 CGCAGAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTCTG 300  
 Db 105 CGCCAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTCTG 46  
 Qy 301 CAAATATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 345  
 Db 45 CAAATATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

## RESULT 7

US-09-755-633-7

; Sequence 7, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: McCall, Catherine A.

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09755,633

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-755-633-7

Query Match 100.0%; Score 345; DB 9; Length 402;

Best Local Similarity 100.0%; Pred. No. 1.1e-95;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
 Db 58 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117  
 Qy 61 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAT 120  
 Db 118 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAT 177  
 Qy 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180  
 Db 178 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 237  
 Qy 181 CACGGGAGGCTGTGGATAAATCTATTCCAAACCTTGTCTTTAATAAAGAACACATAGAG 240  
 Db 238 CACGGGAGGCTGTGGATAAATCTATTCCAAACCTTGTCTTTAATAAAGAACACATAGAG 297  
 Qy 241 CGCCAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTG 300  
 Db 298 CGCCAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTG 357  
 Qy 301 CAAATATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 345  
 Db 358 CAAATATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 402

## RESULT 8

US-09-755-633-8/c

; Sequence 8, Application US/09755633

; Patent No. US20020127200A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Shumin

; APPLICANT: Weber, Eric R.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; FILE REFERENCE: IM-2-C1-C1

; CURRENT APPLICATION NUMBER: US/09755,633

; CURRENT FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-755-633-8

Query Match 100.0%; Score 345; DB 9; Length 402;

Best Local Similarity 100.0%; Pred. No. 1.1e-95;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
 Db 345 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286  
 Qy 61 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAT 120  
 Db 285 CATCGAACTTGGCTGTAGGGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAAT 226  
 Qy 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180  
 Db 225 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 166  
 Qy 181 CACGGGAGGCTGTGGATAAATCTATTCCAAACCTTGTCTTTAATAAAGAACACATAGAG 240  
 Db 185 CACGGGAGGCTGTGGATAAATCTATTCCAAACCTTGTCTTTAATAAAGAACACATAGAG 106  
 Qy 241 CGCCAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTG 300  
 Db 105 CGCCAAAAAAGGTGTGAGGAGAAAGATGGAGAGTGACAAAGTCTCTAGACTACCTG 46  
 Qy 301 CAAATATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 345  
 Db 45 CAAATATTCTTGTGTGTAATAAACACCGAGTGGACACCGGAAAGT 1

## RESULT 9

US-10-218-654-83

; Sequence 83, Application US/10218654

; Publication No. US20030099609A1

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/10/218,654

; CURRENT FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: US/09/322,409

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/087,306

; PRIOR FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 83

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Canis familiaris

US-10-218-654-83



Query Match 100.0%; Score 345; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1.1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 60  
DB 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 117

QY 61 CATCGAACTTGGCTGATAGCGGATGGGAACCTGATCTCTACTCTCTGAAAATAAAAT 120  
DB 118 CATCGAACTTGGCTGATAGCGGATGGGAACCTGATCTCTACTCTCTGAAAATAAAAT 177

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
DB 178 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 237

QY 181 CACGGGAGGCTGTGATAAATCTATCCAAACTTCTTTTAATAAAGAACACATAGAG 240  
DB 238 CACGGGAGGCTGTGATAAATCTATCCAAACTTCTTTTAATAAAGAACACATAGAG 297

QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTG 300  
DB 298 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTG 357

QY 301 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 345  
DB 358 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 402

RESULT 10  
US-10-218-654-84/c  
; Sequence 84, Application US/10218654  
; Publication No. US2003009609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-84

Query Match 100.0%; Score 345; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1.1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 60  
DB 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 286

QY 61 CATCGAACTTGGCTGATAGCGGATGGGAACCTGATCTCTACTCTCTGAAAATAAAAT 120  
DB 285 CATCGAACTTGGCTGATAGCGGATGGGAACCTGATCTCTACTCTCTGAAAATAAAAT 226

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
DB 225 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 166

QY 181 CACGGGAGGCTGTGATAAATCTATTCAAAAGTTCTTTTAATAAAGAACACATAGAG 240

DB 165 CACGGGAGGCTGTGATAAATCTATTCAAAAGTTCTTTTAATAAAGAACACATAGAG 106  
QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTG 300  
DB 105 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTG 46  
QY 301 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 345  
DB 45 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 1

RESULT 11  
US-10-262-439-83  
; Sequence 83, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-83

Query Match 100.0%; Score 345; DB 15; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1.1e-95;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 60  
DB 58 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGTCTCCACT 117

QY 61 CATCGAACTTGGCTGATAGCGGATGGGAACCTGATCTCTACTCTCTGAAAATAAAAT 120  
DB 118 CATCGAACTTGGCTGATAGCGGATGGGAACCTGATCTCTACTCTCTGAAAATAAAAT 177

QY 121 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 180  
DB 178 CACCAACTGTGCATTAAAGAAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC 237

QY 181 CACGGGAGGCTGTGATAAATCTATTCAAAAGTTCTTTTAATAAAGAACACATAGAG 240  
DB 238 CACGGGAGGCTGTGATAAATCTATTCAAAAGTTCTTTTAATAAAGAACACATAGAG 297

QY 241 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTG 300  
DB 298 CGCCAAAAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCTCTAGACTACCTG 357

QY 301 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 345  
DB 358 CAAGTATTTCTTGGTGTATAAATACACCGAGTGACACCGGAAAGT 402

RESULT 12  
US-10-262-439-84/c  
; Sequence 84, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:

```
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-262-439-84

Query Match      100.0%; Score 345; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB
QY      61  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT 120
DB
QY      181  CACGGGAGGCTGTGGATAAATCTATTCAAAACCTTGCTTTTAATAAAGAACACATAGAG 240
DB
QY      241  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300
DB
QY      301  CAAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345
DB
QY      45  CAAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 13
US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match      100.0%; Score 345; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB
QY      525  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466
DB
QY      61  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120
DB
QY      465  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 406
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; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-755-633-4

Query Match      100.0%; Score 345; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB
QY      86  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145
DB
QY      61  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120
DB
QY      146  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 205
DB
QY      121  CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 180
DB
QY      206  CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTTGAAGAACCAACTGCC 265
DB
QY      181  CACGGGAGGCTGTGGATAAATCTATTCAAAACCTTGCTTTTAATAAAGAACACATAGAG 240
DB
QY      266  CACGGGAGGCTGTGGATAAATCTATTCAAAACCTTGCTTTTAATAAAGAACACATAGAG 325
DB
QY      241  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300
DB
QY      326  CGCCAAAAAAGCTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 385
DB
QY      301  CAAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345
DB
QY      386  CAAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 14
US-09-755-633-6/c
; Sequence 6, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-6

Query Match      100.0%; Score 345; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB
QY      525  TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466
DB
QY      61  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120
DB
QY      465  CATCGAACTTGGCTGTAGCGGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 406
DB
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QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
Db 405 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 346
QY 181 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 240
Db 345 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 286
QY 241 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGCACAAAGTTCTAGACTACCTG 300
Db 285 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGCACAAAGTTCTAGACTACCTG 226
QY 301 CAAGTATTTCTTGGTGTATAAACAACCGAGTGACACCGGAAAGT 345
Db 225 CAAGTATTTCTTGGTGTATAAACAACCGAGTGACACCGGAAAGT 181
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RESULT 15

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US-10-218-654-80
; Sequence 80, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kea
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-10-218-654-80
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Query Match 100.0%; Score 345; DB 15; Length 610;
Best Local Similarity 100.0%; Pred. No. 1.4e-95;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db 86 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 145
QY 61 CATCGAAGTTCGCTGATAGCGGAACTGATGATTCCTCTCTGAAAATAAAAT 120
Db 146 CATCGAAGTTCGCTGATAGCGGAACTGATGATTCCTCTCTGAAAATAAAAT 205
QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
Db 206 CACCAACTGTGCATTAAAGAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 265
QY 181 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 240
Db 286 CACGGGAGGCTGTGATAAACTATTCCAAAACCTTCTTTTAAATAAAGAACACATAGAG 325
QY 241 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGCACAAAGTTCTAGACTACCTG 300
Db 326 CGCCAAAAAAGAGTGTGCAGAGAAAGATGAGAGTGCACAAAGTTCTAGACTACCTG 385
QY 301 CAAGTATTTCTTGGTGTATAAACAACCGAGTGACACCGGAAAGT 345
Db 386 CAAGTATTTCTTGGTGTATAAACAACCGAGTGACACCGGAAAGT 430
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
6219.989 Million cell updates/sec

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Perfect score: 345  
Sequence: 1 ttgtgctgtagaaatcccat.....ccgagtgacacccggaagt 345

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
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4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	345	100.0	345	4	US-09-322-409-87
3	345	100.0	345	4	US-09-451-527-85
4	345	100.0	345	4	US-09-451-527-87
5	345	100.0	402	4	US-09-322-409-83
6	345	100.0	402	4	US-09-322-409-84
7	345	100.0	402	4	US-09-451-527-83
8	345	100.0	402	4	US-09-451-527-84
9	345	100.0	610	4	US-09-322-409-80
10	345	100.0	610	4	US-09-322-409-82
11	345	100.0	610	4	US-09-451-527-80
12	345	100.0	610	4	US-09-451-527-82
13	341.8	99.1	405	4	US-09-371-615A-1
14	231.4	67.1	816	3	US-09-079-839-2
15	229.8	66.6	816	4	US-09-023-655-1236
16	206	59.7	377	4	US-09-180-864-1
17	196.4	56.9	1534	3	US-08-629-643A-4
18	196.4	56.9	1534	3	US-09-155-884-4
19	90.6	26.3	6727	3	US-08-629-643A-5
20	90.6	26.3	6727	3	US-09-280-799-1
21	90.6	26.3	6727	3	US-09-155-884-5
22	90.2	26.1	3230	3	US-09-280-799-78
23	90.2	26.1	3230	6	5324640-1
24	38	11.0	7218	1	US-08-232-463-14
25	34.4	10.0	4843	3	US-08-986-485-1
26	33.4	9.7	22846	2	US-08-469-461-3
27	33.4	9.7	22846	3	US-07-890-609-3

C 28	32.4	9.4	2797	4	US-09-453-702B-244	Sequence 244, Appl
C 29	31.8	9.2	1902	4	US-09-220-132-74	Sequence 74, Appl
C 30	31.6	9.2	927	4	US-09-134-001C-150	Sequence 150, Appl
C 31	31.6	9.2	1642	4	US-09-737-898B-24	Sequence 24, Appl
C 32	31.6	9.2	1642	4	US-09-737-826A-24	Sequence 24, Appl
C 33	31.6	9.2	9626	4	US-09-150-867-2	Sequence 2, Appl
C 34	31.6	9.2	174493	4	US-09-804-471A-3	Sequence 3, Appl
C 35	31.6	9.2	174493	4	US-10-238-709-3	Sequence 1, Appl
C 36	31.6	9.2	1664976	4	US-08-916-421B-1	Sequence 3, Appl
C 37	31.4	9.1	21338	4	US-08-961-527-20	Sequence 20, Appl
C 38	31.2	9.0	505	4	US-09-621-976-15639	Sequence 15639, A
C 39	31.2	9.0	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 40	31	9.0	222	4	US-09-543-681A-1166	Sequence 1166, Ap
C 41	31	9.0	3434	4	US-09-388-743-9	Sequence 9, Appl
C 42	30.8	8.9	1842	4	US-09-328-352-2806	Sequence 2806, Ap
C 43	30.8	8.9	9421	2	US-08-370-319C-2	Sequence 2, Appl
C 44	30.8	8.9	9421	3	US-09-224-834-2	Sequence 2, Appl
C 45	30.8	8.9	12124	1	US-08-181-271A-36	Sequence 36, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-322-409-85

; Sequence 85, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Kee

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/09/322,409

; CURRENT FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 85

; LENGTH: 345

; TYPE: DNA

; ORGANISM: Canis familiaris

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(345)

US-09-322-409-85

Query Match 100.0%; Score 345; DB 4; Length 345;

Best Local Similarity 100.0%; Pred. No. 1.4e-100; Mismatches 0; Indels 0; Gaps 0;

Matches 345; Conservative 0;

QY	1	TTTGCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT	60
DB	1	TTTGCTGTAGAAAATCCCATGAATAGACTGTGGCAGAGACCTTGACACTGCTCTCCACT	60
QY	61	CATCGAACTTGGCTGATAGCGCATGGACCTGTATCTCTACTCTGAAATAAAT	120
DB	61	CATCGAACTTGGCTGATAGCGCATGGACCTGTATCTCTACTCTGAAATAAAT	120
QY	121	CACCAACTGTGATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC	180
DB	121	CACCAACTGTGATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC	180
QY	181	CACGGGAGGCTGTGGATAAATCTATTCAAAACCTTCTTTTAAATAAAGAACACATAGAG	240
DB	181	CACGGGAGGCTGTGGATAAATCTATTCAAAACCTTCTTTTAAATAAAGAACACATAGAG	240
QY	241	CGCCAAAAAAGAGGTGTCAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG	300
DB	241	CGCCAAAAAAGAGGTGTCAGAGAAAGATGAGAGTGCACAAAGTTCTTAGACTACCTG	300

Qy		301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 345
Db		301 CAAGTATTTCTTGGTGTAATAAACACCGAGTGGACACCGGAAAGT 345

## RESULT 2

RESOL 2  
 US-09-322-409-87/c  
 ; Sequence 87, Application US/09322409  
 ; Patent No. 6471957  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE: IM-2-C1  
 ; CURRENT APPLICATION NUMBER: US/09/322,409  
 ; CURRENT FILING DATE: 1999-05-28  
 ; EARLIER APPLICATION NUMBER: 60/087,306  
 ; EARLIER FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 87  
 ; LENGTH: 345  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 US-09-322-409-87

RESIST 3

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: RESULT 3
: US-09-451-527-85
: Sequence 85, Application US/09451527
: Patent No. 6482403
: GENERAL INFORMATION:
: APPLICANT: Sim, Gek-Kee
: APPLICANT: Yang, Shumin
: APPLICANT: Dreitz, Matthew J.
: APPLICANT: Wonderling, Ramani S.
: TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
: FILE REFERENCE: IM-2-C2
: CURRENT APPLICATION NUMBER: US/09/451.527
: CURRENT FILING DATE: 1999-12-01
:

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; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0

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Query Match	100.0%;	Score 345;	DB 4;	Length 345;
Best Local Similarity	100.0%;	Pred. No. 1.4e-100;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

## RESULT 4

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US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

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	Query Match	100.0%	Score 345;	DB 4;	Length 402;
	Best Local Similarity	100.0%;	Pred. No. 1.15e-100;		
	Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TTTGTCTGAGAAAATCCCATGAATAGACTGTGTGGCAGAGACCTTGCACATGCTCTCCACT	60		
Db	58	TTTGTCTGAGAAAATCCCATGAATAGACTGTGTGGCAGAGACCTTGCACATGCTCTCCACT	117		
Qy	61	CATCGAACTTGGCTGATAGGGGATGGAACTCGATGATTCCTACTCTCGTGAATAAATAAT	120		
Db	118	CATCGAACTTGGCTGATAGGGGATGGAACTCGATGATTCCTACTCTCGTGAATAAATAAT	177		
Qy	121	CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAGAAGACCAAACTGCC	180		
Db	178	CACCAACTGTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTGAGAAGACCAAACTGCC	237		
Qy	181	CACGGGAGGCTGTGGATAACTATTCCAAACCTGTCTTTTAATAAAGAACACATAGAG	240		
Db	238	CACGGGAGGCTGTGGATAACTATTCCAAACCTGTCTTTTAATAAAGAACACATAGAG	297		
Qy	241	CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	300		
Db	298	CGCCAAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	357		

RESULT 7  
US-09-451-527-83  
; Sequence 83, Application US/09451527  
; Patent No. 6492403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Keo  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/451.527  
; CURRENT FILING DATE: 1999-12-01

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;
;   EARLIER APPLICATION NUMBER: 09/322,409
;   EARLIER FILING DATE: 1999-05-28
;   EARLIER APPLICATION NUMBER: 60/087,306
;   EARLIER FILING DATE: 1998-05-29
;   NUMBER OF SEQ ID NOS: 174
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO. 83
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-451-527-83

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Query Match	100.0%;	Score 345;	DB 4;	Length 402;
Best Local Similarity	100.0%;	Pred. No. 1.5e-100;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TTTGTCTGTAGAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTCTCCACT	60	
Db	58	TTTGTCTGTAGAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGCTCTCCACT	117	
Qy	61	CATCGAACTTGGCTGTATAGGCGATGGGAACCTGATGATCTCTACTCTCTGAAAATAAAAAAT	120	
Db	118	CATCGAATCTTGGCTGTATAGGCGATGGGAACCTGATGATCTCTACTCTCTGAAAATAAAAAAT	177	
Qy	121	CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC	180	
Db	178	CACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC	237	
Qy	181	CACGGGGAGGCTGTGGATAAATCTTCCAAAACTTGTCTTTAATAAAGAACAATAGAG	240	
Db	238	CACGGGGAGGCTGTGGATAAATCTTCCAAAACTTGTCTTTAATAAAGAACAATAGAG	297	
Qy	241	CGCCCAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTTACCTG	300	
Db	298	CGCCCAAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTTACCTG	357	
Qy	301	CAAGTATTTCTTGGTGAATAAACAACCGAGTGGACACCGGAAAGT	345	
Db	358	CAAGTATTTCTTGGTGAATAAACAACCGAGTGGACACCGGAAAGT	402	

```

RESULT 8
US-09-451-527-84/c
; Sequence 84, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Keo
; APPLICANT: Yang, Shumin
; APPLICANT: Dretz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE
; TITLE OF INVENTION: ACID MOLECULES,
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451-527-84
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,478
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,144
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1/4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84

```

Query Match 100.0%; Score 345; DB 4; Length 402;  
Best Local Similarity 100.0%; Pred. No. 1.5e-100;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTGCTGTAGAAATCCCATGATACACTGGTGGCAGACCTTCACACTGCTCTCCACT 60

Db	345	TTTGTGTGTAAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT	288
Qy	61	CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT	120
Db	285	CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT	226
Qy	121	CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC	180
Db	225	CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCC	166
Qy	181	CACGGGAGGCTGTGCATAAACTATTCCAAACTTTGCTTTTAATAAAAGAACACATAGAG	240
Db	165	CACGGGAGGCTGTGCATAAACTATTCCAAACTTTGCTTTTAATAAAAGAACACATAGAG	106
Qy	241	CGCCAAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	300
Db	105	CGCCAAAAAAAAGGTGTGCAGGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	46
Qy	301	CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	345
Db	45	CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	1

RESULT 9  
 US-09-322-409-80  
 ; Sequence 80, Application US/09322409  
 ; Patent No. 6471957  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-Kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE: IM-2-C1  
 ; CURRENT APPLICATION NUMBER: US/09/322,409  
 ; CURRENT FILING DATE: 1999-05-28  
 ; EARLIER APPLICATION NUMBER: 60/087,306  
 ; EARLIER FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS: 154  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 80  
 ; LENGTH: 610  
 ; TYPE: DNA  
 ; ORGANISM: Canis familiaris  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (29)..(430)  
 ; US-09-322-409-80

Query Match	100.0%;	Score 345;	DB 4;	Length 610;
Best Local Similarity	100.0%;	Pred. No. 1.9e-100;		
Matches 345;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TTTCTGTGAAGATCCCATGAAATGACATGCTGGTGAGAGACCTTCACACTGCTCTCCACT	60	
Db	86	TTTGTGTGAGAAAAATCCCATGAATGACTGGTGAGAGACCTTCACACTGCTCTCCACT	145	
QY	61	CATCGAACTTGGCTGATAGCGCGATGGGAACCTGATGATTCCTCTCTCAAAAATAAAAT	120	
Db	146	CATCGAACTTGGCTGATAGCGGATGGGAACCTGATGATTCCTCTCTGAAAAATAAAAT	205	
QY	121	CACCAACTGTGCATTAAGAAGTTTTTTCAGGTATAGACATTTGAAGAACCAAACTGCC	180	
Db	206	CACCAACTGTGCATTAAGAAGTTTTTTCAGGTATAGACATTTGAAGAACCAAACTGCC	265	
QY	181	CACGGGAGGCTGTGGATAACTATTCCAAAACCTTGTTCTTTTAATAAAGAACACATGAG	240	
Db	266	CACGGGAGGCTGTGGTAAACTATTTCAAAACCTTGTTCTTTTAATAAAGAACACATGAG	325	
QY	241	CGCCAAAAAAGAGGTGTGCGAGGAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG	300	



; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-03-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-09-451-527-80

Query Match      100.0%; Score 345; DB 4; Length 610;  
Best Local Similarity    100.0%; Pred.No. 1.9e-100;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY	1	TTTGCTGTAGAAAATCCCATGAATAGACTGGTGCACGACCCTTGACACTGTCTCCTCACT
DB	86	TTTTGCTGTAGAAATCCCATTGAATAGACTGGTGCACGACCCTTGACACTGTCTCCTCACT

QY	61	CATCGAACTTCGGCTGTATAGGCCATGGGAACCTGATGATGTTCCTTAATAAAAAATAAAAT
DB	146	CATCGAACCTTCGGCTGTATAGGCCATGGGAACCTGATGATTCCTTAATAAAAAATAAAAT

QY	121	CACCAAACCTGTGATTAAAGAAGTTTTTCAGGTTATAGACACATTGAAGAACAACAACCTGCC
DB	206	CACCAAACCTGTGATTAAAGAAGTTTTTCAGGTTATAGACACATTGAAGAACAACAACCTGCC

QY	181	CACGGGAGGCTGTGGATPAAACTATTCCAATACTTGCTTTTANAAAAACAACATAGAG
DB	266	CACGGGAGGCTGTGGATPAAACTATTCCAATACTTGCTTTTANAAAAACAACATAGAG

QY	241	CCCCAAAAAAAAAGGTGTCAGGAAGAAAGATGGAGTAGCACAAAGTTCCCTAGACTACCTG
DB	326	CCCCAAAAAAAAAGGTGTCAGGAAGAAAGATGGAGTAGCACAAAGTTCCCTAGACTACCTG

QY	301	CAAGTATTTCITGGTGTAATAAACAACCGAGTGGACACCGGAAAGT
DB	386	CAAGTATTTCITGGTGTAATAAACAACCGAGTGGACACCGGAAAGT

RESULT 12  
US-09-451-527-82/c  
Sequence 82, Application US/09451527  
Patent No. 6482403  
GENERAL INFORMATION:  
APPLICANT: Sim, Gek-Kee  
APPLICANT: Yang, Shumlin  
APPLICANT: Dreitz, Matthew J.  
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
FILE REFERENCE: IM-2-C2  
CURRENT APPLICATION NUMBER: US/09/451,527  
CURRENT FILING DATE: 1999-12-01  
EARLIER APPLICATION NUMBER: 09/322,409  
EARLIER FILING DATE: 1999-05-28  
EARLIER APPLICATION NUMBER: 60/087,306  
EARLIER FILING DATE: 1998-05-29  
NUMBER OF SEQ ID NOS: 174  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 82  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Canis familiaris  
US-09-451-527-82

Query Match      100.0%; Score 345; DB 4; Length 610;  
Best Local Similarity    100.0%; Pred.No. 1.9e-100;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY	301	CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	345
Db	386	CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	430

RESULT 10

US-09-322-409-82/c

; Sequence 82, Application US/09322409

; Patent No. 6471957

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Ke

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C1

; CURRENT APPLICATION NUMBER: US/09/322.409

; EARLIER FILING DATE: 1999-05-28

; EARLIER FILING DATE: 1998-05-29

; NUMBER OF SEQ ID NOS: 154

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 82

; LENGTH: 610

; TYPE: DNA

; ORGANISM: Canis familiaris

US-09-322-409-82

Query Match 100.0%; Score 345; DB 4; Length 610;

Best Local Similarity 100.0%; Pred. No. 1.9e-100;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACATGCTCTCCACT	60
Db	525	TTTGCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACATGCTCTCCACT	466
QY	61	CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT	120
Db	465	CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAAT	405
QY	121	CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAGAGAACCAACTGCC	180
Db	405	CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTTGAGAGAACCAACTGCC	346
QY	181	CACGGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAG	240
Db	345	CACGGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAG	286
QY	241	CGCCAAAAAAAACGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG	300
Db	285	CGCCAAAAAAAACGGTGTGCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACCTG	226
QY	301	CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	345
Db	225	CAAGTATTTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT	181

RESULT 11

US-09-451-527-80

; Sequence 80, Application US/09451527

; Patent No. 6482403

; GENERAL INFORMATION:

; APPLICANT: Sim, Gek-Ke

; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.

; APPLICANT: Wonderling, Ramani S.

; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

; FILE REFERENCE: IM-2-C2

; CURRENT APPLICATION NUMBER: US/09/451.527

; CURRENT FILING DATE: 1999-12-01



Wed Sep 1 08:34:23 2004

APPLICATION NUMBER: US/09/023,655  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1236:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 816 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: G288309  
US-09-023-655-1236

Query Match 56.6%; Score 229.8; DB 4; Length 816;  
Best Local Similarity 80.1%; Pred. No. 1.2e-63;  
Matches 270; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy	9	AGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACACTGCTCTCCACTCATCGAAC	68
Db	110	AGAAATCCCAAGTCATGTGGAAGAGACCTTGGCACTGCTTTCTACTCATCGAAC	159
Qy	69	TTGGCTGATAGGGGATGGAACTCTGATGATTCCTCTGAAATAAAATCACCACCT	128
Db	170	TCGTCTGATAGCCCAATGAGACTCTGAGGATTCCTGTTCTGTGTACATAAAATCACCACCT	229
Qy	129	GTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCCACGGGGA	188
Db	230	GTGCACCTGAAGAAATCTTTTCAGGGAATAGGACACACTGGAGAGTCAAACTGTGCAAGGGG	289
Qy	189	GGCTGTGGATAAACTATTCCAAAACTTGTCTTTTAATAAAGAACACATAGAGGCCAAAA	248
Db	290	TACTGTGGAAGACTATTGAAAACTTGTCTTTAATAAAGAAATACATTGACGGCCAAAA	349
Qy	249	AAAAGGTGTCAGAGAGAGATCGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT	308
Db	350	AAAAAAGTGTGGAGAGAGACCGAGAGTAAACCAATTCTCTAGACTACCTGCAAGAGTT	409
Qy	309	TCITGGTGTATAAACACCGAGTGGACACCGGAAAGT	345
Db	410	TCITGGTGTATGAACACCGAGTGGATAATAGAAAGT	446

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Job time : 31.7811 secs

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Sheet

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 164.547 Seconds  
(without alignments)  
8907.036 Million cell updates/sec

Title: US-10-787-382-9

Perfect score: 345

Sequence: 1 ttgtgctgtagaaatcccat.....ccgagtgacacggaaagt 345

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 337963 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	345	100.0	345	3	Aaz5550 Canine ma
C 2	345	100.0	345	3	Aaz5551 Canine ma
3	345	100.0	402	3	Aaz55548 Canine in
C 4	345	100.0	402	3	Aaz55549 Canine in
5	345	100.0	610	3	Aaz55546 Canine in
C 6	345	100.0	610	3	Aaz55547 Canine in
7	341.8	99.1	405	4	Aaf74300 Canine in
8	289.6	83.9	838	3	Aaz44265 Porcine I
9	287.4	83.3	393	4	Aaf74306 Canine in
10	274.8	79.7	399	2	Aat50756 Ovine IL-
11	274.8	79.7	520	2	Aat50755 Ovine IL-
12	271.4	67.1	816	3	Aaa34857 Human ade
13	271.4	67.1	816	3	Aaa13338 Human int
14	271.4	67.1	816	3	Aaf20979 Human low
15	231.4	67.1	816	7	Abz96673 Human nuc
16	231.4	67.1	816	7	Acf63368 Human int
17	231.4	67.1	858	8	Aal61293 h115-P2-P
18	231.4	67.1	858	8	AAL61294 h115-P30-
19	231.4	67.1	864	8	AAL61296 h115.37 v
20	231.4	67.1	864	8	AAL61295 h115.36 v
21	231.4	67.1	4057	3	Aaa34858 Human ade
22	231.4	67.1	4057	3	Aaf20980 Human low
23	231.4	67.1	4057	7	Abz96674 Human nuc

24	229.8	66.6	402	1	AAN81380
25	224.6	65.1	370	1	AAN91647
26	206	59.7	377	2	Aav01595 Human int
27	196.4	56.9	348	2	Aat14922 T cell re
28	196.4	56.9	399	2	Aav64061 T cell re
29	196.4	56.9	402	2	Aat14921 T cell re
30	196.4	56.9	1533	1	AAN82431 B cell di
31	196.4	56.9	1534	2	AAT88013 Murine in
32	196.4	56.9	1623	2	AAT14925 T cell re
33	196.4	56.9	1623	2	Aav64062 Plasmid p
34	195	56.5	252	4	Aaf74305 Canine in
35	194.6	56.4	342	2	Aat14923 T cell re
36	194.2	56.3	339	2	Aat14924 T cell re
37	190.6	55.2	1945	9	ADB53890 Primary r
38	190	55.1	481	1	AAN80461 Clone 115
39	183.6	53.2	385	3	AA43842 Human sec
40	178.4	51.7	375	3	Aac68870 Modified
41	175.6	50.9	357	3	AAC68871 Modified
42	169.2	49.0	381	3	Aac68867 Modified
43	166.4	48.2	399	3	AAC68873 Modified
44	166	48.1	444	3	AAC68875 Modified
45	165.6	48.0	375	3	AAC68872 Modified

#### ALIGNMENTS

RESULT 1  
AAZ55550  
ID AAZ55550 standard; cDNA; 345 BP.

XX AC AAZ55550;

XX DT 14-MAR-2000 (first entry)

XX DE Canine mature interleukin-5 (IL-5) cDNA.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-C087306P.

XX (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WFI; 2000-072623/06.

XX P-PSDB; AAY58220.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
useful for treating or preventing e.g. tumors or autoimmune disease.

XX PS Claim 1h; Page 226-227; 264pp; English.

XX CC Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
feline Flt-3 ligand, canine or feline CD40, canine or feline (IFN-alpha)  
ligand, canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
nucleotides which encode these immunoregulatory proteins. The proteins,  
their associated nucleic acids, specific antibodies and inhibitors may be  
used as vaccines for therapeutic or prophylactic regulation of an immune  
response in animals (particularly cats, dogs, horses and humans). They  
may be used to treat autoimmune or infectious diseases including  
allergies, tumours, inflammation and graft rejection, and to increase the

CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Query Match 100.0%; Score 345; DB 3; Length 345;

Best Local Similarity 100.0%; Pred. No. 4e-93;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Db 1 TTTCCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Qy 61 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120

Db 61 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120

Qy 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 180

Db 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 180

Qy 181 CACGGGAGGCTGGGATAAATATCCAAACTTGTCTTTTAAATAAAGAACACATAGAG 240

Db 181 CACGGGAGGCTGGGATAAATATCCAAACTTGTCTTTTAAATAAAGAACACATAGAG 240

Qy 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300

Db 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300

Qy 301 CAAGTATTTCTTGGTGTAAATAAACCCAGAGTGACACCCGGAAGT 345

Db 301 CAAGTATTTCTTGGTGTAAATAAACCCAGAGTGACACCCGGAAGT 345

RESULT 2

AAZ5551/G

ID AAZ55551 standard; cDNA; 345 BP.

XX AAZ55551;

AC AAZ55551;

DT 14-MAR-2000 (first entry)

XX Canine mature interleukin-5 (IL-5) cDNA complement.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

DR P-PSDB; AAY58220.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

PT useful for treating or preventing e.g. tumours or autoimmune disease.

XX Claim 1h; Page 228; 264pp; English.

XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases, including the  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 345; DB 3; Length 345;

Best Local Similarity 100.0%; Pred. No. 4e-93;

Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60

Db 345 TTTCCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286

Qy 61 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 120

Db 285 CATCGAACTTGGCTGATAGCGCATGGGAACCTGATGATTCCTACTCTGAAAAATAAAAT 226

Qy 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 180

Db 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATGTAAGAACCAAACTGCC 166

Qy 181 CACGGGAGGCTGGGATAAATATCCAAACTTGTCTTTTAAATAAAGAACACATAGAG 240

Db 165 CACGGGAGGCTGGGATAAATATCCAAACTTGTCTTTTAAATAAAGAACACATAGAG 106

Qy 241 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300

Db 105 CGCCAAAAAAGAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 46

Qy 301 CAAGTATTTCTTGGTGTAAATAAACCCAGAGTGACACCCGGAAGT 345

Db 45 CAAGTATTTCTTGGTGTAAATAAACCCAGAGTGACACCCGGAAGT 1

RESULT 3

AAZ55548

ID AAZ55548 standard; cDNA; 402 BP.

XX AAZ55548;

AC AAZ55548;

DT 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA coding region.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;

KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

```
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
XX P-PSDB; AAY58219.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX Claim 1h; Page 225; 264pp; English.
XX
XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting.
XX
XX Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 345; DB 3; Length 402;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-93;
XX Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 58 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117
QY 61 CATCGAACTTGGCTGTAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAT 120
DB 118 CATCGAACTTGGCTGTAGCGATGGGAACCTGATGATTCCTACTCTGAAAATAAAAT 177
QY 121 CACCACTGTGCATTAAAGAGTTTTCAGGATATAGACACATTGAGACCAACTGCC 180
DB 178 CACCACTGTGCATTAAAGAGTTTTCAGGATATAGACACATTGAGACCAACTGCC 237
QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 240
DB 238 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 297
QY 241 CGCCAAAAAAGGTGTGAGGAAAGATGGAGATGACAAAGTCTCTAGACTACCTG 300
DB 298 CGCCAAAAAAGGTGTGAGGAAAGATGGAGATGACAAAGTCTCTAGACTACCTG 357
QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 345
DB 358 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 402
XX
RESULT 4
AAZ55549/c
ID AAZ55549 standard; cDNA; 402 BP.
XX
XX AAZ55549;
AC AAZ55549;
XX
XX 14-MAR-2000 (first entry)
DT
XX Canine interleukin-5 (IL-5) cDNA coding region complement.
DE
XX
```

```
XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011942.
XX
XX 29-MAY-1998; 98US-0087306P.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
XX P-PSDB; AAY58219.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease.
XX
XX Claim 1h; Page 226; 264pp; English.
XX
XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and
XX nucleotides which encode these immunoregulatory proteins. The proteins,
XX their associated nucleic acids, specific antibodies and inhibitors may be
XX used as vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans). They
XX may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase the
XX response from a co-administered antigen. The nucleotide sequences can
XX also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for modulators
XX of activity, while the antibodies may be used in detection, and in drug
XX targeting.
XX
XX Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 345; DB 3; Length 402;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-93;
XX Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
DB 345 TTGCTGTAGAAATCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
QY 61 CATCGAACTTGGCTGTAGCGATGGGAACCTGATGATTCCTCTGAAAATAAAAT 120
DB 285 CATCGAACTTGGCTGTAGCGATGGGAACCTGATGATTCCTCTGAAAATAAAAT 226
QY 121 CACCAACTGTGCATTAAAGAGTTTTCAGGATATAGACACATTGAGACCAACTGCC 180
DB 225 CACCAACTGTGCATTAAAGAGTTTTCAGGATATAGACACATTGAGACCAACTGCC 166
QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 240
DB 165 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 106
QY 241 CGCCAAAAAAGGTGTGAGGAAAGATGGAGATGACAAAGTCTCTAGACTACCTG 300
DB 105 CGCCAAAAAAGGTGTGAGGAAAGATGGAGATGACAAAGTCTCTAGACTACCTG 46
QY 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 345
DB 45 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGACACCGGAAAGT 1
```

RESULT 5  
 ID AA255546 standard; cDNA; 610 BP.  
 XX  
 AC AA255546;  
 XX  
 DT 14-MAR-2000 (first entry)  
 XX  
 DE Canine interleukin-5 (IL-5) cDNA.  
 XX  
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 29..433  
 FT /\*tag= a  
 FT /product= "Canine IL-5"  
 XX  
 PN WO9961618-A2.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-US011942.  
 XX  
 PR 29-MAY-1998; 98US-0087306P.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX  
 DR WPI; 2000-072623/06.  
 DR P-PSDB; AAY58219.  
 XX  
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 PS Claim 1h; Page 223-224; 264pp; English.  
 XX  
 CC Sequences AA255546-Z55551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting  
 XX  
 SQ Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 345; DB 3; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-93;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTCCTGTAGAAATCCATGATAGCTGGTGGGAGACCTTGACATGCTCTCCACT 60  
 DB 86 TTTCCTGTAGAAATCCATGATAGCTGGTGGGAGACCTTGACATGCTCTCCACT 145  
 QY 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTTACTCTCTGAAATAAATAA 120

Db 146 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTTACTCTCTGAAATAAATAA 205  
 QY 121 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 180  
 Db 206 CACCAACTGTGCATTAAAGAAAGTTTTCAGGGTATAGACATTTGAAGAACCAACTGCC 265  
 QY 181 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACCATAGAG 240  
 Db 266 CACGGGAGGCTGTGGATAAACTATTCCAAAACCTTGTCTTTAATAAAGAACCATAGAG 325  
 QY 241 GCCCAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACTG 300  
 Db 326 GCCCAAAAAAAGGTGTCAGGAGAAAGATGGAGAGTGACAAAGTTCTTAGACTACTG 385  
 QY 301 CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 345  
 Db 386 CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 430

RESULT 6  
 AA255547/c  
 ID AA255547 standard; cDNA; 610 BP.  
 XX  
 AC AA255547;  
 XX  
 DT 14-MAR-2000 (first entry)  
 XX  
 DE Canine interleukin-5 (IL-5) cDNA complement.  
 XX  
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS complement(178..582)  
 FT /\*tag= a  
 FT /product= "Canine IL-5"  
 XX  
 PN WO9961618-A2.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 28-MAY-1999; 99WO-US011942.  
 XX  
 PR 29-MAY-1998; 98US-0087306P.  
 XX  
 PA (HESK-) HESKA CORP.  
 XX  
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX  
 DR WPI; 2000-072623/06.  
 DR P-PSDB; AAY58219.  
 XX  
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 PS Claim 1h; Page 224-225; 264pp; English.  
 XX  
 CC Sequences AA255546-Z55551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting



CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 345; DB 3; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-93;  
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
 DB 525 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 466  
 QY 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTTACTCTCTGAAATATAAAT 120  
 DB 465 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTTACTCTCTGAAATATAAAT 406  
 QY 121 CACCACTGTCATTAAAGAGTTTTTCAGGGTATAGACACATTTGAGAACCAACTGCC 180  
 DB 405 CACCACTGTCATTAAAGAGTTTTTCAGGGTATAGACACATTTGAGAACCAACTGCC 346  
 QY 181 CACGGGAGGCTGTGGATAAATCTATCCAAAATCTTCTTTATAAAGAACACATAGAG 240  
 DB 345 CACGGGAGGCTGTGGATAAATCTATCCAAAATCTTCTTTATAAAGAACACATAGAG 286  
 QY 241 CGCCAAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300  
 DB 285 CGCCAAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 226  
 QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 345  
 DB 225 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 181

RESULT 7  
 AAF74300  
 ID AAF74300 standard; DNA; 405 BP.  
 AC AAF74300;  
 XX  
 XX  
 DT 04-MAY-2001 (first entry)  
 DE  
 DE Canine interleukin-5 coding sequence #1.  
 XX  
 XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
 KW inflammatory reaction; ds.  
 XX  
 XX Canis sp.  
 OS  
 XX WO200111049-A2.  
 PN  
 XX  
 PD 15-FEB-2001.  
 XX  
 XX 09-AUG-2000; 2000WO-US021651.  
 PF  
 XX  
 XX 10-AUG-1999; 99US-00371615.  
 PR  
 XX  
 XX (IDEX-) IDEX LAB INC.  
 PA  
 XX  
 XX Guo H, Lawton R, Mermer B, Aiyappa AP;  
 PI  
 XX  
 XX WPI; 2001-191542/19.  
 DR  
 DR P-PSDB; AAB72615.  
 XX  
 XX Novel canine interleukin 5 polynucleotide and polypeptides are used for  
 PT generating antibodies which are useful in treating allergies in dogs.  
 XX  
 XX Claim 31; Page 46; 48pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences of the  
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies.

CC cancer and inflammatory reactions in dogs. The present sequence is one  
 CC version of the IL-5 coding sequence shown in the specification  
 XX  
 SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Query Match 99.1%; Score 341.8; DB 4; Length 405;  
 Best Local Similarity 99.4%; Pred. No. 3.8e-92;  
 Matches 343; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
 DB 58 TTTGCTGTAGAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 117  
 QY 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTTACTCTCTGAAATATAAAT 120  
 DB 118 CATCGAACTTGGCTGATAGCGGATGGAACTGATCTTACTCTCTGAAATATAAAT 177  
 QY 121 CACCACTGTGCATTAAAGAGTTTTTCAGGGTATAGACACATTTGAGAACCAACTGCC 180  
 DB 178 CACCACTGTGCATTAAAGAGTTTTTCAGGGTATAGACACATTTGAGAACCAACTGCC 237  
 QY 181 CACGGGAGGCTGTGGATAAATCTATCCAAAATCTTCTTTATAAAGAACACATAGAG 240  
 DB 238 CACGGGAGGCTGTGGATAAATCTATCCAAAATCTTCTTTATAAAGAACACATAGAG 297  
 QY 241 CGCCAAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 300  
 DB 298 CGCCAAAAAAGGTGTGAGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTG 357  
 QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 345  
 DB 358 CAAGTATTTCTTGGTGTAAATAACACCGAGTGACACCGGAAAGT 402

RESULT 8  
 AAZ44265  
 ID AAZ44265 standard; DNA; 838 BP.  
 AC AAZ44265;  
 XX  
 XX 31-MAR-2000 (first entry)  
 DT  
 DT Porcine IL-5 DNA.  
 XX  
 DE  
 DE Pig; vaccine; cysticercosis; protective antigen; cC1; cC3; cC4; ss.  
 KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5;  
 XX  
 XX Sus scrofa.  
 OS  
 XX CN1231339-A.  
 FN  
 XX 13-OCT-1999.  
 PD  
 XX 29-JAN-1999; 99CN-00113447.  
 PF  
 XX 29-JAN-1999; 99CN-00113447.  
 PR  
 XX (UYTW-) UNIV NO 2 MILITARY MEDICAL PLA.  
 PA  
 XX Sun S, Dai J;  
 PI  
 XX WPI; 2000-087904/08.  
 DR  
 XX Nucleic acid vaccine for cysticercosis co-contracted by human and pig.  
 PT  
 XX  
 XX Claim 3; Page 9; 21pp; Chinese.

This invention describes a novel nucleic acid vaccine for preventing and  
 curing human and porcine cysticercosis. The invention involves the formation  
 of a eukaryotic expression plasmid from fusion transcript expression unit  
 consisting of three protective antigen genes (cC1, cC3 and cC4) of pig  
 tenial cysticercus and coexpression unit of related cell factor gamma  
 interferon (IFN-gamma) and pork interleukin 5 (IL-5)] genes. The

CC	production and purification process of said nucleic acid vaccine is
CC	simple and convenient, the physical and chemical properties of the
CC	vaccine are stable, and the vaccine is easy to store and transport, and
CC	possesses effective immunological protective function for human and pig
CC	cysticercosis. This sequence represents the pig IL-5 gene used in the
CC	method of the invention
XX	
SQ	Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;
	Query Match                83.9%; Score 289.6; DB 3; Length 838;
	Best Local Similarity 90.1%; Pred. No. 2.le-76;
	Matches 310; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY	2 TTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTTCCTCACT 61 
Db	103 TTGCTGTACAAGGTPCCCATGAATAGGCTGGTGGCAGAGACCTTGGCACTGCTTCCA 162 
QY	62 ATCGAAGTTGGCTGATAGGCATGGGAACCTGATGATTCTCTACTCCCTGAAATAAAAAATC 121 
Db	163 ATCGAAGTTACTGATAGGCGACGGGAACCTGATGATTCTCTCTGAAACAATCAACT 222 
QY	122 ACCAACTGTGCATTAAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAACTGCC 181 
Db	223 ACCAACTGTGCATTGAAGAAGTCTTTTCAGGGTATAGACACATTAAAGAAATCGCACTGTGC 282 
QY	182 ACGGGGAGGCTGTGGATAAACTATTCCAAACCTTGCTTTTAATAAAGAACAATAGAGC 241 
Db	283 CGGGGGAGTGTGTGGAAAAGCTTTTCGAAACCTGTCTTTTAATAAAGAACAATAGAGC 342 
QY	242 GCCAAAAAAAAGGTGTGCGAGGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACTCTGC 301 
Db	343 GCCAAAAAAAAGGTGTGGAGGAGGAAGATGGAGAGTAAAAAAGTTCCTAGACTACTCTGC 402 
QY	302 AAGTATTTCTTGGTGTAAATAAAACCGAGGTGGACACCGGAAAGT 345 
Db	403 AAGTGTTCCTTGGTGTAAATAAAACACTGAGTGGCAATGGAAAGT 446 

RESULT 9	
AAF74306	
ID	AAF74306 standard; DNA; 393 BP.
XX	
XX	AAF74306;
XX	
XX	04-MAY-2001 (first entry)
DT	
XX	
XX	Canine interleukin-5 coding sequence #3.
DE	
XX	Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
KW	inflammatory reaction; ds.
KW	
XX	
OS	Canis sp.
XX	
XX	WO200111049-A2.
PN	
XX	
XX	15-FEB-2001.
XX	
XX	09-AUG-2000; 2000WO-US021651.
PF	
XX	
PR	10-AUG-1999; 99US-00371615.
XX	
XX	(IDEX-) IDEXX LAB INC.
PA	
XX	
XX	Guo H, Lawton R, Mermer B, Aiyappa AP;
PI	
PI	WPI; 2001-191542/19.
XX	
DR	
XX	
XX	Novel canine interleukin 5 polynucleotide and polypeptides are used for
PT	generating antibodies which are useful in treating allergies in dogs.
PT	
XX	
XX	Claim 1; Page 35; 48pp; English.
PS	
XX	
XX	
CC	The present invention provides the protein and coding sequences of the

CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies  
CC cancer and inflammatory reactions in dogs. The present sequence is one  
CC version of the IL-5 coding sequence shown in the specification  
XX  
SQ Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;

Query Match 83.3%; Score 287.4; DB 4; Length 393;  
Best Local Similarity 99.7%; Pred. No. 7.2e-76;  
Matches 288; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 46 ACATGCTCTCCACTCATCGAACCTGGCTGATAGGCGATGGGAACCTGATGATTCCTACT 105  
Db 1 ACACTGCTCTCCACTCATCGAACCTGGCTGATAGGCGATGGGAACCTGATGATTCCTACT 60  
QY 106 CCTGAAATAAAAAATCACCAACTGTCATTAAAGAAAGTTTTTCAGGGTATAGACACATTG 165  
Db 61 CCTGAAATAAAAAATCACCAACTGTCATTAAAGAAAGTTTTTCAGGGTATAGACACATTG 120  
QY 166 AGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCAAAACCTGCTTTTAATA 225  
Db 121 AGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCAAAACCTGCTTTTAATA 180  
QY 226 AAGAACAACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAG 285  
Db 181 AAGAACAACATAGAGCGCCAAAAAAGGTGTGCAGGAGAAAGATGGAGAGTGACAAAG 240  
QY 286 TTCCTAGACTACCTCGAAGTATTTCTTGCTGTAATAAACACCGAGTGGGA 334  
Db 241 TTCCTAGACTACCTCGAAGTATTTCTTGCTGTAATAAACACCGAGTGGGA 289

RESULT 10  
AAT50756  
ID AAT50756 standard; cDNA; 399 BP.  
XX AC AAT50756;  
XX  
DT 17-OCT-2003 (revised)  
DT 24-SEP-1997 (first entry)  
XX  
DE Ovine IL-5 cDNA.  
XX  
KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;  
KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;  
KW immunosuppression; allergy; reproductive system; growth; early maturity;  
KW antibody; diagnosis; immunopotentiator;  
KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;  
KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.  
XX  
OS Ovis aries.  
XX  
PN WC9700321-Al.  
XX  
PD 03-JAN-1997.  
XX  
XX 14-JUN-1996; 96WO-AU000360.  
XX  
XX 14-JUN-1995; 95AU-00003502.  
PR 27-OCT-1995; 95AU-00006244.  
XX  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX  
XX Seow H, Wood P;  
XX  
XX WPI; 1997-077528/07.  
DR P-PSDB; AAW08479.  
XX  
XX Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine  
PT adjuvants and to treat or prevent microbial infections in livestock.  
XX  
XX Claim 6; Page 41-42; 78pp; English.  
XX  
CC The sequences given in AAT50755-56 encode ovine interleukin-5 (IL-5).

Ovine IL-5 or IL-12 are used to treat and/or prevent infections in livestock (esp. cows and sheep), particularly where the animals are stressed, e.g. during transport. IL-5 and IL-12 can also be used as adjuvants in vaccines for veterinary use (partic. weakly immunogenic subunit or synthetic peptide vaccines). They may also be used to treat cancer, immunosuppression and allergy. They may also be used to treat reproductive system and to promote growth or early maturity. Optionally interleukin can be delivered from constructs or delivery cells and antibodies are useful in enzyme immunoassays for rapid diagnosis of infection. The interleukins are immunopotentiators, especially IL-5 promotes growth of early haematopoietic progenitor cells and generation of cytotoxic cells from thymocytes, also it stimulates production and secretion of IgM and IgA (in synergism with bacterial endotoxin). IL-12 induces production of gamma-interferon by, and proliferation of, T and NK cells and increases the (non-)specific cytolytic lymphocyte response. The genetic constructs can also be used for in vitro production of IL-5 or -12. (Updated on 17-OCT-2003 to standardise OS field)

Sequence 399 BP; 130 A; 77 C; 93 G; 99 T; 0 U; 0 Other;

Query Match 79.7%; Score 274.8; DB 2; Length 399;

Best Local Similarity 87.7%; Pred. No. 4.3e-72; Mismatches 0; Gaps 0;

Matches 300; Conservative 0; Indels 42; Indels 0; Gaps 0;

3 TGCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCA 62

54 TGCTGTAGAAAGTACCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACGCA 113

63 TCGAAGTGGCTGATAGCGGATGGAACTGATGATTCCTTACCTCTGAAATTAATAATCA 122

114 TCAAACTCTGCTGATAGGTGAGGAACCTTGATGATTCCTTACCTCTGAGCATACAATCA 173

123 CCAACTGTGATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCCA 182

174 CCAACTATGATTAAGAAAGTTTTCAGGGTATAGACACATTTGAAGAACCAAACTGCCCA 233

183 CGGGAGGCTGTGATGATTAATTCCTTACCTCTGAAATTAATAATCA 242

234 AGGGATGCTGTGAAAAAATATTCGAAACTTGTCTTTAATAAAGATATACATAGACCT 293

243 CCAAAAAAAGGTGTCAGGAGAAAGATGGAGGTGACAAAGTTCTTACACTACCTGCA 302

294 CCAAAAAAAGGTGTCAGGAGAAAGATGGAGGTGACAAAGTTCTTACACTACCTGCA 353

303 AGTATTTCCTGGTGTAAATCAACCGAGTGGACACCGGAAAG 344

354 AGTTTCTTGGTGTGATAAACACAGAGTGGACGATGGAAG 395

RESULT 11

AAT50755

.ID AAT50755 standard; DNA; 520 BP.

XX AC AAT50755;

XX DT 17-OCT-2003 (revised)

XX DT 24-SEP-1997 (first entry)

XX DE Ovine IL-5 gene.

XX KW Cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;

XX KW livestock; cow; stress; transport; vaccine adjuvant; veterinary; cancer;

XX KW immunosuppression; allergy; reproductive system; growth; early maturity;

XX KW antibody; diagnosis; immunopotentiator;

XX KW early haematopoietic progenitor cell; cytotoxic cell; thymocyte;

XX KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss.

XX OS Ovis aries.

XX FH Key

XX CDS

FT Location/Qualifiers

FT 46..444

FT /\*tag= a

FT /product= "Ovine\_IL-5"

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/\*tag= c

/number= 2

217..345

/\*tag= d

/number= 3

346..480

/\*tag= e

/number= 4

WO9700321-A1.

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/number= 4

WO9700321-A1.

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 Db 399 AGTTTCTTGTGTATAAACAACAGAGTGACGATGGAAG 440

## RESULT 12

ID AAA34857 standard; DNA; 816 BP.  
 XX AC AAA34857;

28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide SEQ ID NO:2546...

Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 phosphorothioate; impaired respiration; inflammation; allergy;  
 allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US017712.

03-AUG-1998; 98US-0095212P.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary  
 vasoconstriction, inflammation, allergies, asthma, hypertension,  
 bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 cancers.

Disclosure; Page 716; 1343pp; English.

The present invention describes a new composition comprising an antisense  
 oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 nucleic acids involved in bronchoconstriction, allergies, and/or  
 inflammation. The ON can have antiinflammatory, antiallergic,  
 antiasthmatic, cytostatic and analgesic activities. The compositions are  
 useful for the treatment of diseases associated with inflammation,  
 impaired airways, including lung disease and diseases whose secondary  
 effects afflict the lungs of a subject. They can be used for treating  
 e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 carcinomas, and cancers which may metastasize to the lungs, including  
 breast and prostate cancer. The reduction of the adenosine content of the  
 ONs reduces side effects. The A-containing ONs break down with the  
 release of deoxyadenosine which activates adenosine receptors causing  
 bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 nucleotide sequences given in the sequence listing from the present  
 invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 sequences are also called SEQ ID NO:1 to 185, but the sequences differ

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing

XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 67.1%; Score 231.4; DB 3; Length 816;

Best Local Similarity 80.4%; Pred. No. 5.4e-59; Indels 0; Gaps 0;

Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 9 AGAAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGTCTCTCATCTCGAAC 68

Db 110 AGAAATTCACCAAGTCATTGGTGAAGAGACCTTGGCACTGCTTCTACTCATCGAAC 169

Qy 69 TTGGCTGATAGCGGATGGAACTGATGATTCCTACTCTCTGAAATATAAATACCAACT 128

Db 170 TCTGTGATAGCCAAATGAGACTCTGAGGATTCCTGTTCTGTACATAAAATACCAACT 229

Qy 129 GTGCATTAAGAAGTTTTTTCAGGGTATAGACACATTCGAAGAACCAACTGCCACGGGA 188

Db 230 GTGCACTGAGAAATCTTTTCAGGGAATAGGCACACTGGAGAGTCAACTGTGCAAGGGG 289

Qy 189 GGCTGTGATAAACTATTTCAAAACTTGTCTTTTAAATAAGAACACATAGAGCCGCAAAA 248

Db 290 TACTGTGGAAGACTATTTCAAAACTTGTCTTTTAAATAAGAACATACATTGACGGCCAAA 349

Qy 249 AAAAAGGTGTCCAGGAGAAAGATCGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT 308

Db 350 AAAAAGTGTGGAAGAAAGACGAGAGTAACCAATTCCTAGACTACCTGCAAGAGTT 409

Qy 309 TCTTGGTGTATAAACACCGAGTGGACACCGGAAAGT 345

Db 410 TCTTGGTGTATAAACACCGAGTGGATAATAGAAAGT 446

## RESULT 13

ID AAA13338 standard; cDNA; 816 BP.

XX AC AAA13338;

25-JUL-2000 (first entry)

Human interleukin-5 (IL-5) nucleotide sequence.

Human; interleukin-5; IL-5; inflammatory disease; asthma; eczema;  
 antisense oligonucleotide; allergic rhinitis; inflammatory skin disease;  
 allergic conjunctivitis; inhibitor; ss.

Homo sapiens.

US6048726-A.

11-APR-2000.

15-MAY-1998; 98US-00079839.

15-MAY-1998; 98US-00079839.

(WELT/) WELTMAN J K.

(KARI/) KARIM A S.

Welman JK, Karim AS;

WPI; 2000-302784/26.

Oligonucleotide comprising non-natural internucleoside linkage, useful  
 for inhibiting interleukin-5 expression and treating inflammatory  
 diseases, asthma, allergic rhinitis, allergic conjunctivitis.  
 Disclosure; Col 3-4; 11pp; English.



## RESULT 15

ABZ96673  
ID ABZ96673 standard; DNA; 816 BP.

XX AC ABZ96673;

XX DT 17-OCT-2003 (first entry)

XX DE Human nucleic acid sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PX (EPIC-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.

XX PS Disclosure; SEQ ID NO 11915; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a  
XX first active agent comprising an oligonucleotide antisense to the  
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX junctions of genes encoding a polypeptide associated with lung and/or  
XX nasal airway dysfunction and a second active agent comprising an  
XX antiinflammatory steroid and ubiquinone. A composition of the invention  
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX immunosuppressive, and cytostatic activity. The composition may have a  
XX use in antisense gene therapy. The composition is useful for treating or  
XX preventing a respiratory, lung or malignant disease or condition, also  
XX for enhancing the prophylactic or therapeutic respiratory effect of an  
XX antiinflammatory steroid in a subject, for reducing or depleting levels  
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX lung inflammation, lung allergies, or a respiratory disease or condition.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 816 BP; 277 A; 137 C; 164 G; 238 T; 0 U; 0 Other;

Query Match 67.1%; Score 231.4; DB 7; Length 816;

Best Local Similarity 80.4%; Pred. No. 5.4e-59;

Matches 271; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 9 AGAAATCCCATGAATAGACTGTGGCAGACCTTGACACTGCTTCCACTCATCGAAC 69

Db 110 AGAAATCCCATGAATAGACTGTGGCAGACCTTGACACTGCTTCCACTCATCGAAC 169

QY 69 TTGGCTGATAGCGGATGGAAACCTGATGATTCTTACTCTCTGAAATAAAAAATCACCACCT 128  
Db 170 TCTGCTGATAGCCAAATGAGACTCTGAGGATTCTTCTGTACATAAAAAATCACCACCT 229  
QY 129 GTGCATTAAAGAGTCTTTTCAGGGTATAGACACATTGAGAACCAAACTGCCACGGGA 188  
Db 230 GTGCACCTGAAGAAATCTTTTCAGGGATAGGCACACTGGAGAGTCAAACTGTGCAAGGGG 289  
QY 189 GGCTGTGGATAAACTATTTCCTTTCTTTTAAATAAAGAACACATAGAGCCGCAAAA 248  
Db 290 TACTGTGGAAGACTATTTCCTTTCTTTTAAATAAAGAAATACATTGACGCGCAAAA 349  
QY 249 AAAAAAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTTCCTAGACTACCTGCAAGTATT 308  
Db 350 AAAAAAGTGTGAGGAGAAAGACGAGAGTAAACCAATTCCTAGACTACCTGCAAGTATT 409  
QY 309 TCTTGTGTGTAATAACACCGAGTGGACACCGGAAAGT 345  
Db 410 TCTTGTGTGTAATGACACCGAGTGGATAATAGAAAGT 446

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Job time : 164.547 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:21:12 ; Search time 1491.34 Seconds  
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Title: US-10-787-382-9

Perfect score: 345

Sequence: 1 ttctgctgtagaaatcccat.....ccgagtgacacccgaaagt 345

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: gb\_pr:  
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12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
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41: em\_hgt\_other:

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	345	100.0	345	6	AR241541
3	345	100.0	345	6	AR254496
4	345	100.0	345	6	AR254497
5	345	100.0	345	6	BD211562
6	345	100.0	345	6	BD211563
7	345	100.0	402	6	AR241538
8	345	100.0	402	6	AR241539
9	345	100.0	402	6	AR254494
10	345	100.0	402	6	AR254495
11	345	100.0	402	6	BD211560
12	345	100.0	402	6	BD211561
13	345	100.0	610	4	AF331919
14	345	100.0	610	6	AR241536
15	345	100.0	610	6	AR241537
16	345	100.0	610	6	AR254492
17	345	100.0	610	6	AR254493
18	345	100.0	610	6	BD211558
19	345	100.0	610	6	BD211559
20	341.8	99.1	405	6	AR300436
21	341.8	99.1	405	6	AX083939
22	322.8	93.6	356	4	AF091133
23	290.2	84.1	405	4	ECU91947
24	289.6	83.9	838	4	AF025436
25	285.4	82.7	405	4	AF068770
26	283.8	82.3	405	4	BTINTLEUS
27	280	81.2	529	4	SSC133452
28	278.4	80.7	405	4	S8C010088
29	274.8	79.7	520	4	OU35038
30	259.4	75.2	354	4	AF051372
31	250	72.5	343	6	AX083948
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34	231.4	67.1	816	6	E01639
35	231.4	67.1	816	6	E13591
36	231.4	67.1	816	9	HSIL5R
37	231.4	67.1	858	6	AX766521
38	231.4	67.1	858	6	AX766523
39	231.4	67.1	864	6	AX766525
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41	229.8	66.6	816	6	AR380691
42	229.8	66.6	816	9	HSBCDFIA
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# ALIGNMENTS

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LOCUS

DEFINITION

AR241540

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

AR241540  
Sequence 85 from patent US 6471957.

AR241540

AR241540.1

GI:27287249

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 345)

Sim.G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.

Canine IL-4 immunoregulatory proteins and uses thereof

Patent: US 6471957-A 85 29-OCt-2002;

Location/Qualifiers

linear

DNA

345 bp

FAT 20-DEC-2002

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QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACACCGGAAAGT 345
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DEFINITION Sequence 87 from patent US 6471957.
ACCESSION AR241541
VERSION AR241541.1 GI:27287250
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 345)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 87 29-Oct-2002;
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Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 285 CATCGAAGCTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAATATAAAT 226

QY 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
DB 225 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 166

QY 181 CACGGGAGGCTGGGATTAACCTATTCGAAACTTGTCTTTAATAAAGAACACATAGAG 240
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DEFINITION Sequence 85 from patent US 6482403.
ACCESSION AR254496
VERSION AR254496.1 GI:27303384
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 345)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 85 19-Nov-2002;
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
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QY 61 CATCGAAGCTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAATATAAAT 120
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QY 121 CACCAACTGTGCATTAAGAAGTTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180
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QY 301 CAAGTATTTCTTGGTGTAAATAACACCGAGTGGACACCGGAAAGT 345
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RESULT 4
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LOCUS AR254497 345 bp DNA linear PAT 20-DEC-2002
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ACCESSION AR254497
VERSION AR254497.1 GI:27303385
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 345)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 87 19-Nov-2002;

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FEATURES  
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RESULT 6  
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LOCUS  
DEFINITION  
Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same.  
ACCESSION  
BD211563  
VERSION  
BD211563.1 GI:33021332  
KEYWORDS  
JP 2002516104-A/69.  
SOURCE  
Canis familiaris (dog)  
ORGANISM  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE  
1 (bases 1 to 345)  
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
Patent: JP 2002516104-A 69 04-JUN-2002;  
JOURNAL  
HESKA CORP  
COMMENT  
OS Canis familiaris (dog)  
PN JP 2002516104-A/69  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000551002  
PR 29-MAY-1998 US 60/087306  
PI GEKKEE SIM,SHUNIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC  
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,  
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and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FH Key Location/Qualifiers  
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Location/Qualifiers  
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Db 285 CATCGAACTTGGCTGATAGGCGATGGGAACCTGATGATTCCTACTCTCTGAAAAATAAAT 226  
Qy 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATTCATTAAGAAGCAACCACTGCC 180  
Db 225 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACATTCATTAAGAAGCAACCACTGCC 166  
Qy 181 CACGGGAGGCTGTGGATAAATACTATCCAAACTTGTCTTTAATAAAGAACAATAGAG 240  
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RESULT 5  
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LOCUS  
DEFINITION  
Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same.  
ACCESSION  
BD211562  
VERSION  
BD211562.1 GI:33021332  
KEYWORDS  
JP 2002516104-A/68.  
SOURCE  
Canis familiaris (dog)  
ORGANISM  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE  
1 (bases 1 to 345)  
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
Canine and feline immunoregulatory proteins, nucleic acid molecules  
and method of using the same  
Patent: JP 2002516104-A 68 04-JUN-2002;  
JOURNAL  
HESKA CORP  
COMMENT  
OS Canis familiaris (dog)  
PN JP 2002516104-A/68  
PD 04-JUN-2002  
PF 28-MAY-1999 JP 2000551002  
PR 29-MAY-1998 US 60/087306  
PI GEKKEE SIM,SHUNIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC  
C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,  
PC A61K39/395,  
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,  
PC C07K14/54,  
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC  
G01N33/15,  
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine  
and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FH Key Location/Qualifiers  
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/organism="Canis familiaris"  
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Query Match 100.0%; Score 345; DB 6; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.3e-83;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60  
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## RESULT 7

AR241538  
LOCUS AR241538 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6471957.  
ACCESSION AR241538  
VERSION AR241538.1 GI:27287247  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 83 29-OCT-2002;  
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Query Match 100.0%; Score 345; DB 6; Length 402;  
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Qy 121 CACCAACTGTGCATTAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAAACTGCC 180  
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Qy 241 CGCCAAAAAAGGTTGTGCAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 300  
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Qy 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACCCGGAAGT 345  
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## RESULT 8

AR241539/c  
LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 84 from patent US 6471957.  
ACCESSION AR241539  
VERSION AR241539.1 GI:27287248  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 84 29-OCT-2002;  
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Qy 181 CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 240  
Db CACGGGAGGCTGGGATAAATCTTCCAAAACCTGTCTTTAATAAAGAACACATAGAG 106

Qy 241 CGCCAAAAAAGGTTGTGCAGGAGAAAGATGGAGAGTGCACAAAGTTCTTAGACTACCTG 300  
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Qy 301 CAAGTATTTCTTGGTGTAAATAAACACCGAGTGCACCCGGAAGT 345  
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## RESULT 9

AR254494  
LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6482403.  
ACCESSION AR254494  
VERSION AR254494.1 GI:27303382  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;

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**LOCUS**  
 AR254495 402 bp DNA linear PAT 20-DEC-2002  
**DEFINITION**  
 Sequence 84 from patent US 6482403.  
**ACCESSION**  
 AR254495  
**VERSION**  
 AR254495.1 GI:27303383  
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**SOURCE**  
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**ORGANISM**  
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**REFERENCE**  
 1 (bases 1 to 402)  
 AUTHORS  
 Sim G.-K., Yang S., Dreitz, M. J. and Wonderling, R. S.  
 TITLE  
 Caniney IL-13 immunoregulatory proteins and uses thereof  
 JOURNAL  
 Patent: US 6482403-A 84 19-NOV-2002;  
 LOCATION/Qualifiers  
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 Qy 61 CATCGAACTTGGCTGTATAGGCGATGGGAACTCTACTCTCTGAAAATAAAAAAT 120  
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Db      238  CACGGGAGGCTGTGGATAAATATTCCAAAATTGCTTTTAATAAAGAACACATAGAG 297
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Db      358  CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 402

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LOCUS      402 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211561
VERSION BD211561.1 GI:33021331
KEYWORDS JP 2002516104-A/67.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 402)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
JOURNAL Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP
COMMENT OS Canis familiaris (dog)
PN JP 2002516104-A/67
PD 04-JUN-2002
PF 28-MAY-1998 JP 2000551002
PI 29-MAY-1998 US 60/087306
PR GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAWANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
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molecules and method of using the same
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Best Local Similarity 100.0%; Pred No. 3.2e-83;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 60
Db 345 TTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACT 286
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Qy 121 CACCAACTGTGCATTAAAGAGTTTTTCAGGGGTATAGACACATTGAAGAACCAAACTGCC 180
Db 225 CACCAACTGTGCATTAAAGAGTTTTTCAGGGGTATAGACACATTGAAGAACCAAACTGCC 166
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Db      165  CACGGGAGGCTGTGGATAAATATTCCAAAATTGCTTTTAATAAAGAACACATAGAG 106
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Db      45  CAAGTATTCTTGGTGTAAATAAACACCGAGTGGACACCGGAAAGT 1

RESULT 13
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LOCUS      610 bp mRNA linear MAM 04-OCT-2001
DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION AF331919
VERSION AF331919.1 GI:15919180
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Yang,S., Sellins,K.S., Weber,E. and McCall,C.
TITLE Canine interleukin-5: molecular characterization of the gene and
expression of biologically active recombinant protein
JOURNAL J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
MEDLINE 21334408
PUBMED 11440633
REFERENCE 2 (bases 1 to 610)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
Prospect Parkway, Ft Collins, CO 80525, USA
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Best Local Similarity 100.0%; Pred. No. 3.1e-83;
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RESULT 14  
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DEFINITION Sequence 80 from patent US 6471957.  
ACCESSION AR241536  
VERSION AR241536.1 GI:27287245  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G.-K., Yang,S., Dretz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 80 29-OCT-2002;  
FEATURES Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 345; DB 6; Length 610;  
Best Local Similarity 100.0%; Pred. No. 3.1e-83;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR241537 610 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 82 from patent US 6471957.  
ACCESSION AR241537  
VERSION AR241537.1 GI:27287246  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Sim,G.-K., Yang,S., Dretz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 82 29-OCT-2002;  
FEATURES Location/Qualifiers  
source 1..610  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 345; DB 6; Length 610;  
Best Local Similarity 100.0%; Pred. No. 3.1e-83;  
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CATCGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATAAAAAAT 120  
Db 146 CATCGAACTTGGCTGATAGCGGATGGAACTGATGATTCCTACTCCTGAAATAAAAAAT 205  
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Qy 181 CACGGGAGGCTGTGGATTAACCTATTCCAAACTTGTCTTTAATAAAGAACACATAGAG 240  
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Qy 241 CGCCAAATAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 300  
Db 326 CGCCAAATAAAGAGTGTGCAGGAGAAAGATGGAGAGTGACAAAAGTTCCCTAGACTACCTG 385  
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Search completed: August 31, 2004, 01:25:42  
Job time : 1492.34 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:25:57 ; Search time 981.052 Seconds  
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Title: US-10-787-382-18  
Perfect score: 1658  
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Scoring table: IDENTITY NUC  
Gap 10.0 , Gapext 1.0

Searched: 323270 seqs, 2460713050 residues 6474540  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*  
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19: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1631.8	98.4	1658	9	US-09-755-633-19
3	600.6	36.2	3230	9	US-09-800-629A-78
4	600.6	36.2	3230	17	US-10-679-533-78
5	406	24.5	671	9	US-09-755-633-21
6	171.8	10.4	610	9	US-09-755-633-4
7	171.8	10.4	610	9	US-09-755-633-6
8	171.8	10.4	610	15	US-10-218-654-80
9	171.8	10.4	610	15	US-10-218-654-82
10	171.8	10.4	610	15	US-10-218-654-82
11	171.8	10.4	610	15	US-10-262-439-80
12	150.6	9.1	5397	15	US-10-311-455-1017
13	145.8	8.8	402	9	US-09-755-633-7
14	145.8	8.8	402	9	US-09-755-633-8

15	145.8	8.8	402	15	US-10-218-654-83	Sequence 83, Appl
16	145.8	8.8	402	15	US-10-218-654-84	Sequence 84, Appl
17	145.8	8.8	402	15	US-10-262-439-83	Sequence 83, Appl
18	145.8	8.8	402	15	US-10-262-439-84	Sequence 84, Appl
19	134.6	8.1	5397	15	US-10-311-455-1018	Sequence 1018, Ap
20	131.6	7.9	345	9	US-09-755-633-9	Sequence 9, Appl
21	131.6	7.9	345	9	US-09-755-633-11	Sequence 11, Appl
22	131.6	7.9	345	15	US-10-218-654-85	Sequence 85, Appl
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28	108	6.5	6727	9	US-09-800-629A-1	Sequence 1, Appl
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30	96.2	5.8	858	15	US-10-295-074-8	Sequence 8, Appl
31	96.2	5.8	858	15	US-10-295-074-10	Sequence 10, Appl
32	89	5.4	864	15	US-10-295-074-12	Sequence 12, Appl
33	89	5.4	864	15	US-10-295-074-14	Sequence 14, Appl
34	61.8	3.7	7348	13	US-10-433-793-52	Sequence 52, Appl
35	61.2	3.7	4661	17	US-10-312-841-1	Sequence 1, Appl
36	60.8	3.7	3673778	15	US-10-311-455-954	Sequence 954, App
37	60.8	3.7	6876	15	US-10-311-455-954	Sequence 954, App
38	60.6	3.7	6280	17	US-10-340-589C-74	Sequence 74, Appl
39	60	3.6	10328	15	US-10-311-455-1517	Sequence 1517, Ap
40	58.4	3.5	6365	15	US-10-311-455-98	Sequence 98, Appl
41	57.4	3.5	9741	15	US-10-311-455-1296	Sequence 1296, Ap
42	56.6	3.4	4985	15	US-10-094-240-10	Sequence 10, Appl
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44	56.2	3.4	335913	10	US-09-754-853A-2	Sequence 3, Appl
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ALIGNMENTS

RESULT 1

US-09-755-633-18  
; Sequence 18, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09755.633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 1658  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (171)..(373)  
; NAME/KEY: Intron  
; LOCATION: (407)..(1275)  
; NAME/KEY: Intron  
; LOCATION: (1405)..(1522)  
US-09-755-633-18

Query Match 100.0%; Score 1658; DB 9; Length 1658;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Sequence 78, Application US/09800629A  
 ; Patent No. US20020128216A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Karraes, James G.  
 ; APPLICANT: McKay, Robert  
 ; APPLICANT: Mancharan, Muthiah  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
 ; TITLE OF INVENTION: TRANSDUCTION  
 ; FILE REFERENCE: ISPH-0537  
 ; CURRENT APPLICATION NUMBER: US/09/800,629A  
 ; CURRENT FILING DATE: 2001-03-07  
 ; PRIOR APPLICATION NUMBER: PCT/US00/07318  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: 09/280,799  
 ; PRIOR FILING DATE: 1999-03-26  
 ; NUMBER OF SEQ ID NOS: 210  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 78  
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 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-800-629A-78

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DB 2206 TAGAAAGTTGAGACTAACTGGTTGTTGTCAGCCAAAGATTTTGGAG 2252

## RESULT 4

US-10-679-532-78  
; Sequence 78, Application US/10679532  
; Publication No. US20040121376A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Karyas, James G.  
; APPLICANT: McKay, Robert  
; APPLICANT: Manoharan, Muthiah  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL  
; FILE REFERENCE: ISPH-0537  
; CURRENT APPLICATION NUMBER: US/10/679,532  
; PRIOR FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: US/09/800,629A  
; PRIOR FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: PCT/US00/07318  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 09/280,799  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 210  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 3230  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-679-532-78

Query Match 36.2%; Score 600.6; DB 17; Length 3230;  
Best Local Similarity 57.8%; Pred. No. 1.4e-116;  
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

QY 1 AGGCAAACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTAGCTC 60

Db 527 AGGCAACAGCAGAACGCTTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTGTAGTCT 586  
Qy 61 TTGGGCTCGCTATGTTCTGCTTTGCTGTAGAAAATCCCATGATAGACTGGTGGCAG 120  
Db 587 TTGGAGCTGCTACGTGTATGCCATCCACAGAAATCCACAGTGCATTTGGTGAAG 646  
Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGCGATGTTCT 180  
Db 647 AGACCTTGGCACTGCTTCTACTCATCGAATCTGCTGATAGCAATGAGGTAATTTCT 706  
Qy 181 TTTTGAATCTCAGCTCTTTAAATGCAATGGGTAATTTGGTGGTGGTCTAGTT----- 234  
Db 707 TTAATGATCTCAGTCTCTGTAAGTGCATAGGTAATCATTTGGTGGTCTTTACTAT 766  
Qy 235 -TTTAAAGATCCATTAATGAATGAATGAGTGTAAATATAATATAATATGAGTAACT 293  
Db 767 ATATAGAGATCTGTTATATAATAATAGATCTGAG-CACATTAGTACATGGGTGATACT 825  
Qy 294 ATGTTACTCAGAGAAATATATAAAGTATGAACCTTACATATACATTAATAAATGAATG 353  
Db 826 ACATCAGCAAGCAACATTTCTTTAAAGATGATGAATGCTGGTGTCTGTAAATAATGATG 885  
Qy 354 TTGCTTCTCTTTCTTTCAGAACCTGATGATCTCTACTCTGAAATATAAATAATGTAAGTT 413  
Db 886 -TATTTCTTCTCTCCAGACTCTGAGGATCTCTGCTGTACATATAAATAATGTAAGTT 944  
Qy 414 AAATAATGATTAATAAATGATATACGAATCAG-----TTTCATATTTTAAGCTATAAA 469  
Db 945 AAATAATGATTAATAAATGATGAGTAAATGAATGTAATTTCTCTTTTAAGCTGTAATA 1004  
Qy 470 GTATCAGTAAATCTGGGATGATTAATTTATCTATTTTGTATTTTGTGCGGATG 529  
Db 1005 TCATTTAGTATCATTTGAACATTTAAATTTCTATTTTGTGTTTCTCATATGGTGGCTGT 1064  
Qy 530 AAAT-TATGCTTTATGAATPATTTAGGAATGCTGTAGGAATGCTCTACAATATTAAGTA 588  
Db 1065 GAATGCTGTACTTATAAATATGAGGAATGACATT-----TTATCAAGTA 1109  
Qy 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGTTGTGATGTTCTCCATCTCAAG 648  
Db 1110 GAATCTCTTTAAAGAGTGGATAGGCTTTTGTGATGTTTGTGTTTGTGTTTCTCCCAAG 1169  
Qy 649 AGCTCTGTGTCAGGATCTTTTCCAAAGAAATCCATATTTGGTTCAGAGATCTTCTCTAG 708  
Db 1170 AGCATCTGTGTCAGG-ATTTCTTCCAGAGGATTTCCACACTGAGTGGTGGTGGTCTAG 1228  
Qy 709 GTTCCATTCCTCTGCTGCTGGTTCCTTCACTCACTCACTGTTTCTGAAAGTACTAGCA 768  
Db 1229 TCTCCGTGCTGCTGAC-----TCTTCTCACTTCACTCACTGTTTCTGAAAGTATTAGCA 1283  
Qy 769 ACTTGGGTTATATTTTGAATPATTTAGTGTGATGATGATGATGATGATGATGATGATGAT 828  
Db 1284 ACTCAGAAATATATTTTGAACCATGATCAGTAGACATTAATAATATATAACAAATGCC- 1342  
Qy 829 ATATTAATAGTCACTTCCACATATTTAAATGATTTTAACTTAATGGAATCATATACAT 888  
Db 1343 --CTATATTAATATCTGCATCTTAAATAATATGATGATGATGATGATGATGATGATGAT 1400  
Qy 889 CTGAGTATGTCATGCTATTAATTAATGTTTAAATGATGATGATGATGATGATGATGATGAT 948  
Db 1401 TGAATAG-CCCTGGTCAATTAATAATGTAATAATATATAGTTT-ATATGCTTAATAAGA 1456  
Qy 949 ATAAATATACCAGCTAGAACATATACAGGAAATCTGAGGTGAGGTAAATCAGTAAGGCA 1008  
Db 1457 ATAAATATACCAGCTAGAACATATACAGGAAATCTGAGGTGAGGTAAATCAGTAAGGCA 1513  
Qy 1009 GTTGTATATACCTGTAAGCAATTTATTTTCAATATCATTTTCAATATCATTTTATATCATTTGTA 1068  
Db 1514 -----ATTACATCTTCCAAACATTTTTCAGTTTACATAATTAAGTATATATCTTTATA 1568  
Qy 1069 ACATCTCTCAGTAATATATAAATCATCTTTAC-TTATGGTAATATAGTTTAGTATAAG 1127

Db 1569 AAATCTCTCAGTAATCATATATAAGCTTCACTACTTTTGGAAATTTTATCTTAATATGTG 1628  
Qy 1128 GTGTTTCCCATCTGGGAAAGACACAAGTAAACCTCTTTGGAGAGAGGAACCTTGTGTA 1187  
Db 1629 GTGTTTGTGCTCTAGAAA-----ACAAACAAAAACTCTTTGGAGAAAGGAACCTCATGTA 1684  
Qy 1188 AACCCCAAAACAAAGCTCTAACTTTT----- 1214  
Db 1685 AATACCAAAACAAAGCTTAACTTTTGGACCAAAATTTGTTTAAATAATTTTAA 1744  
Qy 1215 ----- 1214  
Db 1745 TTGATGAATTAATAAGTATATATTTTATTTGTGTACAAATATGATGTTTGAAGTATGTAT 1804  
Qy 1215 -----TGGACCAAAATTTTATGCTCTGTTTGTGATGAATTTATTTT 1256  
Db 1805 ACATTCAGAAATGACAAATGACCAAAATTTTATACCTTTGCTTGATTTTGA-TTTT 1863  
Qy 1257 TAAATCTTCTCTCAATTTAGCACCAACTGTGCAITTTAAAGAAAGTTTTTTCAGGTATAGACAC 1316  
Db 1864 AAAATTTTCTCTCATTTAGCACCAACTGTGCACTGAAAGAAATCTTTTCAGGGAATAGGCAC 1923  
Qy 1317 ATTGAAGAACCAACTGCTCCGAGGCTGTGTGATAAACTATTTCCAAAACCTTGTCTTT 1376  
Db 1924 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAAACCTTGTCTTT 1983  
Qy 1377 AATAAAAGACACATAGAGCGCCAAAGTAAAGTAAAGACATTTTGGCAAAACCTTAAGT 1436  
Db 1984 AATAAAGAAATACATTTGACGCGCAAAAGTAAAGTACACACATTTCAATGGAAGCTATATT 2043  
Qy 1437 ATATTGTCTGACTCTGCTCTTTTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTCTA 1496  
Db 2044 TGTCTGCTGCTG-----TGCCTATTCTATGGAATTTGACAGTTTCTCTG 2085  
Qy 1497 CAATATCT-----CCTCTGTTCTTTTAAACAGAAAAGTGTGAGGAGAAAGATGGAGAG 1550  
Db 2086 TAATACCTTATTTGCTCATTTTTTTTTCACAGAAAAGTGTGAGAGAAAGACGAGAG 2145  
Qy 1551 TGACAAAAGTCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCCAGTGGACAC 1610  
Db 2146 TAAACCAATCTCTAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACCCAGTGGATAA 2205  
Qy 1611 CGGAAAGTGTAGAACAAACCGCTTATTTGTAGTGGAGATTTTGGAG 1657  
Db 2206 TAGAAAAGTGTAGACTTAAACTGTTTGTGTCAGCCAAAGATTTTGGAG 2252

RESULT 5

US-09-755-633-21  
; Sequence 21, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-Cl-Cl  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 671  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; US-09-755-633-21

Query Match

24.5%; Score 406; DB 9; Length 671;

Best Local Similarity 100.0%; Pred. No. 9e-76;		
Matches	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AGGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGGCTAGCTC	60
Db	1 AGGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGGCTAGCTC	60
QY	61 TTGGGGCTGCGCTATGTTTCTTGCCTTTTGCCTGTAGAAAATCCCATGAATAGACTGGTGGCAG	120
Db	61 TTGGGGCTGCGCTATGTTTCTTGCCTTTTGCCTGTAGAAAATCCCATGAATAGACTGGTGGCAG	120
QY	121 AGACCTTGACACTGCTCTCCACTCATCGAACTTTGGCTGATAGCGCATGGGTAAATTTTCT	180
Db	121 AGACCTTGACACTGCTCTCCACTCATCGAACTTTGGCTGATAGCGCATGGGTAAATTTTCT	180
QY	181 TTTTGATTCCTACAGTCTTTTAAAAATGCATGGGTAAATTGGTGGTGGCTAGTTTAAAA	240
Db	181 TTTTGATTCCTACAGTCTTTTAAAAATGCATGGGTAAATTGGTGGTGGCTAGTTTAAAA	240
QY	241 GATCCATTATCAATAATGAAGTAATGAGTGTGTAATAATATATAATGGGTACCATTATC	300
Db	241 GATCCATTATCAATAATGAAGTAATGAGTGTGTAATAATATATAATGGGTACCATTATC	300
QY	301 TCAGAAGAATTTATTTAAAAAGTTTATGAACCTTTACAAATACATTAAAAATGGAATGTTGTTTC	360
Db	301 TCAGAAGAATTTATTTAAAAAGTTTATGAACCTTTACAAATACATTAAAAATGGAATGTTGTTTC	360
QY	361 CTTTCTTTTTCAGAACCTGATGATTTCCCTACTCTCCTGAAAATAAAAT	406
Db	361 CTTTCTTTTTCAGAACCTGATGATTTCCCTACTCTCCTGAAAATAAAAT	406

```

RESULT 6
US-09-755-633-4
; Sequence 4, Application US/09755633
; Patent No. US2002012700A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IW-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09755.633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(430)
US-09-755-633-4

Query Match      10.4%; Score 171.8; DB 9; Length 610;
Best Local Similarity 93.7%; Pred. No. 3e-26;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0

2y      1  AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGCTAGCTC 60
db      1  AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGCTAGCTC 60
2y      3  AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGCTAGCTC 62
db      3  AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTTGCTAGCTC 62
2y      61  TTGGGGTGCCTATGTTTCTTCCTTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120
db      61  TTGGGGTGCCTATGTTTCTTCCTTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120
2y      63  TTGGGGTGCCTATGTTTCTTCCTTGTAGAAAATCCCATGAATAGACTGGTGGCAG 122
db      63  TTGGGGTGCCTATGTTTCTTCCTTGTAGAAAATCCCATGAATAGACTGGTGGCAG 122
2y      121  AGCCTTGAACACTGCTCTCCATCATCGAACTTGGCTGATAGCCGATGGGTAATTTTCT 180
db      121  AGCCTTGAACACTGCTCTCCATCATCGAACTTGGCTGATAGCCGATGGGTAATTTTCT 180

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[illegible]

RESULT 8  
 US-10-218-654-80  
 ; Sequence 80, Application US/10218654  
 ; Publication No. US2003099609A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sim, Gek-kee  
 ; APPLICANT: Yang, Shumin  
 ; APPLICANT: Dreitz, Matthew J.  
 ; APPLICANT: Wonderling, Ramani S.  
 ; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 ; FILE REFERENCE: IM-2-C1  
 ; CURRENT APPLICATION NUMBER: US/10/218,654  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: US/09/322,409  
 ; PRIOR FILING DATE: 1999-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087,306  
 ; PRIOR FILING DATE: 1998-05-29  
 ; NUMBER OF SEQ ID NOS:154

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-218-654-80

Query Match 10.4%; Score 171.8; DB 15; Length 610;  
Best Local Similarity 93.7%; Pred. No. 3e-26;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 181 TTTTGATTCCT 191  
Db 428 TTCCTACTCCT 418

RESULT 10

US-10-262-439-80  
; Sequence 80, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-262-439-80

Query Match 10.4%; Score 171.8; DB 15; Length 610;  
Best Local Similarity 93.7%; Pred. No. 3e-26;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 60  
Db 3 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 62

QY 61 TTGGGGCTGCCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120  
Db 63 TTGGGGCTGCCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 122

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGGTAAATTTCT 180  
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGGTAAATTTCT 182

QY 181 TTTTGATTCCT 191  
Db 183 TTCCTACTCCT 193

RESULT 11

US-10-262-439-82/c  
; Sequence 82, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-218-654-80

Query Match 10.4%; Score 171.8; DB 15; Length 610;  
Best Local Similarity 93.7%; Pred. No. 3e-26;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 60  
Db 3 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 62

QY 61 TTGGGGCTGCCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120  
Db 63 TTGGGGCTGCCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 122

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGGTAAATTTCT 180  
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGGTAAATTTCT 182

QY 181 TTTTGATTCCT 191  
Db 183 TTCCTACTCCT 193

RESULT 9

US-10-218-654-82/c  
; Sequence 82, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-82

Query Match 10.4%; Score 171.8; DB 15; Length 610;  
Best Local Similarity 93.7%; Pred. No. 3e-26;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 60  
Db 608 AGGCAAACTGAACTTTCAGAGCTATGAGAAATGCTTCTGAAATTCGATTGCTAGCTC 549

QY 61 TTGGGGCTGCCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120  
Db 548 TTGGGGCTGCCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGGTAAATTTCT 180  
Db 488 AGACCTTGACACTGCTCTCCACTCATCGAATTCGCTGATAGGCGATGGGTAAATTTCT 429

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; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-439-82

Query Match
Best Local Similarity 10.4%; Score 171.8; DB 15; Length 610;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTC 60
DB 608 AGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTC 549

QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
DB 548 TTGGGGCTGCTATGTTTCTGCTTTGCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAAATTTCT 180
DB 488 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAAATTTCT 429

QY 181 TTTGATTTCT 191
DB 428 TTTGATTTCT 418

RESULT 12
US-10-311-455-1017
; Sequence 1017, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1017
; LENGTH: 5397
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1017

Query Match
Best Local Similarity 9.1%; Score 150.6; DB 15; Length 5397;
Matches 250; Conservative 0; Mismatches 119; Indels 8; Gaps 2;

QY 1 AGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTC 60
DB 5019 AGGTAAACCTAGACGTTTATAGATGATGAGATGTTTGTATTTGAGTTTGTATTT 5078

QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
DB 5079 TTGGAGTTGTTTACGTGTATGTTATTTTATAGAAAATTTTATAGAAATTTTATAGTGTATTTGGTGAAG 5138

; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-439-82

Query Match
Best Local Similarity 10.4%; Score 171.8; DB 15; Length 610;
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTC 60
DB 608 AGCAAAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGTCTAGCTC 549

QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
DB 548 TTGGGGCTGCTATGTTTCTGCTTTGCTCTAGAAAATCCCATGAATAGACTGGTGGCAG 489

QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAAATTTCT 180
DB 488 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAAATTTCT 429

QY 181 TTTGATTTCT 191
DB 428 TTTGATTTCT 418

RESULT 13
US-09-755-633-7
; Sequence 7, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-7

Query Match
Best Local Similarity 8.8%; Score 145.8; DB 9; Length 402;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTTCTGGGGCTGCTATGTTTCTGCTTT 86
DB 1 ATGAGATGCTTCTGAAATTTGAGTTTGTAGCTTCTGGGGCTGCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGACCTTGACACTGTCTCCACTCAT 120

QY 147 CGAAGTTGGCTGATAGCGGATGGGTAAATTTCTTTTGTATTCCT 191
DB 121 CGAAGTTGGCTGATAGCGGATGGGTAAATTTCTTTTGTATTCCT 165

RESULT 14
US-09-755-633-8/c
; Sequence 8, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
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Search completed: August 31, 2004, 14:03:44  
Job time : 985.052 secs

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FILE REFERENCE: IM-2-C1-C1
CURRENT APPLICATION NUMBER: US/09/755,633
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-09-755-633-8

Query Match      8.8%; Score 145.8; DB 9; Length 402;
Best Local Similarity 92.7%; Pred. No. 7.5e-21;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT 86
Db 402 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT 343

QY 87 GCTGTAGAAAATCCCATGAAATGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGAAATGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGCATGGGTAATTTCTTTTTCATTCT 191
Db 282 CGAACTTGGCTGATAGCGCATGGGTAATTTCTTTTTCATTCT 238

RESULT 15
US-10-218-654-83
Sequence 83, Application US/10218654
Publication No US20030099609A1
GENERAL INFORMATION:
APPLICANT: Sim, Gek-kee
APPLICANT: Yang, Shumin
APPLICANT: Dzeitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/10/218,654
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
PRIOR FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 83
LENGTH: 402
TYPE: DNA
ORGANISM: Canis familiaris
US-10-218-654-83

Query Match      8.8%; Score 145.8; DB 15; Length 402;
Best Local Similarity 92.7%; Pred. No. 7.5e-21;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT 86
Db 1 ATGAGAATCCTTCTGAAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT 60

QY 87 GCTGTAGAAAATCCCATGAAATGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGAAATGACTGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGCATGGGTAATTTCTTTTTCATTCT 191
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Blank Sheet



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 21:24:28 ; Search time 5570.11 Seconds  
(without alignments)  
8888.782 Million cell updates/sec

Title: US-10-787-382-18  
Perfect score: 1658  
Sequence: 1 aggaacactgaacatttc.....gtatgggaatttggaga 1658

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	398	24.0	622	29	CE331159 tigr-gss-
2	114.8	6.9	463	14	CD559535 AGENCOURT
3	114.4	6.9	467	14	CD559688 AGENCOURT
4	114.4	6.9	467	14	CD559690 AGENCOURT

C	5	114.4	6.9	470	14	CD559687
C	6	114.4	6.9	473	14	CD559689 AGENCOURT
C	7	114.4	6.9	478	14	CD559534 AGENCOURT
	8	114.4	6.9	492	14	CD559533 AGENCOURT
	9	113.2	6.8	489	14	CD559536 AGENCOURT
C	10	111.2	6.7	456	14	CD559686 AGENCOURT
	11	110.8	6.7	456	14	CD559532 AGENCOURT
	12	97.8	5.9	405	29	AY412020 Homo sapi
	13	96.2	5.8	405	29	AY412021 Pan trogl
	14	95.8	5.8	477	14	CD559608 AGENCOURT
C	15	95.2	5.7	503	13	BQ598873 MI-P-B4-a
	16	85.8	5.2	399	29	AY412022 Mus muscu
C	17	83	5.0	1101	29	CNS0039G Drosophil
	18	78.4	4.7	1200	13	EX437758 BX437758
	19	72.8	4.4	987	29	CNS014PQ Drosophil
	20	71.2	4.3	1200	13	EX437739 BX437739
	21	70	4.2	854	9	AL522840 AL522840
C	22	69.8	4.2	1200	13	EX437758 BX437758
C	23	69.2	4.2	1200	13	EX415878 BX415878
C	24	69	4.2	994	13	EX414650 BX414650
	25	68.2	4.1	1201	9	AL536104 AL536104
	26	68	4.1	1101	29	CNS0039G Drosophil
C	27	68	4.1	1190	29	CNS020N7 Tetradon
C	28	67.6	4.1	1201	13	EX443774 BX443774
C	29	67.4	4.1	1201	13	EX355654 BX355654
	30	67	4.0	1201	9	AL532464 AL532464
C	31	66.6	4.0	1101	29	CNS017L2 Drosophil
C	32	66.4	4.0	1201	13	EX439779 BX439779
C	33	66.2	4.0	1165	13	EX338369 BX338369
C	34	65.8	4.0	1101	29	CNS00EVL Drosophil
	35	65.6	4.0	1124	13	EX436282 BX436282
	36	65.2	3.9	928	29	CNS00DKY Drosophil
	37	65	3.9	1101	29	CNS00EVL Drosophil
	38	64.6	3.9	508	28	AQ248202 HS_2045 B
	39	64.6	3.9	1146	13	EX462546 BX462546
C	40	64.2	3.9	1056	13	EX415058 BX415058
	41	64.2	3.9	1200	13	EX415878 BX415878
	42	64	3.9	999	13	EX380865 BX380865
C	43	64	3.9	1101	29	CNS004ZW Drosophil
C	44	63.4	3.8	1190	29	CNS020N7 Tetradon
C	45	63	3.8	1201	13	EX442997 BX442997

#### ALIGNMENTS

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LOCUS tigr-gss-dog-1700033986568 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE331159  
VERSION CE331159.1 GI:36147469  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
REFERENCE 1 (bases 1 to 622)  
AUTHORS Kirness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,J.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org

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Class: shotgun.
Location/Qualifiers
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    /organism="Canis familiaris"
    /mol_type="genomic DNA"
    /strain="Standard Poodle"
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    peripheral blood"

ORIGIN
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  Best Local Similarity 96.4%; Pred. No. 4.2e-09;
  Matches 407; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1237 TTTTGATGAATTATATTTTAAATCTTCTCATTTAGCACCAACTGTGCATTAAGAA 1296
Db 3 TTGTTTGATGAATATATTTTAAATCTTCTCATTTAGCACCAACTGTGCATTAAGAA 62

Qy 1297 GTTTTTCAGGTATAGACATTAAGAACCAAACTGCCACGGGAGGCTGTGGATAA 1356
Db 63 GTTTTTCAGGTATAGACATTAAGAACCAAACTGCCACGGGAGGCTGTGGATAA 122

Qy 1357 CTATTCACAAACTGTCTTTAAATAAAGAACACATAGAGCGCCAAAGTAAGTTAAAG 1416
Db 123 CTATTCACAAACTGTCTTTAAATAAAGAACACATAGAGCGCCAAAGTAAGTTAAAG 182

Qy 1417 CATTTGCAAAACTTAAGTATATTTGCTGACTGCTGCTGTTTTTTTTTTTTTTT 1476
Db 183 CATTTGCAAAACTTAAGTATATTTGCTGACTGCTGCTGTTTTTTTTTTTTTTT 242

Qy 1477 CAGAATGTACAGTTTCTTCAATATCTCTCTGTTCTTTTACACAAAGGTGCGAG 1536
Db 243 CAGAATGTACAGTTTCTTCAATATCTCTCTGTTCTTTTACACAAAGGTGCGAG 302

Qy 1537 AGAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGTATAA 1596
Db 303 AGAAGATGGAGAGTGACAAAGTTCTTAGACTACCTGCAAGTATTTCTTGGTGTATAA 362

Qy 1597 CACGAGTGACACCGCAAGTTGAGAACAAACCGGCTTATTTAGTGAAGATTTTGA 1656
Db 363 CACGAGTGACACCGCAAGTTGAGAACAAACCGGCTTATTTAGTGAAGATTTTGA 422

Qy 1657 GA 1658
Db 423 GA 424

RESULT 2
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LOCUS
DEFINITION
  AGENCOURT 14496865 NIH MGC 195 Homo sapiens cDNA clone
  IMAGE:6971769 5', mRNA sequence.
ACCESSION
  CD559535
VERSION
  CD559535.2 GI:38558950
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 463)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  On Jun 10, 2003 this sequence version replaced gi:31585603.
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genetics / NIH
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgaps-remail.nih.gov
  Tissue Procurement: Narayan Bhat
  cDNA Library Preparation: Bhat Laboratory

REFERENCE
  AUTHORS
  TITLE
  JOURNAL
  COMMENT
  On Jun 10, 2003 this sequence version replaced gi:31585603.

CD559688
LOCUS
DEFINITION
  AGENCOURT 14496964 NIH MGC 195 Homo sapiens cDNA clone
  IMAGE:6971770 5', mRNA sequence.
ACCESSION
  CD559688
VERSION
  CD559688.2 GI:38453486
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 467)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  On Jun 10, 2003 this sequence version replaced gi:31585756.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBKI row: 9 column: 08
High quality sequence stop: 463.
Location/Qualifiers
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    /clone_lib="IMAGE:6971769"
    /tissue_type="mixed"
    /lab_host="DH5A (TI phage-resistant)"
    /clone_lib="NIH MGC 195"
    /note="Vector: pDNR-Dual; Site 1: loxP-Sali; Site 2:
    loxP-HindIII; Clones from this library have been
    PCR-amplified using gene-specific primers to contain the
    complete open reading frame (based on known gene sequences
    available from NCBI's RefSeq). Template for PCR is cDNA
    derived from either pooled cytoplasmic polyA RNA from 30
    cells lines or pooled total RNA from 10 different tissues
    (from BD Biosciences/Clontech and Washington University).
    PCR products are directionally cloned into the loxP sites
    of the pDNR-Dual vector. Library constructed by Dr.
    Narayan Bhat, Earl Bere III and Hongling Liao (Gene
    Expression Laboratory, Research Technology Program, SAIC
    Frederick, NCI-Frederick, Frederick, MD 21702). For
    information on which gene each clone represents, please
    visit our anonymous ftp site at
    ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
    A Note: this is a NIH_MGC Library."

ORIGIN
  Query Match      6.9%; Score 114.8; DB 14; Length 463;
  Best Local Similarity 75.3%; Pred. No. 1.2e-09;
  Matches 143; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 2 GGCAACACATGACATTTGAGGATGAGAGTCTCTGCAATTTGAGTTGTAGCTCT 61
Db 3 GACAAACGAGAGCTTTGAGGATGAGAGTCTCTGCAATTTGAGTTGTAGCTCT 62

Qy 62 TGGGGCTGCTTATTTTCTGCTTTGCTGTAGAAAATCCCATGATAGCTGTGGCAGA 121
Db 63 TGGAGCTGCTTACGTGTATGCTATCCCAAGAAATCCCAAGTGCATTTGGTGAAGA 122

Qy 122 GACCTTGACACTGCTCTCCACTCATCGAACTTGGCTATAGGCGATGGGTATTTCTT 181
Db 123 GACCTTGACACTGCTCTCTTCTACTCATCGAACTTGGCTATAGGCGATGGGTATTTCTT 182

Qy 182 TTTGATTTCTT 191
Db 183 TCTGTCTTCTT 192

RESULT 3
CD559688/c
LOCUS
DEFINITION
  AGENCOURT 14496964 NIH MGC 195 Homo sapiens cDNA clone
  IMAGE:6971770 5', mRNA sequence.
ACCESSION
  CD559688
VERSION
  CD559688.2 GI:38453486
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 467)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  On Jun 10, 2003 this sequence version replaced gi:31585756.

```

Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Narayan Bhat  
cDNA Library Preparation: Bhat Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRBK1 row: g column: 09  
High quality sequence start: 11  
High quality sequence stop: 467.  
Location/Qualifiers

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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue\_type="mixed"  
/lab\_host="DH5A (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC 195"  
/notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:  
loxP-HindIII; Clones from this library have been  
PCR-amplified using gene-specific primers to contain the  
complete open reading frame (based on known gene sequences  
available from NCBI's RefSeq). Template for PCR is cDNA  
derived from either pooled cytoplasmic polyA RNA from 30  
cells lines or pooled total RNA from 10 different tissues  
(from BD Biosciences/Clontech and Washington University).  
PCR products are directionally cloned into the loxp sites  
of the pDNR-Dual vector. Library constructed by Dr.  
Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
Expression Laboratory, Research Technology Program, SAIC  
Frederick, NCI-Frederick, Frederick, MD 21702). For  
information on which gene each clone represents, please  
visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat  
a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 6.9%; Score 114.4; DB 14; Length 467;  
Best Local Similarity 75.5%; Pred. No. 1.4e-09;  
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 4 CAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGCTAGCTCTTG 63  
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Db 466 CAACCGAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGATTTGCTAGCTCTTG 407  
| | | | |  
Qy 64 GGGCTGCTATGTTTCTGCTTGTAGAAAATCCCATGAATAGACTGGTGCGAGAGA 123  
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Db 406 GAGCTGCTACGTGTATGCCATCCCAAGAAATTCACCAAGTGCATTGGTGAAGAGA 347  
| | | | |  
Qy 124 CTTTGACATGCTCTCCACTCAGACTGGCTGATAGCGATGGGTAATTTCTTTT 183  
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Db 346 CTTTGGCACTGCTTTCTACTCATGCAACTCTGCTGATAGCAATGAGACTCTGAGGATTC 287  
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Qy 184 TGATTCCT 191  
| | | | |  
Db 286 CTGTTCCT 279  
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RESULT 4  
CD559690/c  
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DEFINITION AGENCOURT 14496838 NIH\_MGC\_195 Homo sapiens cDNA clone  
IMAGE:6971768 5', mRNA sequence.  
ACCESSION CD559690  
VERSION CD559690.2 GI:38453490  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

# ORGANISM

## Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 467)

## AUTHORS

NIH-MGC http://mgs.nci.nih.gov/.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

On Jun 10, 2003 this sequence version replaced gi:31585758.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRBK1 row: g column: 07

High quality sequence stop: 467.

Location/Qualifiers

1. 467

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/tissue\_type="mixed"

/lab\_host="DH5A (T1 phage-resistant)"

/clone\_lib="NIH\_MGC 195"

/note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:

loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the

complete open reading frame (based on known gene sequences

available from NCBI's RefSeq). Template for PCR is cDNA

derived from either pooled cytoplasmic polyA RNA from 30

cells lines or pooled total RNA from 10 different tissues

(from BD Biosciences/Clontech and Washington University).

PCR products are directionally cloned into the loxp sites

of the pDNR-Dual vector. Library constructed by Dr.

Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Expression Laboratory, Research Technology Program, SAIC

Frederick, NCI-Frederick, Frederick, MD 21702). For

information on which gene each clone represents, please

visit our anonymous ftp site at

ftp://image.llnl.gov/image/rearrayed\_plates/IRBK.presv.dat

a Note: this is a NIH\_MGC Library."

Query Match 6.9%; Score 114.4; DB 14; Length 467;

Best Local Similarity 75.5%; Pred. No. 1.4e-09;

Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 4 CAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGCTAGCTCTTG 63

| | | | |

Db 466 CAACCGAGACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGATTTGCTAGCTCTTG 407

| | | | |

Qy 64 GGGCTGCTATGTTTCTGCTTGTAGAAAATCCCATGAATAGACTGGTGCGAGAGA 123

| | | | |

Db 406 GAGCTGCTACGTGTATGCCATCCCAAGAAATTCACCAAGTGCATTGGTGAAGAGA 347

| | | | |

Qy 124 CTTTGACATGCTCTCCACTCATGACTGGCTGATAGCGATGGGTAATTTCTTTT 183

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Db 346 CTTTGGCACTGCTTTCTACTCATGCAACTCTGCTGATAGCAATGAGACTCTGAGGATTC 287

| | | | |

Qy 184 TGATTCCT 191

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Db 286 CTGTTCCT 279

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RESULT 5  
CD559687/c

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LOCUS       CD559687              470 bp    mRNA    linear    EST 19-NOV-2003
DEFINITION  AGENCOURT 14497029 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971771 5', mRNA sequence.
ACCESSION   CD559687
VERSION     CD559687.2 GI:38453484
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 470)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585755.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics / NIH
            National Cancer Institute
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK1 row: g column: 10
            High quality sequence start: 14
            High quality sequence stop: 470.

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                     /lab_host="DH5A (TI phage-resistant)"
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                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxp sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."

ORIGIN
Query Match      6.9%; Score 114.4; DB 14; Length 470;
Best Local Similarity 75.5%; Pred. No. 1.4e-09;
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY      4  CAACACTGAACATTTTCAGAGCTATGAGAAATGCTCTGTAATTTGAGTTGCTAGCTCTTG 63
Db      469  CAACCGCAGAACGTTTCAGAGCCATGAGGATGCTCTGCAATTTGAGTTGCTAGCTCTTG 410

QY      64  GGGCTGCTATGTTTCTGCTTGTGTAGAAATCCCATGATGACTGTTGGGAGAGA 123
Db      409  GAGCTGCTTACGTTGATGCTATCCCAAGAAATCCCAAGATGCTTGGTGAAGAGA 350

QY      124  CCTTGACATGCTCTCCATCGAATCTTGGCTGATAGCGATGGGTAAATTTCTTTT 183
Db      349  CTTTGGCACTGCTTTCTACTCTGCAACTCTGCTGATAGCAATGAGACTCTGAGGATTC 290

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QY      184  TGATTCTCT 191
Db      289  CTGTTCTCT 282

RESULT 6
LOCUS       CD559689/c              473 bp    mRNA    linear    EST 19-NOV-2003
DEFINITION  AGENCOURT 14496901 NIH_MGC_195 Homo sapiens cDNA clone
IMAGE:6971769 5', mRNA sequence.
ACCESSION   CD559689
VERSION     CD559689.2 GI:38453487
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 473)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     On Jun 10, 2003 this sequence version replaced gi:31585757.
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics / NIH
            National Cancer Institute
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Narayan Bhat
            cDNA Library Preparation: Bhat Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBK1 row: g column: 08
            High quality sequence start: 16
            High quality sequence stop: 473.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6971769"
                     /tissue_type="mixed"
                     /lab_host="DH5A (TI phage-resistant)"
                     /notes="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:
                     loxp-HindIII; Clones from this library have been
                     PCR-amplified using gene-specific primers to contain the
                     complete open reading frame (based on known gene sequences
                     available from NCBI's RefSeq). Template for PCR is cDNA
                     derived from either pooled cytoplasmic polyA RNA from 30
                     cells lines or pooled total RNA from 10 different tissues
                     (from BD Biosciences/Clontech and Washington University).
                     PCR products are directionally cloned into the loxp sites
                     of the pDNR-Dual vector. Library constructed by Dr.
                     Narayan Bhat, Earl Bere III and Hongling Liao (Gene
                     Expression Laboratory, Research Technology Program, SAIC
                     Frederick, NCI-Frederick, Frederick, MD 21702). For
                     information on which gene each clone represents, please
                     visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
                     a Note: this is a NIH_MGC Library."

ORIGIN
Query Match      6.9%; Score 114.4; DB 14; Length 473;
Best Local Similarity 75.5%; Pred. No. 1.4e-09;
Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY      4  CAACACTGAACATTTTCAGAGCTATGAGAAATGCTCTGTAATTTGAGTTGCTAGCTCTTG 63
Db      472  CAACCGCAGAACGTTTCAGAGCCATGAGGATGCTCTGCAATTTGAGTTGCTAGCTCTTG 413

```



Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 6.9%; Score 114.4; DB 14; Length 492;  
 Best Local Similarity 75.5%; Pred. No. 1.3e-09;  
 Matches 142; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 4 CAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGGCTAGCTCTTG 63  
 Db |||||  
 33 CAACCGAGAACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGATTTGCTAGCTCTTG 92  
 QY 64 GGGCTGCTATGTTTCTGCTTTCGCTGTAGAAATCCCATGAATGACTGGTGGCAGAGA 123  
 Db |||||  
 93 GAGCTGCTAGCTGTATGCCATCCACACAGAAATCCACAGTGCATTTGGTGAAGAGA 152  
 QY 124 CTTGACACTGCTCTCCACTCATCGAATTTGGCTGTAGTGGTATAGCGGTAAATTTCTTTT 183  
 Db |||||  
 153 CTTGGGACGCTCTTCTACTCATCGAATCTGCTGTATGCCAATGAGACTCTGAGGATTC 212  
 QY 184 TGATTCCT 191  
 Db |||||  
 213 CTGTTCCT 220

## RESULT 9

CD559536  
 LOCUS  
 DEFINITION AGENCOURT 14496804 NIH MGC 195 Homo sapiens cDNA clone  
 IMAGE:6971768 5', mRNA sequence.

ACCESSION CD559536

VERSION CD559536.2 GI:38558953

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 489)

NIH-MGC <http://mgs.nci.nih.gov/>;

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

On Jun 10, 2003 this sequence version replaced gi:31585604.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabs@email.nih.gov](mailto:cgabs@email.nih.gov)

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBK1 row: 5 column: 07

High quality sequence start: 17

High quality sequence stop: 489.

## FEATURES

source

1. .489

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6971768"

/issue\_type="mixed"

/lab\_host="DH5A (T1 phage-resistant)"

/clone\_lib="NIH MGC 195"

/note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2:

loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat)  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 6.8%; Score 113.2; DB 14; Length 489;  
 Best Local Similarity 74.7%; Pred. No. 2.1e-09;  
 Matches 142; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 2 GGCAACACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTGGCTAGCTCT 61  
 Db |||||  
 29 GACCAACGAGAACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGATTTGCTAGCTCT 88  
 QY 62 TGGGGCTGCCCTATGTTTCTGCTTGTAGAAAATCCCATGAATGACTGGTGGCAGA 121  
 Db |||||  
 89 TGGAGCTGCCCTACGTGTATGCCATCCCAACAGAAATCCCAAGTGCATTTGGTGAAGA 148  
 QY 122 GACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGTAGTGGCGATGGGTATTTCTT 181  
 Db |||||  
 149 GACCTTGGCACTGCTTTTCTACTCATGCACTCTGCTGATAGCAATGAGACTCTGAGGAT 208  
 QY 182 TTTCATTCCT 191  
 Db |||||  
 209 TCCTGTTCT 218

## RESULT 10

CD559686/c

LOCUS

DEFINITION AGENCOURT 14497093 NIH MGC 195 Homo sapiens cDNA clone

IMAGE:6971772 3', mRNA sequence.

ACCESSION CD559686

VERSION CD559686.1 GI:31585754

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 456)

NIH-MGC <http://mgs.nci.nih.gov/>;

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabs@email.nih.gov](mailto:cgabs@email.nih.gov)

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: IRBK1 row: 5 column: 11

High quality sequence stop: 456.

Location/Qualifiers

1. .456

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/clone="IMAGE:6971772"
/tissue type="mixed"
/lab host="DH5A (TI phage-resistant)"
/clone lib="NIH MGC 195"
/note="vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

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ORIGIN

Query Match 6.7%; Score 111.2; DB 14; Length 456;  
 Best Local Similarity 74.5%; Pred. No. 4.8e-09;  
 Matches 140; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 CAACACTGACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCTCTTG 63  
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 Db 456 CCAAGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTGCTAGCTCTTG 397  
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 QY 64 GGCCTGCTATGTTTCTGCTTGTGTAGAAATCCCATGATAGACTGGTGGCAGAGA 123  
 |||||  
 Db 396 GAGCTGCTACGTTGTATGTCATCCACAGAAATCCCAAGTGCATTTGGTGAAGAGA 337  
 |||||  
 QY 124 CTTGACACGTCTCTCCACTCACTGCACTTGGCTGATAGCGATGGGGTAATTTCTTTT 183  
 |||||  
 Db 336 CTTGGCAGCTCTTCTTACTCATCGAACCTGCTGATAGCAATGAGACTCTGAGGATTC 277  
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 QY 184 TGATTCCT 191  
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 Db 276 CTGTTCT 269  
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RESULT 11  
 CD559532 456 bp mRNA linear EST 11-JUN-2003  
 LOCUS  
 DEFINITION AGENCOURT\_14497057 NIH MGC 195 Homo sapiens cDNA clone  
 IMAGE:6971772 5', mRNA sequence.

ACCESSION CD559532  
 VERSION CD559532.1 GI:31585600  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 (bases 1 to 456)  
 NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE  
 National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
 Unpublished (1999)

COMMENT  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [csaphe-r@mail.nih.gov](mailto:csaphe-r@mail.nih.gov)  
 Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: IRBK1 row: 9 column: 11

FEATURES  
 source  
 High quality sequence stop: 456.  
 Location/Qualifiers  
 1..456

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971772"
/tissue_type="mixed"
/lab_host="DH5A (TI phage-resistant)"
/clone lib="NIH MGC 195"
/note="vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene
Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

```

ORIGIN

Query Match 6.7%; Score 110.8; DB 14; Length 456;  
 Best Local Similarity 74.7%; Pred. No. 5.6e-09;  
 Matches 139; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 6 AACACTGACATTTTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCTCTTGG 65  
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 Db 1 AAACAGAACGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTGCTAGCTCTTGA 60  
 |||||  
 QY 66 GCTGCTATGTTTCTGCTTGTAGAAATCCCATGATAGACTGGTGGCAGAGACC 125  
 |||||  
 Db 61 GCTGCTACGTGATGCCATCCACAGAAATCCCAAGTGCATTTGGTGAAGAGACC 120  
 |||||  
 QY 126 TTGACACTGCTCTCCACTCATCGAACTGGCTGATAGCGATGGGTAATTTCTTTTG 185  
 |||||  
 Db 121 TTGCACCTGCTTTTACTCTCATCGAACTGCTGTATAGCAATGAGACTCTGAGGATTCCT 180  
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 QY 186 ATTCTCT 191  
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 Db 181 GTTCTCT 186  
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RESULT 12  
 AY412020

LOCUS  
 DEFINITION Homo sapiens IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.

ACCESSION AY412020

VERSION AY412020.1 GI:39767985

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 (bases 1 to 405)

AUTHORS  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

TITLE  
 Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 405)

AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
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 /gene="IL5"  
 /locus\_tag="HCM4418"

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 Best Local Similarity 74.5%; Pred. No. 9e-07;  
 Matches 123; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 86  
 Db 1 ATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146  
 Db 61 CCCACAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAACTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 191  
 Db 121 CGAACTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 165

RESULT 13  
 AY412021  
 LOCUS  
 DEFINITION  
 Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION  
 AY412021  
 VERSION  
 AY412021.1 GI:39767986  
 KEYWORDS  
 GSS.  
 SOURCE  
 Pan troglodytes (chimpanzee)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 1 (bases 1 to 405)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
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 /gene="IL5"

Query Match 5.8%; Score 97.8; DB 29; Length 405;  
 Best Local Similarity 74.5%; Pred. No. 9e-07;  
 Matches 123; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 86  
 Db 1 ATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146  
 Db 61 CCCACAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAACTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 191  
 Db 121 CGAACTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 165

RESULT 13  
 AY412021  
 LOCUS  
 DEFINITION  
 Pan troglodytes IL5 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION  
 AY412021  
 VERSION  
 AY412021.1 GI:39767986  
 KEYWORDS  
 GSS.  
 SOURCE  
 Pan troglodytes (chimpanzee)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 1 (bases 1 to 405)  
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.  
 Location/Qualifiers  
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 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
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/locus\_tag="HCM4418"

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 Best Local Similarity 73.9%; Pred. No. 1.7e-06;  
 Matches 122; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 86  
 Db 1 ATGAGGATGCTTCTGCAATTTGAGTTTGTAGCTCTTGGGGCTGCCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146  
 Db 61 CCCACAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAACTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 191  
 Db 121 CGAACTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 165

RESULT 14  
 CD559608  
 LOCUS  
 DEFINITION  
 AGENCOURT 14496997 NIH MGC 195 Homo sapiens cDNA clone  
 IMAGE:6971867 5', mRNA sequence.  
 ACCESSION  
 CD559608  
 VERSION  
 CD559608.2 GI:38558942  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 477)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585676.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics / NIH  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: [cgabs-f@mail.nih.gov](mailto:cgabs-f@mail.nih.gov)  
 Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRBK2 row: g column: 10  
 High quality sequence start: 107  
 High quality sequence stop: 353.  
 Location/Qualifiers  
 FEATURES  
 source  
 1..477  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6971867"  
 /tissue\_type="mixed"  
 /lab\_host="DH5A (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 195"  
 /note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the pDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC



Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearrayed\\_plates/TRBK.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/TRBK.presv.dat)  
a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 5.8%; Score 95.8; DB 14; Length 477;  
Best Local Similarity 72.3%; Pred. No. 1.8e-06;  
Matches 139; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

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Db 15 GACTAACGCGAAGCGTTTACAGCCGCTGAGACGCTTCTGCTATTTGATTTGCTAGCTC 74  
QY 61 TTGGGGCTGCTATGTTTCTGCTGTGAGAAATCCCATGATAGACTGGTGGCAG 120  
Db 75 TTGAGCTGCTACGTGTATGCCATCCCAAGGAAATCCCAAGTGCATTGGTGAAG 134  
QY 121 AGACCTTGACATGCTCTCCTCACTCATCGAATCTGGCTGATAGCGATGGGTAATTTCT 180  
Db 135 AGACCTTGACATGCTCTTCTACTCGTCACTCTGCTGATAGCAATGAGACTCTGAGGA 194  
QY 181 TTTTGATTCCT 191  
Db 195 TTCTGTTCCT 205

RESULT 15  
BQ598873/c  
LOCUS BQ598873 503 bp mRNA linear EST 24-JUN-2002  
DEFINITION MI-P-E4-ah-e-08-1-UM.s1 MI-P-E4 Sus scrofa cDNA clone  
MI-P-E4-ah-e-08-1-UM 3', mRNA sequence.  
ACCESSION BQ598873  
VERSION BQ598873.1 GI:21545599  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 503)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548  
Contact: Tuggle CK  
Molecular Genetics Laboratory, Department of Animal Science  
Iowa State University  
201 Kildee Hall, Ames, IA 50011-3150, USA  
Tel: 5152944252  
Fax: 5152942401  
Email: [cktuggle@iastate.edu](mailto:cktuggle@iastate.edu)  
Tissue Procurement: Dr. Chris Tuggle, Iowa State University  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)).  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
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/note="Vector: pMT3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: EcoRI; The MI-P-E4

Library is derived from embryo at gestational day 14. For a detailed description of the library from which this clone was derived, please visit our web site at <http://pigest.genome.iastate.edu/>.  
TAG\_TISSUE=postelongation\_d\_14\_conceptus  
TAG\_LIB=MI-P-E4  
TAG\_SEQ=ACTCAC"

ORIGIN

Query Match 5.7%; Score 95.2; DB 13; Length 503;  
Best Local Similarity 80.0%; Pred. No. 2.2e-06;  
Matches 112; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY 1578 TATTCTTGGTGTATAATAAACACCCGAGTGGACACCGGAAAGTTGAGACAAACCGGCTTAT 1637  
Db 442 TTTTCTTGGTGTGATAAATACCGAGTGGACAAATGGAAGTTAAGACCAAACTGCTTAC 383  
QY 1638 TGTAGTGGAAAGATTTTGGAG 1657  
Db 382 CGAAGCAAAAGATTTTTCAG 363

Search completed: August 31, 2004, 13:00:16  
Job time : 5572.11 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: August 30, 2004, 16:21:12 ; Search time 7167.07 Seconds  
(without alignments)  
10026.797 Million cell updates/sec  
Title: US-10-787-382-18  
Perfect score: 1658  
Sequence: 1 aggcacactgaacatttc.....gtatgggaagattttggaga 1658

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22:	em_ov.*	
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31:	em_htg_inv.*	
32:	em_htg_other.*	
33:	em_htg_mus.*	
34:	em_htg_pln.*	
35:	em_htg_rod.*	
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	634.6	38.3	3241	9	HUMIL5A J02971 Human eosin
3	634.6	38.3	5186	9	AF353265 Homo sapi
4	634.6	38.3	57186	9	AC004042 Homo sapi
5	634.6	38.3	180042	9	AC079320 Homo sapi
c	634.6	38.3	16366	9	AC116366 Homo sapi
c	634.6	38.3	16366	9	AC116366 Homo sapi
7	600.6	36.2	3230	6	AR136275 Sequence
8	600.6	36.2	3230	6	BD247730 Antisense
9	600.6	36.2	3230	6	BD247730 Antisense
10	600.6	36.2	3230	6	BD247730 Antisense
11	600.6	36.2	3230	6	BD247730 Antisense
12	600.6	36.2	3230	6	BD247730 Antisense
13	599	36.1	3230	6	BD247730 Antisense
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15	347.4	21.0	1140	4	OAILV1
16	272.6	16.4	700	6	AX182851
17	245.2	14.8	450	4	OAILV2
18	221.6	13.4	700	6	AX182853
19	216	13.0	700	6	AX182850
20	215.4	13.0	700	6	AX182852
21	205.2	12.4	1395	6	A21910
22	171.8	10.4	610	4	AF331919
23	171.8	10.4	610	6	AR241536
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c	171.8	10.4	610	6	AR254493
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ALIGNMENTS

RESULT 1  
AF331920  
LOCUS AF331920  
DEFINITION Canis familiaris interleukin-5 gene, complete cds.  
ACCESSION AF331920  
VERSION AF331920.1  
KEYWORDS GI:15919182  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 1658)  
AUTHORS Yang,S., Sellins,K.S., Weber,E. and McCall,C.  
TITLE Canine interleukin-5: molecular characterization of the gene and expression of biologically active recombinant protein

AF331920 1658 bp DNA linear NAM 04-OCT-2001  
Canis familiaris interleukin-5 gene, complete cds.





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Db      1573 AACTCTCTCAGTAATATATTAAGTCTCATCTCTTTTGAATTTTATCTTAATATG 1632
QY      1128 GTGTTTCCCACTGGAAGACACAAGTAATAAACCTCTTTGGGAGGAGGAACCTTGTA 1187
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QY      1198 AACCCCAACAAAGCTTAACCTTT----- 1213
Db      1689 AATACCAACAAACAAAGCTTAACCTTTGTGACCAAAATGTTTAAATATATTTTAA 1748
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QY      1257 TAAATCTCTCTATTTAGCACCAACTGTCAATTAAGAGAGTTTTCAGGTTATACAC 1316
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RESULT 3
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LOCUS      AF353265      5186 bp      DNA      linear      PRI 20-APR-2001
DEFINITION Homo sapiens interleukin 5 (IL5) gene, complete cds.
ACCESSION  AF353265
VERSION    AF353265.1  GI:13346490
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 5186)
AUTHORS   Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,

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Yi, Q. and Nickerson, D.A.  
 Direct Submission  
 Submitted (25-FEB-2001) Molecular Biotechnology, University of  
 Washington, 1705 NE Pacific, Seattle, WA 98195, USA  
 To cite this work please use: SeattleSNPs. NHUHI Program for  
 Genomic Applications, UW-FHCRC, Seattle, WA (URL:  
 http://pga.mbt.washington.edu).

**FEATURES**  
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Center code: WIBR  
Web site: http://www.seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L10831  
Center clone name: 729\_C\_24  
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DEFINITION Homo sapiens chromosome 5 clone RP11-89G4, complete sequence.  
AC116366  
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VERSION AC116366.2 GI:21070669  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 169385)  
DOE Joint Genome Institute and Stanford Human Genome Center.  
AUTHORS Direct Submission  
TITLE Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 169385)  
DOE Joint Genome Institute.  
AUTHORS Direct Submission  
TITLE Direct Submission  
JOURNAL  
REFERENCE 3 (bases 1 to 169385)  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
DOE Joint Genome Institute and Stanford Human Genome Center.  
Submitted (22-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On May 22, 2002 this sequence version replaced gi:19745048.  
Draft Sequence Produced by DOE Joint Genome Institute  
www.jgi.doe.gov  
Finishing Completed at Stanford Human Genome Center  
www-shgc.stanford.edu  
Quality: Phrap Quality >=40 99.9% of Sequence;  
Estimated Total Number of Errors is 0.1.

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Query Match 38.3%; Score 634.6; DB 9; Length 169385;  
Best Local Similarity 68.6%; Pred. No. 1.2e-105;  
Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;  
QY 1 AGGCAACACATGACATTTTCAGAGCTATGAGAACTCTTGAATTCAGTTTCTAGCTC 60  
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DEFINITION	Sequence 78 from patent US 6136603.					
ACCESSION	AR136275					
VERSION	AR136275.1	GI:14476947				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	Unclassified.					
AUTHORS	1. (bases 1 to 3230)					
TITLE	Dean, N.M., Karras, J.G. and McKay, R.					
JOURNAL	Antisense modulation of interleukin-5 signal transduction					
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Db 1005 TCATTAGTTATCAATGGAACATTAATTTTCTATATTTTGTGTTTATGTTGGGCTGT 1064  
QY 530 AAAT-TATGCTCTATGAATATTAGGAATGGTGTAGGAATGGCTCTACAATATTAAAGTA 588  
Db 1065 GAATGCTGTACTTATAAATATAGGAATGACTTT-----TTATCAAGTA 1109  
QY 589 GAATCCATTAGCAGTGCAGCCCTTTTGTGATGTTGTGATGTTCTCCATCTCAAG 648  
Db 1110 GAATCCTTTAAACAGTGGATAGGCTCTTTGGTGTGATGTTGTAGTTTGGCTTCCCAAG 1169  
QY 649 AGCCTCGTGTAGGCAATCTTTTCCAAAGAAATCCATATTGGGTACAGATATCTTCTAG 708  
Db 1170 AGCATCGTGTAGG-ATTCCTTCCAGAGGATTCACACTGAGTGAGAGGTGGCTGTAG 1228  
QY 709 GCTCATTACCTCTGTGCTGGCTTCTCCCTCACTCAACGTTTTTCTGAAAGTACTAGCA 768  
Db 1229 TCTCGTGCAGTCTGAC-----TCTTCTCACTCACTCAACGTTTCTGAAAGTATTAGCA 1283  
QY 769 ACTTGGGGTATATTTTGAATATTGCTAGTACATGAATAAATATACAGTGAAGTCCT 828  
Db 1284 ACTCAGATTTATTTTGAACCATGATCAGTACATTAATAATATAAACAATGCC- 1342  
QY 829 ATATTATAGTCACTTCCACATATTATAAGATTTTAACTCTAATGGAATCATATACAT 888  
Db 1343 --CTATATTAAATTTCTGCATCTTAATAATATTAGCTATATGATGGTGTGATGCAT 1400  
QY 889 CTGGAGTATGTCATGTCATATTAAATGTTTAAATGTTGATATCATTTAGTCTAAATAGA 948  
Db 1401 TGAATAG--CCTGGTCAATTAATAATGTTAAATATATAGTTT-ATTAGTCTAAATAGA 1456  
QY 949 ATAAATTTACAGCTAGAACATATACGAGGAATTTCTGAGGTGAGGTAAATCAGTAAGCA 1008  
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QY 1009 GTTGTATTATACCTGTAAGATTTATTTTCAATATCATTTCTATATATCATTTGTA 1068  
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QY 1188 AACCCCAACAAAGTCTAACTTTT----- 1214  
Db 1685 AATACCAACAAAGGCTTAACITTTGGGACCAAAATGTTTAAATAATTTTAA 1744  
QY 1215 ----- 1214

Db 1745 TTGATGAATTAAGTATATATATTTATTGTGTACATAATGATGTTTGAAGTATGAT 1804  
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Db 1864 AAAATTTTCTCTCAATTTAGCACCACTGTCACCTGAAGAAATTTTCAGGGAATAGGCAC 1923  
QY 1317 ATGAAGAACCAAACTGCCACGGGAGGCTGTGGATTAACCTTTCCTCAAACTTGTCTTT 1376  
Db 1924 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGACTATTCAAAAAATTTGTCTT 1983  
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Db 1984 AATAAAGAAATACATTTAGCGCCAAAGTAAGTTTACACATTTCAATGGAAGCTATATT 2043  
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Db 2044 TCTCTGGCTG-----TGCTATTTCTATGGAATTTGACAGTTTCTG 2085  
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QY 1551 TGCAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTGTATTAATAACCGAGTGGACAC 1610  
Db 2146 TAAACCAATTCCTAGCTACCTGCAAGAGTTCTTGTGTATTAATAACCGAGTGGATA 2205  
QY 1611 CGAAAGTTGAGAACAAACCGCTTATTTAGTGGAGAAATTTGGAG 1657  
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## RESULT 8

BD247730 3230 bp DNA linear PAT 17-JUL-2003  
LOCUS Antisense modulation of interleukin-5 signal transduction.

DEFINITION BD247730

ACCESSION BD247730

VERSION BD247730.1 GI:33057500

KEYWORDS JP 2002539846-A/78.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 3230)

DEAN,N.M., KARRAS,J.G. and Mckay,R.

Antisense modulation of interleukin-5 signal transduction

Patent: JP-2002539846-A 78 26-NOV-2002;

ISIS PHARMACEUTICALS INC

OS Homo sapiens (human)

PN 2002539846-A/78

PF 17-MAR-2000 JP 2000608790

PR 26-MAR-1999 US 09/280799

PI NICHOLAS M DEAN, JAMES G KARRAS, ROBERT MCKAY

PC C12N15/09, A61K31/711, A61K48/00, A61P11/06, A61P29/00, A61P35/00,

PC A61P43/00,

PC A61P43/00, C12N5/02, C12N15/00

CC Antisense modulation of interleukin-5 signal transduction FH

Key Location/Qualifiers

FT source 1..3230

FT Location/Qualifiers

1..3230

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

## ORIGIN

Query Match 36.2%; Score 600.6; DB 6; Length 3230;  
Best Local Similarity 67.8%; Pred. No. 3.6e-99;

Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

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Db 647 AGACCTTGGCAGCTGCTTTCTACTCATCGAACTCTGCTGATAGCAATGAGGTAAATTTCT 706
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QY 294 ATGTTACTCAGAAGAAATTAATTTAAAAGTTATGAACCTTACAATACATTAATAAATGAATG 353
Db 826 ACATCACCAGCAACATTTCTGTTAAAAGTTATGATGCTGGTGTGCTGTAATAAATGATG 885
QY 354 TTGTTTCTCTTTTTCAGAACTGATGATTCCTACTCTCTGAAATAAATAATGTAAGTT 413
Db 886 -TATTTCTCTCTCTCAGACTCTGAGGATTCCTGTTCTCTGTACATAAATAATGTAAGTT 944
QY 414 AATATTGATTTGTAATAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 469
Db 945 AATATTGATTTGTAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
QY 470 GTATCAGTTAATGAGTGAATTAATTTTATCTATTTTGTGTTTATGTTGTCGGGATG 529
Db 1005 TCATTTGATTTATGTTGAACTTATTTTATTTTCTATATTTTGTGTTTATGTTGTCGGTGT 1064
QY 530 AAAT-TATGTCCTTATGAATATTAGGAATGTTGTTAGGAATGCTCTACAAATATTAGTA 588
Db 1065 GAATGCTGTACTTTATAAATATGAGGAATGACTTT-----TTATCAAGTA 1109
QY 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGATTTGTGATGTTTCTCCATCTCAAAG 648
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QY 649 AGCTCTGTGTCAGCACTCTTTTCAAAGAAATTCATATTTGGTTCAGAGATATCTCTAG 708
Db 1170 AGCATCGTGTGAGG-ATTCTTTCCAGAGGATTTCCACACTGAGTGAGGTTGGTGTCTAG 1228
QY 709 GTCCTATTCACTCTGTCGTGGCTTTCTCACTCAACGTTTCTTGAAGTACTAGCA 768
Db 1229 TCTCCGTGAGTCTGAC-----TCTTTCTCACTCAACGTTTCTTGAAGTATTAGCA 1283
QY 769 ACTTGGGGTTATATTTTAGAATTTAGTTCAGTAGACATGAAAATATACAGTGAAGTCT 828
Db 1284 ACTCAGAATATATTTTGAACCATGATCAGTAGACATTAATAATAATAAATAATTAACAATGCC- 1342
QY 829 ATATTAATAGTCACTTCCACATTTTAAATCAATTTTAACTCAATGGAATCATATACAT 888
Db 1343 --CTATATTAAATTTCTGCATCTTAAATCAATTTATGATATATGATGTTGTTGATGTCAT 1400
QY 889 CTGAGTATGTCATGCTGATATTAATTTTAAATGTTAAATGTTAAATGTTAAATGTTAAATG 948
Db 1401 TGAATATG--CC-TGGTCAATTTAAATGTTAAATGTTAAATGTTAAATGTTAAATGTTAAATG 1456
QY 949 ATAAAAATACAGCTAGACTATACAGAGGAAATTTCTGAGGTGAGGTAAATCAGTAGGCA 1008
Db 1457 ATAAAAATACAGCTAGACTATGTAAGGAAATTTCTGAGGTGAGGTAAATCAGTAGGCA 1513
QY 1009 GTTGTATTATACCTCGTAAGCATTTTATTTTCAATTAATCAATTTTCAATTTATATATTTGTA 1068
Db 1514 -----ATTACACTTCCAAAACATTTTTCAGTTTACATTAATTAAGTTATATCTTTATA 1568
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QY 1128 GTGGTTTCCCACCTCGGAAAAGACACAAGTAAACCTCTTGGGAGAAAGGAACTTGTGTA 1187
Db 1629 GTGGTTTGTGTGCTAGAAA-----ACAAACAAAAAACTCTTTGGAGAGAGGAACATCATGA 1684
QY 1188 AACCCCAACAAACAAAGTCTAACTTTT----- 1214
Db 1685 AATACCAACAAACAAAGCTAACTTTTGGACCAAAATTTGTTTAATTAATTTTAA 1744
QY 1215 ----- 1214
Db 1745 TTGATGAATTAATAAGTATATATATTTATTTGTGTACAATATGATCTTTTGAAGTATGAT 1804
QY 1215 -----TGGACCAAAATTTTATGCTTTTGGCTTTTGGATCAATATATTTT 1256
Db 1805 ACATTTGAGATGGAATGGAACCAATTTTATACCTTGTCTTGTGATTTTTCGCA-TTTT 1863
QY 1257 TAAAAATCTTCTCTCAATTTAGCACCAACTGTGCATTTAAAGAAGTTTTTTCAGGGTATAGACAC 1316
Db 1864 AAAAAATTTCTCTCAATTTAGCACCAACTGTGCATTTAAAGAAGTTTTTTCAGGGTATAGACAC 1923
QY 1317 ATTGAAGAACCAACTGCCACGGGAGGCTGTGGATAAACTATTTCCAAAACCTTGTCTTT 1376
Db 1924 ACTGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGCTATTTCAAAAACTTGTCTTT 1983
QY 1377 AATAAAGAACACATAGAGCGCCAAAAGTAAAGATTTAAAGACATTTGGCAAAAACCTTAAGT 1436
Db 1984 AATAAAGAACATACATTTAGCGCCAAAAGTAAAGTAAAGTACACATTTCAATTTGAGGATATAT 2043
QY 1437 ATATTGTCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTTTCAAGATTTGACAGTTTCTCTA 1496
Db 2044 TCTCTCTGCTG-----TGCCTATTTCTATGGAATTTGACAGTTTCTCTG 2085
QY 1497 CAATATCT-----CCTCTGTTCTTTTAAACAGAAAAGTGTGACAGAAAGATGAGAG 1550
Db 2086 TAATACCTATTGTGCTATTTTCTTTTTCACAGAAAAGTGTGAGAGAAAGACGAGAG 2145
QY 1551 TGACAAAAGTCTCAGACTACCTGCAAGTATTTCTTGGTGTAAATAAACACCGAGTGAAC 1610
Db 2146 TAAACCAATTTCTCAGACTACCTGCAAGAGTTTCTTGGTGTAAATGAACACCGAGTGAATA 2205
QY 1611 CGAAGATTTGAGAACAAACCGCTTATTGTAGTGAAGATTTTCGAG 1657
Db 2206 TAGAAGATTTGAGACTAAACTGTTTGTGACAGCCAAAGATTTTGGAG 2252
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## RESULT 9

E01640

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS Human

PN JP 1998185387-A/2

PF 30-JUL-1998

PR 21-SEP-1987 JP 1987236842

PI 20-SEP-1986 JP 86P 223284

CC HONSHIYO YUJ TAKATSU KIYOSHI, EBA SEBERINSON PC

C12N15/00,C07K13/00,C12N5/00,C12P21/02,C12N5/00,C12R1/91; CC

E01640 3230 bp DNA linear PAT 29-SEP-1997  
gene for human B cell differentiation Factor.

E01640.1 GI:2169893

JP 1988185387-A/2.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3230)

HONSHIYO YUJ, Takatsu, K. and Eba, S.

HUMAN B CELL DIFFERENTIATION FACTOR

Patent: JP 1988185387-A 2 30-JUL-1988;

HONSHIYO YUJ

OS Human

PN JP 1998185387-A/2

PF 30-JUL-1998

PR 21-SEP-1987 JP 1987236842

PI 20-SEP-1986 JP 86P 223284

CC HONSHIYO YUJ TAKATSU KIYOSHI, EBA SEBERINSON PC

C12N15/00,C07K13/00,C12N5/00,C12P21/02,C12N5/00,C12R1/91; CC





Db 2206 TAGAAGTTGAGACTAAAGTGGTTTGTTCAGCCAAAGATTGGAG 2252

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RESULT 10  
LOCUS AR364536 3230 bp DNA linear PAT 03-SEP-2003  
DEFINITION Sequence 1 from patent US 5324640.  
ACCESSION AR364536  
VERSION AR364536.1 GI:34427297  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 3230)  
AUTHORS Honjo, T., Takatsu, K. and Severinson, E.  
TITLE Human B-cell differentiation factor and process of producing said factor  
JOURNAL Patent: US 5324640-A 1 28-JUN-1994;  
FEATURES  
source Location/Qualifiers  
1..3230  
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ORIGIN

Query Match 36.2%; Score 600.6; DB 6; Length 3230;  
Best Local Similarity 67.8%; Pred. No. 3.6e-99;  
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;

Qy 1 AGCAACACTGAACATTTTCAGAGCTATGAGATGCTCTGATTTGAGTTTGGCTAGCTC 60  
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Qy 61 TTGGGGTGGCTATGTTCTGCTTCTGCTGAGAAATCCCATGAATAGACTGGTGGCAG 120  
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Qy 181 TTTTGATCTCTACAGCTTTTAAATGATGGTAAATTTGGTGGTGGCTAGTT----- 234  
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Qy 709 GCTCCATTCACCTGCTGCTGGTGGCTTTCCTCACCTCAACGTTTCTTCTGAAAGTACTAGCA 768  
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Qy 1611 CGAAAGTTGAGAACAAACCGGCTTATTTGTAGTGGAGATTTTGAG 1657



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QY	1215	-----	1214
Db	1745	TTGATGAATTAAAGAAGTATATATATTATTGTGTACAAATGATGTTTTGAAGTATGAT	1804
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QY	1437	ATATTTGCTGCACTCTGCTGTTTTTTTTTTTTTTTACAGAATGTACAGTTTCCTA	1496
Db	2044	TGTCCTGGCTG-----TGCCTATTTCTATGGAATGTACAGTTTCTG	2085
QY	1497	CATATCT-----CCTCTGTTCTTTTAAACAGAAAAGGTGTGACGAGAAGATGGAGAG	1550
Db	2086	TAATACCTATTGTCAATTTTCTTTTTTTCAGAAAAAGTGTGGAGAGAAAGACGGAGAG	2145
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Db	2146	TAAACCAATTCCTAGACTACTGCAAGAGTTTCTTGTTGTAATGAACACCGAGTGGATAA	2205
QY	1611	CGGAAAGTTGAGAACAAACCGGCTTATTGTAGTGGAAAGATTTTGGAG	1657
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RESULT 12			
HUMIL5			
LOCUS		3230 bp	DNA
DEFINITION		Human interleukin 5 (IL-5) gene, complete cds.	linear
ACCESSION		J03478	
VERSION		J03478.1	GI:186338
KEYWORDS		colony stimulating factor; interleukin 5.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE			
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		Tanabe, T., Konishi, M., Mizuta, T., Noma, T. and Honjo, T.	
JOURNAL		Molecular cloning and structure of the human interleukin-5 gene	
MEDLINE		J. Biol. Chem. 262 (34), 16580-16584 (1987)	
PUBMED		88059042	
REFERENCE		2 (bases 1 to 3230)	
AUTHORS		Tanabe, T.	
TITLE		Direct Submission	
JOURNAL		Submitted (09-SEP-1987) T. Tanabe, Department of Medical Chemistry,	
FEATURES		Kyoto University Faculty of Medicine, Japan	
source		Location/Qualifiers	
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Qy	1 AGGCAACACTGAACATTTCCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTTCTAGCTC 60		
Db	527 AGGCAACGAGAAAGTTTCAGAGCCATGAGGATGCTTCTGCATTTGAGTTTCTAGCTC 586		
Qy	61 TTGGGGTGGCTATGTTTCTGCTTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAG 120		
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Qy	121 AGACCTTGACATGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGGGTAATTTTCT 180		
Db	647 AGACCTTGGCACTGCTTTCTACTCATCGAACTCTGCTGATAGCAATGAGTAATTTCT 706		
Qy	181 TTTTGATTCCTACAGTCTTTAAAGTCATGGGTAATTTGGTGGTGGCTAGTT----- 234		
Db	707 TTATGATTCCTACAGTCTGTAAAGTCATAGGTAATCATTTTGTGATGGTTTCTTTACTAT 766		
Qy	235 -TTTAAAGATCCATTATCAATAATGAAGTAATCAGTGTAAATAATATAATGGGTAACC 293		
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Qy	294 ATGTTACTCAGAGAAATATATTTAAAGTTTATGAACCTTACAATA CATTAAAAATGAATG 353		
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Qy	354 TTGTTTCTCTTTCTTTTCAGAACCTGATGATTCCTACTCTCTGAAAAATAAAATGTAAGTT 413		
Db	886 -TATTTCTTCTCTCCAGACTCTGAGGATTCCTGTTCTCTGTCATATAAATGTAAGTT 944		
Qy	414 AAATATGATTTGATAAAATGATTACATGAATCAG-----TTTCAATTTTAAAGCTATAAA 469		
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QY 470 GTATCAGTTAAACATGGGATGATTAATTTAATCTATTTTGTATTTTATGTCGGATGT 529  
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QY 530 AAAT-TATGTCCTTATCAATATAGGAATGGTGTAGGAATGCTCTACAAATATTAGTA 588  
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QY 589 GAATCCATTAAAGCAAGTGGATCAGGCCCTTTTGTATGTTGTCTCAGTTCTCCATCTCAAAG 648  
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QY 649 AGCTCTGTGTCAGCAATCTTTCCAAAGAAATTCCTATTTGGGTGAGAGTACTTCTTAG 708  
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QY 709 GTCCTCATTCACCTCTGCTGTGGCTTTCTCACCTCAACGTTTCTGAAAGTACTAGCA 768  
Db 1229 TCTCGTGCAGTCTGAC-----TCCTTCTCAGTCTAACGTTTCTGAAAGTATTAGCA 1283  
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Db 1284 ACTCAGAATATATTTTGAACCAATGATCAGTAGACATTAATAATATATAACAAATGCC- 1342  
QY 829 ATATTATAGTCACTTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACAT 888  
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QY 1198 AACCCCAAAACAAAGTCTAACTTTT-----1214  
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QY 1215 -----1214  
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Db 1805 ACATTTGCAAGATGCAATGGAACCAATTTTATACCTTGTGATTTATGCA-TTTT 1863  
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Db 1864 AAAATTTTCTCATTTAGACCACTGTCATTAAGAAAGTTTTCAGGAAATAGGCAC 1923  
QY 1317 ATTGAAGAACCAACTGCCACGGGGAGGCTGTGGATAAATACTATTCAAAACCTGTCTTT 1376  
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QY 1377 AATAAAGAACACATAGACGCCAAAGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1436  
Db 1984 AATAAAGAAATACATTTAGCGCCAAAGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2043  
QY 1437 ATATTTGTGACTCTGCTGCTGTTTTTTTTTTTTTTTTTTTTTTTAAAGAAATGACAGTTTCTTA 1496

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Db 2146 TAAACCAATTTCTAGACTACCTGCAAGAGTTTCTTGTGTTAATAAACACCGAGTGGATA 2205  
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Db 2206 TAGAAAGTTGAGACTAACTGTTTGTGACCCAAAGATTTTGGAG 2252

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LOCUS E13592 3230 bp DNA linear PAT 27-APR-1998  
DEFINITION gDNA encoding beta-cell differentiation factor, BCDF.  
ACCESSION E13592  
VERSION E13592.1 GI:3252397  
KEYWORDS JP 1997215496-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 3230)  
HONSHIYO, Y., Takatsu, K. and Eba, S.  
PRODUCTION OF HUMAN B CELL DIFFERENTIATION FACTOR  
Patent: JP 1997215496-A 2 19-AUG-1997;  
HONSHIYO YUU

COMMENT OS Homo sapiens (human)  
PN JP 1997215496-A/2  
PD 19-AUG-1997  
PF 21-SEP-1987 JP 1996206192  
PR 20-SEP-1986 JP 86P 223284  
PI HONSHIYO YUU, TAKATSU KIYOSHI, EBA SEBERINSON PC  
C12N15/09, A61K38/00, A61K38/00, A61K38/00, C07H21/04, C07K14/47, PC  
C12N5/10,  
PC C12P21/02, C12P21/02, C12R1:91);  
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CC topology: linear;  
CC hypothetical: No;  
CC anti-sense: No;  
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FEATURES  
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Query Match	36.1%	Score 599	DB 6	Length 3230
Best Local Similarity	67.8%	Pred. No. 7e-99		
Matches 1211	Conservative	0	Mismatches 385	Indels 191
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QY	61	TTGGGGTGGCTATGTTTCTGCTTTCCTGTAGAAAATCCCATGAATAGACTGGTGGCAG	120	
DB	587	TTGGAGCTGCCTACGTGTATGCCATCCCAACAGAAATCCCAACAGTCATTGCTGAAAG	646	
QY	121	AGACCTTGCACACTGCTCCACTCATCGAACTTCGGCTGATAGGCGATGGGGTAATTTTCT	180	
DB	647	AGACCTTGGCACTGCTTCTACTCATCGAACTCTGCTGATAGCCAAATGAGGTAATTTTCT	706	
QY	181	TTTTGATTCCTACAGTCTTTAAAAATGCATGGGTAAATGGTGGTGGCTAGTT-----	234	
DB	707	TTATGATTCCTACAGTCTGTAAGGTGCATAGGTAATCATTTGTGATGGTTCCTTACTAT	766	
QY	235	-TTTAAAGATCCATTCATATAATGAAGTAAGTAGTGTTAATAATAATATATATGGGTAAAC	293	
DB	767	ATATAGAGATCTGTTATATAATATAAGATTTCTGAG-CACATTAGTACATGGGTGATAACT	825	
QY	294	ATGTTACTCAGAAGAAATATATATAAGTTATGAACCTTCAATACATTAATAAATGAATG	353	
DB	826	ACATCACAGCAACATCTCTGTAAGAGTTATGAATGCTGGTGTGCTGTAATAAATGATTG	885	
QY	354	TTGTTTCTTCTTTTTCAGAACCTGATGATTCCTACTCCTCGAAAAATAAAATGTAAGTT	413	
DB	886	-TATTTCTTCTCTCCAGACTCTGAGGATTCCTGTTCTCTGTACATAAAAAATGTAAGTT	944	
QY	414	AAATTAGATTGTAATAAATGATTACATGAATCAG---TTTCATATTTTAAGCTATAAA	469	
DB	945	AAATTAGATTGTAATAAATGATGGCAATGAATAAGTAATAATTCCTGTTTAAAGCTGTA	1004	
QY	470	GTATCAGTTAACATTTGGGATGATTTAATTTTATCTATTTTGTGTTTATGCTGCGGATG	529	
DB	1005	TCATTAGTTATCATTTGGAACCTATTTAATTTTCTATATTTGTTTTCATATGGGTGGCTG	1064	
QY	530	AAAT-TATGTCTTATGAATATTAGGAATGGTGTTAGGAATGGCTCTACAAATTAAGTA	588	
DB	1065	GAATGCTGTACTTATATAATATGAGGAATGACTTT-----TTATCAAGTA	1109	
QY	589	GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGATGTTGTCTCAGTTCTCCATCTCAAAG	648	
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QY	649	AGCCTGCTGCAGGCATCTTTTCCAAAGAAATCCCATATTGGGTFCAGAGATATCTCTAG	708	
DB	1170	AGCATCGTGTGAG-ATTCTTTCCAGAAGGATTCACACTGAGTGAGAGGTGGTGTGCTAG	1228	
QY	709	GCTCCATTACCTCTGTCGTGGCTTTTCCCTCACCTCAACGTTTTTCTGGAAGTACTAGCA	768	
DB	1229	TCICCGTGCAGTCTGAC-----TCTTTTCTACCTCAACGTTTCTGGAAGTATTAGCA	1283	
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DB	1284	ACTCAGAATTATATTTTTAGAACCATGATCAGTAGAGCATTAATAATATATAACAAATGCC-	1342	
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QY	1069	ACACTTCTCAGTAATTATATAAAACATCATTTTAC--TTATGTGTAATTATAGCTTAGTATAAG	1127
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QY	1128	GTGTTTTCCACCTGGAAAAAGACACAGTAAAAACCTCTTTGGAGAAAGGGAACCTTGTGTA	1187
Db	1629	GTGTTTTGTTGCCCTAGAAA-----ACAAACAAAAAACTCTTTGGAGAGGGAACCTCATGTA	1684
QY	1188	AAACCCACAAAAAAGAGCTCTAACTTTT-----	1214
Db	1685	AATACCACAAAAAAGAGCCTTAACCTTTGTGGACCAAAATGCTTTTAATAATTAITTTTTAA	1744
QY	1215	-----	1214
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QY	1215	-----TGACCAAAATTTTTATGCTCTGTTTTTGATGAATTATATTTTT	1256
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QY	1257	TAAAACTTCCCTCATTTAGCACCAACTGTGCAATTAAGAAGTTTTTTTCAGSGTATAGACAC	1316
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QY	1317	ATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCCAAACTTGTCTTT	1376
Db	1924	ACTGGAGAGTCAAACTGTGCAAGGGGCTACTGTGGAAGNCTATTCAAAAACCTTGTCTTT	1983
QY	1377	AATAAAGAACACATAGAGCGCCAAAGTAAGTTAAAGACATTTGGCAAAAACCTTAAGT	1436
Db	1984	AATAAAGAAATACATTTGACGGCCAAAAAGTAAAGTTACACACATTCATGGAAGCTATATT	2043
QY	1437	ATAATTCGTCGACTCTGCCGTGTTTTTTTTTTTTTTTTTTTTTACAGAAGATTACAGCTTTCCCTA	1496
Db	2044	TGTCCTGGCTG-----TGCCATTTTCTATGGAATTGACAGTTTTCCTG	2085
QY	1497	CAATATCT-----CCTCTGTTCTTTTAAACAGAAAAAGGTGTGCAGAGAAAGATGGAGAG	1550
Db	2086	TAATACCTATTGTCAATTTTTTCTTTTTTTCAGAAAAAAGTGTGGAGAAAGAACCGCGAGAG	2145
QY	1551	TGCABAAGTTCCCTAGACTACCTGCAAGTATTTCTCTGCTGTATAAACAACCGAGTGGACAC	1610
Db	2146	TAAACCAATTCCTAGACTACTCTGCAAGAGTTTCTTGGTGAATGAACACCGAGTGGATAA	2205
QY	1611	CGGAAAGTTGAGAACAAACCGGCTTATTGTAGTGGGAAGATTTTTGGAG	1657
Db	2206	TAGAAAGTTTGAGACTAAAGTGGTTTCTTGTGAGCCAAAGATTTTTGGAG	2252

RESULT 14	HUM21DC94Z	HUM21DC94Z	3507 bp	DNA	linear	PRI 22-OCT-1995
LOCUS		Homo sapiens (subclone 6_e5 from Pl H21)				DNA sequence.
DEFINITION		L48478				
ACCESSION		L48478.1	GI:1032381			
VERSION						
KEYWORDS		interleukin gene cluster.				
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE		1 (bases 1 to 3507)				
AUTHORS		Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A.,				
		Ericsson,C.B., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M.,				
		Mayeda,C.A., Steiert-El Kheir,A. and Palazzolo,M.J.				
TITLE		Sequencing of the interleukin gene cluster of homo sapiens				
JOURNAL		Unpublished (1995)				
COMMENT		Original source text: Homo sapiens (tissue library: Subclones in				
		pOT2 from Pl clone H21) DNA.				
		This subclone overlaps H21 6 b10 and H21 6 b1.				

## Sequence submitted by:

Human Genome Center  
Lawrence Berkeley Laboratory  
Berkeley, CA 94720

e-mail: seq@genome.lbl.gov

The P1, from which this subclone is derived, is adjacent to P1  
(1857) and (5005).

## FEATURES

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/db\_xref="taxon:9606"  
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## ORIGIN

Query Match 29.6%; Score 490.6; DB 9; Length 3507;  
Best Local Similarity 66.9%; Pred. No. 3.1e-79;  
Matches 1061; Conservative 0; Mismatches 339; Indels 187; Gaps 18;

QY 201 AAAATGCATGGTAATTGGTGGTGGCTAGTT-----TTAAGATCCATTATCAA 253  
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QY 374 AACCTGATGATTCCTACTCCTGAAATATAAATGTAAGTTAAATATATATATATATAT 433  
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QY 434 GATTACATGATCAG-----TTTCATATTTAAGCTATAAAGTATCAGTTAAGATCGGAT 489  
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QY 549 ATTAGGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608  
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QY 609 TCAGGCCCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 668  
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QY 669 TTCCAAAGAAATCCATATGTTGGTCAGAGATACATTCCTAGGCTCCATTCACCTCTGTCGT 728  
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QY 729 TGGCTTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 788  
Db 521 ---TCCTTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 577  
QY 789 AATTATGTCAGTACATGAAATATACAGTGAAGTCCATATATATATATATATATATAT 848  
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QY 909 ATTAATAATGTTAAATAATGATATATATATATATATATATATATATATATATATAT 968  
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QY 969 TATACGAGAAATCTTGAGGTGAGTAAATCAGTAAGCGAGTGTGTTATATACCTCGTAAG 1028

Db 756 TGTAGAAACACAT--TGATATGAGTTTAAATGTTATAATGC-----ATTACACTTCCAAA 807  
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QY 1089 AAACATCATTTACTTATGGT-AAATTAGCTTATAGTTAGTTTCCACCTCGGAAAA 1147  
Db 868 AAGCTTCACTACTTTTGTAAATTTTATCTTAATATGTTGTTGTTGTTGTTGTTGTTGTT 926  
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Db 927 ---ACAAAACAAAACCTTTTGGAGAGGAACTCATGTAATACCAACAAACAAAGCCT 983  
QY 1208 AACTTT----- 1213  
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QY 1214 -----TTG 1216  
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QY 1217 GACCAAAATTTTATGCTTGTGTTTGAATCAATATATTTTAAATCTTCTCTCATTTAGC 1276  
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Db 1504 GGTGTTGTCAGCCAAAGATTTTGGAG 1530

RESULT 15  
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LOCUS Ovis aries interleukin-5 (IL5) gene, exons 1 and 2.  
DEFINITION OAILV1  
ACCESSION U17052  
VERSION U17052.1 GI:897558  
KEYWORDS  
SEGMENT 1 of 2  
SOURCE Ovis aries (sheep)  
ORGANISM Ovis aries  
REFERENCE 1 (bases 1 to 1140)  
AUTHORS Bryson,C.E., Viney,E., Brandon,M. and Boyd,A.W.  
TITLE Structure of the sheep interleukin-5 gene  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1140)

AUTHORS Bryson, C.E.  
TITLE Direct Submission  
JOURNAL Submitted (08-NOV-1994) Claire E. Bryson, Department of Veterinary  
Science, University of Melbourne, Flemington Rd., Parkville,  
Victoria, 3052, Australia

## FEATURES

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number=1  
exon  
824..856  
/gene="IL5"  
number=2

## ORIGIN

Query Match 21.0%; Score 347.4; DB 4; Length 1140;  
Best Local Similarity 76.8%; Pred. No. 3.6e-53;  
Matches 529; Conservative 0; Mismatches 121; Indels 39; Gaps 7;  
QY 1 AGCAAACACTGACATTTGAGAGCTATGAGAAATGCTTCTGAATTGAGTTGCTAGCTC 60  
Db 438 AGCAAACGCTGAACATTTGAGAGCTAGAGAAATGCTTCTGAATTGAGTTGCTAGCTC 497  
QY 61 TTGGGCTGCTATGTTCTGCTTGTGTAAGAAATCCCATGAATAGACTGGTGGCAG 120  
Db 498 TTGGAGCTGCTATGTTGCTGCAATGCTGTGAAGATGCTGTAAGATGCTGTTGGCAG 557  
QY 121 AGACCTTGACATGCTCTCCACTCATCGAACTTGGCTGATAGCGGATGGGTAATTTCT 180  
Db 558 AGACCTTGACATGCTCTCCAGCATCAAACTCTGCTGATAGTGTGATGGGTAATTTCT 617  
QY 181 TTTTGATTCCTACAGCTTTTAAATGCATGGTAATTGGTGGTGGTGGTGGTGGTGGTGGT 240  
Db 618 TTTTGATTCCTACAGCTTTTAAATATATAGCTAATCATTTGGTGGTGGTGGTGGTGGT 677  
QY 241 GATCCATTAATCAATAATGAATGAATGATGTTAATAAT-----ATATAATG 286  
Db 678 GATCTGCTATTAGTCATGAATTTGCTGATGATGATGATGATGATGATGATGATGATGAT 737  
QY 287 GGTAAACATGTTACTCAGAGAAATATATATAAGTTATGACCTTACAAATACATTAATA 346  
Db 738 GGTAAACATACAACTAGCAAGCATTTTACTTAAACTTACGAGTGTAGAGTGGCTTTAA 797  
QY 347 ATGAATGTTGTTCTCTTTCTTTTTCAGAACCTGATGATTCCTACTCTGAAAATAAAAT 406  
Db 798 ATGAATG-TAATTCCTTTCTTTTTCAGAACCTGATGATTCCTACTCTGAGCATCAAT 856  
QY 407 GTAAGTTAAATTAAGTTTGAATAAATGATACATGAATCAG---TTTCATATTTTAAG 462  
Db 857 GTAAGTTAAATCATGATTTGATAAATGATGATGATGATGATGATGATGATGATGATGAT 916  
QY 463 CTATTAAGTATCAGTTAACTGGGATGATTAATTTATCTATTTTGTGTTTGTGTTGTTG 522  
Db 917 CTATAAAGCA-AAGTTATCTACTGATGATTTACTTTTCTCCATTTGTTTTTATATAG 975  
QY 523 CGGAT-GTAAATATGCTTATGAATATGGAATGGTGTAGGAATGGCTCTCAATA 581  
Db 976 TGAATACAAAAGTATGATTTAAATAATTAAGATGACTTT-----ATA 1020  
QY 582 TTAAGTAAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGATGTTGTGATTCCTCAT 641  
Db 1021 ACAAGTAAATCCATTAAGCAAGTGGATCAGGCC---TCTGTTGATGTCAGTTCTACAT 1077  
QY 642 CTCAGAGGCTGCTGTCAGGCAATCTTT 670  
Db 1078 TTCAGAGGCTTGAGTCAGGCAATCTTT 1106

Search completed: August 31, 2004, 01:25:54  
Job time : 7179.07 secs

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Sequence 2813, Appl  
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Sequence 288, Appl  
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Sequence 5, Appl  
Sequence 11, Appl  
Sequence 3, Appl  
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Sequence 1, Appl

Sequence 1, Appli

Sequence 73, Appl  
Sequence 153, App  
Sequence 87, Appl

Sequence 288, App  
Sequence 4, Appli  
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Sequence 11, Appl

Sequence 3, Appli  
Sequence 5, Appli  
Sequence 1, Appli

Sequence 1, Appli

5 SIGNAL

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s 191; Gaps 19  
GAGTTTGTAGCTC 60  
GAGTTTGTAGCTC 586  
ATGACTGTGGCAG 120  
ATGCATTGGTAAAG 646  
TGGGTAAATTTTCT 180  
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TGGTAGTT----- 234  
GGTTCCTTACTAT 766  
TATAATGGGTAAAC 293  
TCATGGGTGATAACT 825  
ATATAAAATGAATG 353  
TGTAAAAATGATTG 885  
TAAAAATCTAAGTT 413



QY 470 GTATCAGTTACATGGGATGATTTAAATTTATCTATTTTGTGTTTATGTTGCGGATGT 529  
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QY 1005 TCATTAGTATCATTTGAACATTTAAATTTTCATATTTTGTTCATATGGGTGGCTGT 1064  
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QY 530 AAAT-TATGTCCTTATGAATATTAGGAATGGTGTAGGAATGGCTACAAATATTAAAGTA 588  
Db |||||  
QY 1065 GAATGTCTGTACTTATAAATATGAGGAATGACTTT-----TTATCAAGTA 1109  
Db |||||  
QY 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGTGATTTGTGAGTTCTCCATCTCAAG 648  
Db |||||  
QY 1110 GAATCCCTTTAAACAAGTGGATAGGCTCTTTGGTGATGTTGTAGTTTGGCTTTCCCAAG 1169  
Db |||||  
QY 649 AGCTCGTGTGAGGATCTTTTCCAAAAGAAATCCATATTTGGTTCAGAGATACCTTCTAG 708  
Db |||||  
QY 1170 AGCATGTGTGAGG-ATTCCTTCCAGAGGATTTCCACACTGAGTGAGAGTGGTGTAG 1228  
Db |||||  
QY 709 GTCCCATTCACCTGTGCTGGTGGCTTTCCCTCACCTCACTGCTTTTCTGAAAGTACTAGCA 768  
Db |||||  
QY 1229 TCTCCGTCGAGTTCTGAC-----TCTTCTCACTCAACGTGTCTTCTGAAAGTATTAGCA 1283  
Db |||||  
QY 769 ACTTGGGCTTATATTTTAGAATTTATGCTCAGTAGACATGAAATATACAGTCAAGTCT 828  
Db |||||  
QY 1284 ACTCAGAAATATTATTTTAGACATGATCAGTAGACATTTAAATATATACAAATGCC- 1342  
Db |||||  
QY 829 ATATTAATAGTACTCCACATATTTAAATGATTTTAACTCTAAATGGAATCATATACAT 888  
Db |||||  
QY 1343 --CTATATTAATAATCTGCATACCTTAATAATATGACTATATGATGTTGTGTATGCAT 1400  
Db |||||  
QY 889 CTGAGTATGTCATGTCATATTAATGATTTAAATGTCATATCATCTAGTCTAAATAGA 948  
Db |||||  
QY 1401 TGAATAG-----CTGGTCATATTAATAAGTAAATATATATAGTTT-ATTAGTCTAAATAGA 1456  
Db |||||  
QY 949 ATAAATACCAGTAGAACTATACGAGGAAATCTGAGGTGAGGTAATCAGTAAGGCA 1008  
Db |||||  
QY 1457 ATAAACTACCAGTAGAACTATGAGAACACAT-IGATATGAGTTTAAATGATATGTC- 1513  
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QY 1009 GTTGTATATACCTCGTAAGCATTTATTTTCAATTAATCATTTTCAATTTATCATTTGTA 1068  
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QY 1514 -----ATTACACTTCCAAACATTTTTTCCAGTTACATAATTAAGTTATATCCITTTATA 1568  
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QY 1069 ACACCTCTCAGTAATATATAACATCATTTAC-TTATGTTAATTTAGCTTAGTATAAG 1127  
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QY 1569 AAACCTCTCAGTAATATATAAGTTCATCTACTTTTGGAAATTTTATCTTAATATG 1628  
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QY 1128 GTGGTTTCCACCTGGAAAAGACACAGTAAACCTTTTGGAGAGGAACTTGTGTA 1187  
Db |||||  
QY 1629 GTGGTTTGTGCTAGAAA-----ACAAACAAAACCTTTTGGAGAGGAACTCATGTA 1684  
Db |||||  
QY 1188 AACCCCAAAACAAAGTCTAACTTTT----- 1214  
Db |||||  
QY 1685 AATACCAAAACAAAGCCTTAACCTTTTGTGACCAAAATGTTTTTAATAATTTATTTTAA 1744  
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QY 1215 ----- 1214  
Db |||||  
QY 1745 TTGATGAATTAAGATATATATTTATTGTGTACAAATATGATGTTTGAAGTATGAT 1804  
Db |||||  
QY 1215 -----TGACCAAAATTTTATGCTTGTGTTTGTAGTAATTAATTTT 1256  
Db |||||  
QY 1805 ACATTGAGAAATGACAAATGACCAAAATTTTATACCTTGTCTGTGATTTTGA-TTTT 1863  
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QY 1257 TAAATCTCTCATTTTAGCAACCACTGTGCATTTAAAGAGTTTTCAGGGTATAGACAC 1316  
Db |||||  
QY 1864 AAAAAATTTCTCATTTTAGCAACCACTGTGCATGGAAGATCTTTTTCAGGGAATAGGCAC 1923  
Db |||||  
QY 1317 ATTGAAGAACAACTCCCAAGGGAGGCTGTGGATAAACTATTTCCAAACTGTGCTTT 1376  
Db |||||  
QY 1924 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAACTATTTCAAAACTGTGCTTT 1983  
Db |||||  
QY 1377 AATAAAGAAACACATAGAGCGCAAAAGTAAGTTAAAGACATTTTGGCAAACTTAAGT 1436  
Db |||||  
QY 1984 AATAAAGAAATACATTTGACGCGCAAAAGTAAGTTTACACATTTCAATGGAAGCTATAT 2043  
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QY 1437 ATATTTGTGACTGTGCTGCTTTT-----TTTTTTTATCAAGAAATGACAGTTTCTCTA 1496  
Db |||||

Db 2044 TGTCTGGCTG-----TGCTATTTCTATGGAATTGACAGTTTCTGT 2085  
QY 1497 CAATATCT-----CCTCTGTTCTTTTAAACAGAAAAGTGTGCGAGAGAAAGATGGAG 1550  
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QY 2086 TAATACCTATTGTCTATTTTCTTTTTCACAGAAAAGTGTGGAGAAAGACGAGAG 2145  
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QY 2146 TAAACCAATTTCTAGACTACCTGCAAGAGTTTCTTGGTGTAAATAAACACCGAGTGGATAA 2205  
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QY 1611 CGGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAG 1657  
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QY 2206 TAAAGAGTTGAGACTAAACTGTTTGTGACGCCAAAGATTTTGGAG 2252  
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## RESULT 3

US-09-322-409-80  
; Sequence 80, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)...(430)  
US-09-322-409-80

Query Match 10.4%; Score 171.8; DB 4; Length 610;  
Best Local Similarity 93.7%; Pred. No. 6.4e-31;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGGCAAAACACTGAAACATTTTCAGAGCTATGAGAATGCTTCTGAATTTGAGTTTGTAGCTC 60  
Db |||||  
QY 3 AGGCAAAACACTGAAACATTTTCAGAGCTATGAGAATGCTTCTGAATTTGAGTTTGTAGCTC 62  
Db |||||  
QY 61 TTGGGCTGCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120  
Db |||||  
QY 63 TTGGGCTGCTATGTTTCTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 122  
Db |||||  
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGCGATGGGGTAATTTTCT 180  
Db |||||  
QY 123 AGACCTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGCGATGGGAACTGATGA 182  
Db |||||  
QY 181 TTTTGAATTCCT 191  
Db |||||  
QY 183 TTCTACTTCTCT 193  
Db |||||

## RESULT 4

US-09-322-409-82/c  
; Sequence 82, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.

;; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
;; FILE REFERENCE: IM-2-C1

;; CURRENT APPLICATION NUMBER: US/09/322,409

;; CURRENT FILING DATE: 1999-05-28

;; EARLIER APPLICATION NUMBER: 60/087,306

;; EARLIER FILING DATE: 1998-05-29

;; NUMBER OF SEQ ID NOS: 154

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 82

;; LENGTH: 610

;; TYPE: DNA

;; ORGANISM: Canis familiaris

US-09-322-409-82

Query Match 10.4%; Score 171.8; DB 4; Length 610;  
Best Local Similarity 93.7%; Pred. No. 6.4e-31;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTCAGTTTGTCTAGCTC 60

Db 608 AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTCAGTTTGTCTAGCTC 549

Qy 61 TTGGGGTGGCTATGTTTCTGCTTCCCTAGAGAAATCCCATGAATAGACTGGTGGCAG 120

Db 548 TTGGGGTGGCTATGTTTCTGCTTCCCTAGAGAAATCCCATGAATAGACTGGTGGCAG 489

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGTAATTTTCT 180

Db 488 AGACCTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGTAATTTTCT 429

Qy 181 TTTTGATTCCT 191

Db 428 TTCCTACTCCT 418

## RESULT 5

US-09-451-527-80

;; Sequence 80, Application US/09451527

;; Patent No. 6482403

;; GENERAL INFORMATION:

;; APPLICANT: Sim, Gek-Ke

;; APPLICANT: Yang, Shumin

;; APPLICANT: Dreitz, Matthew J.

;; APPLICANT: Wonderling, Ramani S.

;; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

;; FILE REFERENCE: IM-2-C2

;; CURRENT APPLICATION NUMBER: US/09/451,527

;; CURRENT FILING DATE: 1999-12-01

;; EARLIER APPLICATION NUMBER: 09/322,409

;; EARLIER FILING DATE: 1999-05-28

;; EARLIER APPLICATION NUMBER: 60/087,306

;; EARLIER FILING DATE: 1998-05-29

;; NUMBER OF SEQ ID NOS: 174

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 80

;; LENGTH: 610

;; TYPE: DNA

;; ORGANISM: Canis familiaris

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (29)..(430)

US-09-451-527-80

Query Match 10.4%; Score 171.8; DB 4; Length 610;  
Best Local Similarity 93.7%; Pred. No. 6.4e-31;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTCAGTTTGTCTAGCTC 60

Db 3 AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTCAGTTTGTCTAGCTC 62

Qy 61 TTGGGGTGGCTATGTTTCTGCTTCCCTAGAGAAATCCCATGAATAGACTGGTGGCAG 120

Db 63 TTGGGGTGGCTATGTTTCTGCTTCCCTAGAGAAATCCCATGAATAGACTGGTGGCAG 122

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGTAATTTTCT 180

Db 123 AGACCTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGTAATTTTCT 182

Qy 181 TTTTGATTCCT 191

Db 183 TTCCTACTCCT 193

## RESULT 6

US-09-451-527-82/c

;; Sequence 82, Application US/09451527

;; Patent No. 6482403

;; GENERAL INFORMATION:

;; APPLICANT: Sim, Gek-Ke

;; APPLICANT: Yang, Shumin

;; APPLICANT: Dreitz, Matthew J.

;; APPLICANT: Wonderling, Ramani S.

;; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

;; FILE REFERENCE: IM-2-C2

;; CURRENT APPLICATION NUMBER: US/09/451,527

;; CURRENT FILING DATE: 1999-12-01

;; EARLIER APPLICATION NUMBER: 09/322,409

;; EARLIER FILING DATE: 1999-05-28

;; EARLIER APPLICATION NUMBER: 60/087,306

;; EARLIER FILING DATE: 1998-05-29

;; NUMBER OF SEQ ID NOS: 174

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 82

;; LENGTH: 610

;; TYPE: DNA

;; ORGANISM: Canis familiaris

US-09-451-527-82

Query Match 10.4%; Score 171.8; DB 4; Length 610;  
Best Local Similarity 93.7%; Pred. No. 6.4e-31;  
Matches 179; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTCAGTTTGTCTAGCTC 60

Db 608 AGGCAACACTGAACATTTTCAGAGCTATGAGAAATGCTTCTGAAATTCAGTTTGTCTAGCTC 549

Qy 61 TTGGGGTGGCTATGTTTCTGCTTCCCTAGAGAAATCCCATGAATAGACTGGTGGCAG 120

Db 548 TTGGGGTGGCTATGTTTCTGCTTCCCTAGAGAAATCCCATGAATAGACTGGTGGCAG 489

Qy 121 AGACCTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGTAATTTTCT 180

Db 488 AGACCTTGACACTGCTCTCCACTCATCGAATTCGGCTGATAGGCGATGGGTAATTTTCT 182

Qy 181 TTTTGATTCCT 191

Db 428 TTCCTACTCCT 418

## RESULT 7

US-09-322-409-83

;; Sequence 83, Application US/09322409

;; Patent No. 6471957

;; GENERAL INFORMATION:

;; APPLICANT: Sim, Gek-Ke

;; APPLICANT: Yang, Shumin

;; APPLICANT: Dreitz, Matthew J.

;; APPLICANT: Wonderling, Ramani S.

;; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC

;; FILE REFERENCE: IM-2-C1

;; CURRENT APPLICATION NUMBER: US/09/322,409

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; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-83

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 191
Db 121 CGAACTTGGCTGATAGCGATGGGAACCTGATCTTCTACTCCT 165

RESULT 8
US-09-322-409-84/c
; Sequence 84, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-84.

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 342 GCTGTAGAAAATCCCATGATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGATGGGTAATTTCTTTTGTATTCCT 191
Db 282 CGAACTTGGCTGATAGCGATGGGAACCTGATGATCTTCTACTCCT 238

RESULT 9
US-09-451-527-83
; Sequence 83, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-84.

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 343

; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-83.

Query Match      8.8%; Score 145.8; DB 4; Length 402;
Best Local Similarity 92.7%; Pred. No. 6.1e-25;
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 86
Db 402 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTTGGGGCTGCTATGTTTCTGCTTT 343
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Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTTGCTCTCCACTCAT 146  
Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTTGCTCTCCACTCAT 283  
Qy 147 CGAATTGGCTGATAGCGGATGGGTAAATTTCTTTTGATTCCT 191  
Db 282 CGAATTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCCT 238

## RESULT 11

US-09-371-615A-1  
; Sequence 1, Application US/09371615A  
; Patent No. 6537781  
; GENERAL INFORMATION:  
; APPLICANT: IDEXX LABORATORIES  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING  
; FILE REFERENCE: CANINE INTERLEUKIN 5  
; FILE REFERENCE: 03604001700US00  
; CURRENT APPLICATION NUMBER: US/09/371,615A  
; CURRENT FILING DATE: 1999-08-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 405  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-371-615A-1

Query Match 8.8%; Score 145.8; DB 4; Length 405;  
Best Local Similarity 92.7%; Pred. No. 6.1e-25;  
Matches 153; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 27 ATGAGATGCTTCTGAATTTGACTTTGCTAGCTCTTGGGCTGCCATGTTCTGCTTT 86  
Db 1 ATGAGATGCTTCTGAATTTGACTTTGCTAGCTCTTGGGCTGCCATGTTCTGCTTT 60  
Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTTGCTCTCCACTCAT 146  
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTTGCTCTCCACTCAT 120  
Qy 147 CGAATTGGCTGATAGCGGATGGGTAAATTTCTTTTGATTCCT 191  
Db 121 CGAATTGGCTGATAGCGGATGGGAACCTGATGATTCCTACTCCT 165

## RESULT 12

US-09-322-409-85  
; Sequence 85, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Ke  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-09-322-409-85

Query Match 7.9%; Score 131.6; DB 4; Length 345;

Best Local Similarity 97.1%; Pred. No. 1.1e-21;  
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1274 AGCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGGAAGAACCAAACTG 1333  
Db 119 ATCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGGAAGAACCAAACTG 178  
Qy 1334 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGTCTTTTAATAAAGAACACATAG 1393  
Db 179 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGTCTTTTAATAAAGAACACATAG 238  
Qy 1394 AGCGCCAAAAGTAAGTT 1411  
Db 239 AGCGCCAAAAGTAAGTT 256

## RESULT 13

US-09-322-409-87/C  
; Sequence 87, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Ke  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-322-409-87

Query Match 7.9%; Score 131.6; DB 4; Length 345;  
Best Local Similarity 97.1%; Pred. No. 1.1e-21;  
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1274 AGCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGGAAGAACCAAACTG 1333  
Db 227 ATCACCAACTGTGCATTAAAGAGCTTTTTCAGGGTATAGACACATTGGAAGAACCAAACTG 168  
Qy 1334 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGTCTTTTAATAAAGAACACATAG 1393  
Db 167 CCCACGGGGAGGCTGTGATAAACTATTCACAAAACCTTGTCTTTTAATAAAGAACACATAG 108  
Qy 1394 AGCGCCAAAAGTAAGTT 1411  
Db 107 AGCGCCAAAAGTAAGTT 90

## RESULT 14

US-09-451-527-85  
; Sequence 85, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Ke  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28

; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 85  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(345)  
US-09-451-527-85

Query Match 7.9%; Score 131.6; DB 4; Length 345;  
Best Local Similarity 97.1%; Pred. No. 1.1e-21;  
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1274 AGCACCACCTGTCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAACTG 1333  
DB 119 ATCACCACCTGTCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAACTG 178  
QY 1334 CCCACGGGGAGGCTGGGATAAATACTATCCAAAACCTGTCTTTAATAAAGAACACATAG 1393  
DB 179 CCCACGGGGAGGCTGGGATAAATACTATCCAAAACCTGTCTTTAATAAAGAACACATAG 238  
QY 1394 AGCGCCAAAAGTAAGTT 1411  
DB 239 AGCGCCAAAAGTAAGTT 256

RESULT 15  
US-09-451-527-87/c  
; Sequence 87, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kea  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; EARLIER FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 87  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-451-527-87

Query Match 7.9%; Score 131.6; DB 4; Length 345;  
Best Local Similarity 97.1%; Pred. No. 1.1e-21;  
Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1274 AGCACCACCTGTCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAACTG 1333  
DB 227 ATCACCACCTGTCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCAACTG 168  
QY 1334 CCCACGGGGAGGCTGGGATAAATACTATCCAAAACCTGTCTTTAATAAAGAACACATAG 1393  
DB 167 CCCACGGGGAGGCTGGGATAAATACTATCCAAAACCTGTCTTTAATAAAGAACACATAG 108  
QY 1394 AGCGCCAAAAGTAAGTT 1411  
DB 107 AGCGCCAAAAGTAAGTT 90

Search completed: August 31, 2004, 06:34:51  
Job time : 151.928 secs

Blank Sheet



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 13:00:28 ; Search time 4443 Seconds  
(without alignments)  
11143.708 Million cell updates/sec

Title: US-10-787-382-18

Perfect score: 1658

Sequence: 1 agcacaactgaacatttc.....gtagtgaagatttggaga 1658

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_man.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	389	23.5	622	29	CE331159 tigr-gss-
2	29	1.7	528	13	EX493336 DKFZp781I
3	28	1.7	556	13	EX467653 BX467653
4	28	1.7	684	14	CB076419 hf42h04.g

5	28	1.7	915	10	BE897924
6	27	1.6	522	9	AL370520
7	27	1.6	534	9	AW102086
8	27	1.6	559	13	BU571592
9	27	1.6	614	14	CA429123
10	27	1.6	687	14	CB824053
11	27	1.6	720	14	CD038829
12	27	1.6	818	29	CNS04725
13	26	1.6	114	14	CB972911
14	26	1.6	114	14	CD407086
15	26	1.6	120	10	BE153390
16	26	1.6	140	12	BQ022057
17	26	1.6	145	12	BM710374
18	26	1.6	202	10	AW524394
19	26	1.6	206	9	AA475329
20	26	1.6	271	12	BG651868
21	26	1.6	273	13	BQ156344
22	26	1.6	287	12	BG157100
23	26	1.6	299	9	AL836569
24	26	1.6	299	9	AL836604
25	26	1.6	322	12	BI708412
26	26	1.6	352	10	BE474681
27	26	1.6	363	13	BU700148
28	26	1.6	371	12	BI299610
29	26	1.6	390	13	BU759812
30	26	1.6	411	9	AI274359
31	26	1.6	415	12	BI301007
32	26	1.6	418	14	CD424543
33	26	1.6	426	10	AW124901
34	26	1.6	426	10	BE687063
35	26	1.6	428	14	R68705
36	26	1.6	429	12	BI376645
37	26	1.6	431	10	BF465903
38	26	1.6	440	14	CA894542
39	26	1.6	441	9	AA028711
40	26	1.6	441	9	AI716899
41	26	1.6	441	14	CA830267
42	26	1.6	443	14	CB250412
43	26	1.6	446	9	AU183176
44	26	1.6	453	12	BG374060
45	26	1.6	455	12	BG377615

#### ALIGNMENTS

RESULT 1  
CE331159  
LOCUS  
DEFINITION  
tigr-gss-dog-17000333986568 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION  
CE331159  
VERSION  
CE331159.1  
KEYWORDS  
GSS:  
Canis familiaris (dog)  
Canis familiaris  
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE  
1 (bases 1 to 622)  
Kirknes, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, M., Fraser, C.W. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
JOURNAL  
MEDLINE  
22875432  
PUBMED  
14512627  
COMMENT  
Contact: Kirknes EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org

Class: shotgun.  
 Location/Qualifiers  
 1. 622  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 23.5%; Score 389; DB 29; Length 622;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-66;  
 Matches 389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1270 ATTTAGCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAGAACCAA 1329  
 Db ATTTAGCACCACCTGTCATTAAAGAGTTTTCAGGGTATAGACACATTGAGAACCAA 95

QY 1330 ACTGCCACCGGGAGGCTGGATAACTATTCACAACTTGTCTTAATAAAGAACAC 1389  
 Db ACTGCCACCGGGAGGCTGGATAACTATTCACAACTTGTCTTAATAAAGAACAC 155

QY 1390 ATAGAGCGCCAAAGTAAGTAAAGACATTTCGCAAAACTTAAGTATATTTGCTGAC 1449  
 Db ATAGAGCGCCAAAGTAAGTAAAGACATTTCGCAAAACTTAAGTATATTTGCTGAC 215

QY 1450 TCTGCTGTTTTTTTTTTTTTTTACAAAGATTGACAGTTTCTTACAAATATCTCTCT 1509  
 Db TCTGCTGTTTTTTTTTTTTTTTACAAAGATTGACAGTTTCTTACAAATATCTCTCT 275

QY 1510 GTTCTTTTACAGAAAAGGTGCGAGGAGAAAGATGAGAGTGCACAAAGTTCCTAGACTA 1569  
 Db GTTCTTTTACAGAAAAGGTGCGAGGAGAAAGATGAGAGTGCACAAAGTTCCTAGACTA 335

QY 1570 CTTCAAGTATTTCTTGGTGTAAATAACACCGAGTGCACACCGGAAGTTGAGAACAAAC 1629  
 Db CTTCAAGTATTTCTTGGTGTAAATAACACCGAGTGCACACCGGAAGTTGAGAACAAAC 395

QY 1630 CGGCTTATGAGTGGAGAGATTGAGGA 1658  
 Db CGGCTTATGAGTGGAGAGATTGAGGA 424

RESULT 2  
 BX493336  
 LOCUS  
 DEFINITION DKFZP7811243\_s1 781 (synonym: hicc4) Homo sapiens cDNA clone  
 DKFZP7811243\_3', mRNA sequence.

ACCESSION BX493336  
 VERSION BX493336.1 GI:32005734  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 528)  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fob, G., Han, M. and Wiemann, S.  
 EST (Bioecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.)  
 Unpublished (2003)  
 Contact: MIPS

MIPS  
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
 This is the 3' sequence of the clone insert.  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
 sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
 r1 sequence also available.  
 This clone (DKFZP7811243) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
 source  
 Location/Qualifiers  
 1. 528  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="DKFZP7811243"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="781 (synonym: hicc4)"  
 /note="Vector: pSport1\_Sfi; Site\_1: SfiI; Site\_2: SfiI; CDNA-collection"

ORIGIN

Query Match 1.7%; Score 29; DB 13; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1456 TGTGTTTTTTTTTTTTTTTACAGAATT 1484  
 Db TGTGTTTTTTTTTTTTTTTACAGAATT 29

RESULT 3  
 BX467653/c  
 LOCUS  
 DEFINITION BX467653 NAPI Anopheles gambiae cDNA clone NAPI-Pl26-D-10-5, mRNA  
 sequence.  
 ACCESSION BX467653  
 VERSION BX467653.1 GI:31658594  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae

REFERENCE 1 (bases 1 to 556)  
 AUTHORS Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouch, R., Benes, V. and Kafatos, F.C.  
 TITLE Anopheles gambiae EST, European Molecular Biology Laboratory  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Christophides GK  
 Fotis C. Kafatos Laboratory  
 European Molecular Biology Laboratory  
 Meyerhofstrasse 1, 69117 Heidelberg, Germany  
 Tel: +49 6221 387-440  
 Fax: +49 6221 387-306  
 Email: christophe@mbi-heidelberg.de  
 Contact: Christophides G.K.  
 European Molecular Biology Laboratory  
 Meyerhofstr. 1, 69117 Heidelberg, Germany.  
 Tel: +49 6221 387-440  
 Fax: +49 6221 387-306  
 Email: christophe@mbi-heidelberg.de  
 Plate: Pl26 row: D column: 10.  
 Location/Qualifiers  
 1. 556  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7165"  
 /clone="NAPI-Pl26-D-10-5"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAPI"  
 /note="Vector: pT7T3D-Pac (Pharmacia); Site 1: NotI; Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAPI is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 1.7%; Score 28; DB 13; Length 556;  
Best Local Similarity 100.0%; Pred. No. 9e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1452 TGCGTGTGTTTTTTTTTTTTTTTACAA 1479  
|||||  
Db 552 TGCGTGTGTTTTTTTTTTTTTTTACAA 525  
|||||

RESULT 4  
CB076419/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CB076419 684 bp mRNA linear EST 24-JAN-2003  
hf42h04.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis  
terminalis cDNA clone hf42h04, mRNA sequence.

CB076419  
EST.  
CB076419.1 GI:27889856  
Hedyotis terminalis  
Hedyotis terminalis  
Hedyotis terminalis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Gentianales; Rubiaceae; Rubioideae;  
Spermacoceae; Hedyotis.  
1 (bases 1 to 684)  
Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,  
O'Shaughnessy, A.L., Ballija, V., Martensen, R.A., McCombie, R.W.,  
Benfey, P. and Stevenson, D.  
Expressed tag sequences from Hedyotis terminalis flower - Stage 2  
(NYBG)  
Unpublished (2003)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcombie@cshl.org  
Plate: hf42 row: h column: 04  
Seq primer: -21M13UnivRev  
High quality sequence rev: 684.  
High quality sequence stop: 684.  
Location/Qualifiers  
1..684  
/organism="Hedyotis terminalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:219667"  
/clone="hf42h04"  
/dev\_stage="pre-anthesis; Stage 2"  
/clone\_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"  
/note="Organ: flower; Vector: pBK-CMV; Site: 1: XhoI;  
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to  
CGH 12/21/01 Library: Stratagene ZAP Express cDNA  
Synthesis Kit. The library was size-fractionated to enrich  
for large inserts. Sample: collected on the island of  
Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN

Query Match 1.7%; Score 28; DB 14; Length 684;  
Best Local Similarity 100.0%; Pred. No. 7.3e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTTTACAGATTG 1485  
|||||  
Db 620 TTTTITTTTTTTTTTTTTTTTACAGATTG 593  
|||||

RESULT 5  
BE997924

LOCUS  
DEFINITION  
ACCESSION

BE997924 915 bp mRNA linear EST 20-OCT-2000  
601440409F1 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:3925155 5',  
mRNA sequence.

ORIGIN

Query Match 1.7%; Score 28; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTTTACAGATTG 1485  
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Db 21 TTTTITTTTTTTTTTTTTTTTACAGATTG 48  
|||||

RESULT 6  
AL370520/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL370520 522 bp mRNA linear EST 03-AUG-2000  
MCBA38C10R1 McBA Medicago truncatula cDNA clone McBA38C10 T7, mRNA  
sequence.  
AL370520  
AL370520.1 GI:9670273  
EST.  
Medicago truncatula (barrel medic)  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 522)  
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,  
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D.,  
Gianinazzi-Pearson, V. and Gamas, P.  
Medicago truncatula ESTs from nitrogen-starved roots  
Unpublished (2000)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de  
Biologie Molculaire des Relations Plantes-Microorganismes,  
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:  
MT-est@toulouse.inra.fr Website: )

ORIGIN

Query Match 1.7%; Score 28; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTTTACAGATTG 1485  
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Db 21 TTTTITTTTTTTTTTTTTTTTACAGATTG 48  
|||||

RESULT 6  
AL370520/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL370520 522 bp mRNA linear EST 03-AUG-2000  
MCBA38C10R1 McBA Medicago truncatula cDNA clone McBA38C10 T7, mRNA  
sequence.  
AL370520  
AL370520.1 GI:9670273  
EST.  
Medicago truncatula (barrel medic)  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 522)  
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,  
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D.,  
Gianinazzi-Pearson, V. and Gamas, P.  
Medicago truncatula ESTs from nitrogen-starved roots  
Unpublished (2000)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de  
Biologie Molculaire des Relations Plantes-Microorganismes,  
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:  
MT-est@toulouse.inra.fr Website: )

ORIGIN

Query Match 1.7%; Score 28; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTTTACAGATTG 1485  
|||||  
Db 21 TTTTITTTTTTTTTTTTTTTTACAGATTG 48  
|||||

RESULT 6  
AL370520/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL370520 522 bp mRNA linear EST 03-AUG-2000  
MCBA38C10R1 McBA Medicago truncatula cDNA clone McBA38C10 T7, mRNA  
sequence.  
AL370520  
AL370520.1 GI:9670273  
EST.  
Medicago truncatula (barrel medic)  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 522)  
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,  
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D.,  
Gianinazzi-Pearson, V. and Gamas, P.  
Medicago truncatula ESTs from nitrogen-starved roots  
Unpublished (2000)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de  
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CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:  
MT-est@toulouse.inra.fr Website: )

ORIGIN

Query Match 1.7%; Score 28; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTTTACAGATTG 1485  
|||||  
Db 21 TTTTITTTTTTTTTTTTTTTTACAGATTG 48  
|||||

RESULT 6  
AL370520/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL370520 522 bp mRNA linear EST 03-AUG-2000  
MCBA38C10R1 McBA Medicago truncatula cDNA clone McBA38C10 T7, mRNA  
sequence.  
AL370520  
AL370520.1 GI:9670273  
EST.  
Medicago truncatula (barrel medic)  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 522)  
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,  
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D.,  
Gianinazzi-Pearson, V. and Gamas, P.  
Medicago truncatula ESTs from nitrogen-starved roots  
Unpublished (2000)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de  
Biologie Molculaire des Relations Plantes-Microorganismes,  
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:  
MT-est@toulouse.inra.fr Website: )

ORIGIN

Query Match 1.7%; Score 28; DB 10; Length 915;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTTTTTACAGATTG 1485  
|||||  
Db 21 TTTTITTTTTTTTTTTTTTTTACAGATTG 48  
|||||

RESULT 6  
AL370520/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL370520 522 bp mRNA linear EST 03-AUG-2000  
MCBA38C10R1 McBA Medicago truncatula cDNA clone McBA38C10 T7, mRNA  
sequence.  
AL370520  
AL370520.1 GI:9670273  
EST.  
Medicago truncatula (barrel medic)  
Medicago truncatula  
Eukaryota;



	normalized according to Bonaldo, Lennon and Soares, Genomew Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pV773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag (dT)18 tail. The sequence tag for this library is AGAAATCCGGC. The cell line was provided by Dr. James Martin from the University of Iowa.
	TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1 Chondrosarcoma
	TAG_LIB=UI-H-FH1
	TAG_SEQ=AGAATCCGGC"
ORIGIN	
Query Match	1.6%; Score 27; DB 14; Length 614;
Best Local Similarity	100.0%; Pred. No. 1.3e+04;
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1458 TTTTITTTTTTTTTTTTACAGAATT 1484
Db	1 TTTTITTTTTTTTTTTTACAGAATT 27
RESULT 10	
CB824053	687 bp mRNA linear EST 16-MAY-2003
LOCUS	EST 5277 Ripe Apricot Fruit Lambda Zap II Library Prunus armeniaca
DEFINITION	cDNA clone bh002p09 3', mRNA sequence.
ACCESSION	CB824053
VERSION	CB824053.1 GI:29959806
KEYWORDS	EST.
SOURCE	Prunus armeniaca (apricot)
ORGANISM	Prunus armeniaca
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
AUTHORS	1 (bases 1 to 687) Grimplet,J., Romieu,C., Audergon,J.M., Albagnac,G., Lambert,P., Bouchet,J.P. and Terrier,N.
TITLE	High Throughput Detection of Isogenes among 5724 3' EST from Apricot Fruit(Prunus armeniaca)
JOURNAL	Unpublished (2003)
COMMENT	Contact: Audergon JM Unité de génétique et amélioration des fruits et légumes Institut National de la Recherche Agronomique Domaine Saint-Maurice BP 94 84143 Montfavet cedex Tel: 00-33-(0)4-32-72-26-68 Fax: 00-33-(0)4-32-72-26-62 Email: audergon@avignon.inra.fr
FEATURES	Seq primer: 17. Location/Qualifiers 1..687 /organism="Prunus armeniaca" /mol_type="mRNA" /cultivar="Bergeron" /db_xref="taxon:36596" /clone="bh002p09" /dev_stage="Ripe stage" /clone_lib="Ripe Apricot Fruit Lambda Zap II Library" /note="Organ: Fruit; Vector: Lambda Zap II; Site 1: Eco RI; Site 2: XhoI; Oriented library, construction described in Molecular cloning and expression of a cDNA encoding l-aminocyclopropane-l-carboxylate (ACC) oxidase from apricot fruit (Prunus armeniaca cv. Bergeron) by Mbegue-Mbegue D, Chahine H, Gomez RM, Gouble B, Audergon JM, Souty M, Albagnac G, Fils-Lycaon B in Physiol Plant 105:294-303 1999"
ORIGIN	
Query Match	1.6%; Score 27; DB 14; Length 687;
Best Local Similarity	100.0%; Pred. No. 1.3e+04;
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1458 TTTTITTTTTTTTTTTTACAGAATT 1484
Db	6 TTTTITTTTTTTTTTTTACAGAATT 32
RESULT 9	
CA429123	614 bp mRNA linear EST 07-NOV-2002
LOCUS	UI-H-FH1-bfh-1-16-0-UI.61 NCI CGAP FH1 Homo sapiens cDNA clone
DEFINITION	UI-H-FH1-bfh-1-16-0-UI 3', mRNA sequence.
ACCESSION	CA429123.1 GI:24791849
VERSION	EST.
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 614) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE	Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov
COMMENT	Tissue Procurement: James Martin cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bent-soares@uiowa.edu The following repetitive elements were found in this cDNA sequence: 1-45, >AT-richLow_complexity 46-166, >ALU (matched complement) 500-599, >AUU Seq primer: M13 FORWARD POLYA=Yes.
FEATURES	Location/Qualifiers 1..614 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-FH1-bfh-1-16-0-UI" /tissue types="Cell Line" /dev stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI CGAP_FH1" /note="Organ: Chondrosarcoma; Vector: pV773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library obtained from a cell line derived from grade I chondrosarcoma tissue. The library was constructed and

Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 TTTT...TTTACAGAATT 1484  
 Db 3 TTTT...TTTACAGAATT 29

RESULT 11  
 CD038829  
 LOCUS  
 DEFINITION UTPI012 G08 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)  
 ACCESSION CD038829  
 VERSION  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Arachis hypogaea (peanut)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aescynomeneae; Arachis.  
 REFERENCE 1 (bases 1 to 720)  
 AUTHORS Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bauscher, M.G. and Lynch, R.E.  
 TITLE Generation and Analyses of ESTs for Arachis hypogaea  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Baozhu Guo  
 Molecular Genetics  
 USDA/ARS, Crop Protection and Management Research Unit  
 2747 Davis Rd., Tifton, GA 31794, USA  
 Tel: 229-387-2334  
 Fax: 229-387-2321  
 Email: bguo@tifton.usda.gov  
 Seq primer: T3.

FEATURES  
 source  
 1. 720  
 /organism="Arachis hypogaea"  
 /mol\_type="mRNA"  
 /cultivar="A13"  
 /db\_xref="taxon:3818"  
 /clone="UTPI012\_G08"  
 /tissue\_type="Immature pods"  
 /dev\_stage="R6"  
 /lab\_host="X11-blue"  
 /clone\_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"  
 /notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV1XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adaptors. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN  
 Query Match 1.6%; Score 27; DB 14; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 1458 TTTT...TTTACAGAATT 1484

Db 11 TTTT...TTTACAGAATT 37

RESULT 12  
 CNS04725  
 LOCUS  
 DEFINITION Tetraodon nigroviridis genome survey sequence pUC-Ori end of clone 089D09 of library G from Tetraodon nigroviridis, genomic survey sequence.  
 ACCESSION AL278618  
 VERSION AL278618.1 GI:8014612  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Tetraodon nigroviridis  
 ORGANISM Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.  
 REFERENCE 1  
 AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
 TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
 JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
 MEDLINE 20296633  
 PUBMED 10835645  
 REFERENCE 2  
 AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
 JOURNAL Genome Res. 10 (7), 939-949 (2000)  
 MEDLINE 20359837  
 PUBMED 10899143  
 REFERENCE 3 (bases 1 to 818)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.  
 FEATURES  
 source  
 1. 818  
 /organism="Tetraodon nigroviridis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:99883"  
 /clone="089D09"  
 /clone\_lib="G"  
 /note="Genoscope sequence ID : C0BG089C05SP1-end : PUC-Ori"

ORIGIN  
 Query Match 1.6%; Score 27; DB 29; Length 818;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+03; Mismatches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1449 CTCTGCTGTTTTTTTTTTTTTTTTTTT 1475  
 Db 585 CTCTGCTGTTTTTTTTTTTTTTTTTTT 611

RESULT 13  
 CB972911/c  
 LOCUS  
 DEFINITION CAB30001 Ib Fb F11 Cabernet Sauvignon Berry Stage I - CAB3 Vitis vinifera cDNA clone CAB30001\_ib\_Fb\_F11 5', mRNA sequence.  
 ACCESSION CB972911

Zhang, J.-S., Chen, S.-Y. and Yu, J.  
Soybean Expressed Sequence Tags Sequencing  
Unpublished (2003)  
Contact: Chen S-Y  
Plant Biotechnology Laboratory  
Institute of Genetics and Developmental Biology, CAS, China  
Datun road, Beijing 100101, China  
Tel: 86-10-64886859  
Fax: 86-10-64873428  
Email: sychen@genetics.ac.cn  
Email: sychen@genetics.ac.cn  
Seq primer: 17 primer  
Location/Qualifiers  
1. 114  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="kefeng 1"  
/db\_xref="taxon:3847"  
/tissue\_type="Seedlings"  
/dev\_stage="two-week seedlings"  
/lab\_host="XLI-Blue MRF, strain"  
/clone\_lib="Soybean induced by Salicylic Acid"  
/note="Vector: pBluescript SK+; Site 1: EcoR I; Site 2: Xho I; The cDNA library was constructed by He, C-Y from mRNA isolated from two-week seedlings (cultivar Kefeng 1) treated by spraying 2.0mM salicylic acid for 24, 36, 48 and 72 h. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLI-Blue MRF host cells (Stratagene)."

ORIGIN  
Query Match 1.6%; Score 26; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1458 TTTTITTTTTTTTTTTTACAGAAAT 1483  
|||||  
Db 29 TTTTITTTTTTTTTTTTACAGAAAT 54  
|||||

RESULT 15  
BE155390/c 120 bp mRNA linear EST 21-JUN-2000  
LOCUS  
DEFINITION PM1-HT0350-270300-010-d06 HT0350 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE155390  
VERSION BE155390.1 GI:8618111  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ngai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

CB972911.1 GI:30296117  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis..  
1 (bases 1 to 114)  
Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Jones, K. and Cook, D.  
Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon' berries at various developmental stages  
Unpublished (2003)  
Contact: Douglas Cook, PhD  
CAES Genome Facility  
UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcook@ucdavis.edu  
Seq primer: AGGTACGGACATATGCC.  
Location/Qualifiers  
1. 114  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/cultivar="Cabernet Sauvignon"  
/db\_xref="taxon:29760"  
/clone="CAB30001-1b Pb\_F11"  
/sex="Hermaphrodite"  
/dev\_stage="Berry stage 1"  
/lab\_host="DH5alpha"  
/clone\_lib="Cabernet Sauvignon Berry Stage 1 - CAB3"  
/note="Organ: Berry; Vector: pONR; Site 1: SfiI; Site 2: SfiI; CAB3 is a cDNA library of Vitis vinifera 'Cabernet Sauvignon'. Clone 8 berries. Samples were collected after berry set from field-grown vines during stage 1 of berry growth, 17 days after full bloom. The average berry size was 6 millimeters. Sampled vines were located at the University of California, Davis, Experimental Vineyard. DNAs were made by oligo-dT priming and directionally cloned 5' and 3' adaptors were used in cloning as follows: 5'-AACAGTGTATCAGCGAGTGCATCGCGCG-3' and 5'-ATTCTAGCGCGCGCGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN  
Query Match 1.6%; Score 26; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e+05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1458 TTTTITTTTTTTTTTTTACAGAAAT 1483  
|||||  
Db 112 TTTTITTTTTTTTTTTTACAGAAAT 87  
|||||

RESULT 14  
CD407086 114 bp mRNA linear EST 07-JUN-2003  
LOCUS  
DEFINITION Gm ck32086 Soybean induced by Salicylic Acid Glycine max cDNA 3', mRNA sequence.  
ACCESSION CD407086  
VERSION CD407086.1 GI:31465058  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
1 (bases 1 to 114)  
Tian, A.-G., Wang, J., Cui, P., Han, Y.-J., Xu, H., Cong, L.-J., Huang, X.-G., Wang, X.-L., Jiao, Y.-Z., Wang, B.-J., Wang, Y.-J.,

REFERENCE  
AUTHORS

Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=PM1-HT0350-270>)  
 300-010-d06&t3=2000-03-27&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 4  
 High quality sequence stop: 68.

## FEATURES

source

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="HT0350"  
 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 1..68; Score 26; DB 10; Length 120;  
 Best Local Similarity 100.0%; Pred. NO. 1e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1453 GCCTGTTTTTTTTTTTTTTTAC 1478  
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 Db 112 GCCTGTTTTTTTTTTTTTTTAC 87

Search completed: August 31, 2004, 17:42:19  
 Job time : 4449 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 14:34:40 ; Search time 770 Seconds

(without alignments)  
10597.045 Million cell updates/sec

Title: US-10-787-382-18

Perfect score: 1658

Sequence: 1 aggcacactgaacatttc.....gtagtgaagatttggaga 1658

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3237270 seqs, 2460713050 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/prodata/1/pubpna/PCTU5\_PUBCOMB.seq.\*
- 7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 14: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1658	100.0	1658	9	US-09-755-633-18
2	1335	80.5	1658	9	US-09-755-633-19
3	406	24.5	671	9	US-09-755-633-21
4	170	10.3	610	9	US-09-755-633-4
5	170	10.3	610	9	US-09-755-633-6
6	170	10.3	610	15	US-10-218-654-80
7	170	10.3	610	15	US-10-218-654-82
8	170	10.3	610	15	US-10-262-439-80
9	170	10.3	610	15	US-10-262-439-82
10	144	8.7	402	9	US-09-755-633-7
11	144	8.7	402	9	US-09-755-633-8
12	144	8.7	402	15	US-10-218-654-83
13	144	8.7	402	15	US-10-218-654-84
14	144	8.7	402	15	US-10-262-439-83

C 15	144	8.7	402	15	US-10-262-439-84	Sequence 84, Appl
C 16	129	7.8	345	9	US-09-755-633-9	Sequence 9, Appl
C 17	129	7.8	345	9	US-09-755-633-11	Sequence 11, Appl
C 18	129	7.8	345	15	US-10-218-654-85	Sequence 85, Appl
C 19	129	7.8	345	15	US-10-218-654-87	Sequence 87, Appl
C 20	129	7.8	345	15	US-10-262-439-85	Sequence 85, Appl
C 21	129	7.8	345	15	US-10-262-439-87	Sequence 87, Appl
C 22	28	1.7	2122	13	US-10-424-599-35126	Sequence 35126, A
C 23	26	1.6	394	17	US-10-437-963-99632	Sequence 99632, A
C 24	26	1.6	2235	15	US-10-318-780-20	Sequence 20, Appl
C 25	26	1.6	3230	9	US-09-800-629A-78	Sequence 78, Appl
C 26	26	1.6	3230	17	US-10-679-532-78	Sequence 78, Appl
C 27	25	1.5	407	15	US-10-198-846-13075	Sequence 13075, A
C 28	25	1.5	461	15	US-10-198-846-6011	Sequence 6011, Ap
C 29	25	1.5	512	13	US-10-621-901-295	Sequence 295, App
C 30	25	1.5	516	17	US-10-437-963-51964	Sequence 51964, A
C 31	25	1.5	586	13	US-10-027-632-220494	Sequence 220494, A
C 32	25	1.5	586	16	US-10-027-632-220494	Sequence 220494, A
C 33	25	1.5	596	13	US-09-770-152-6	Sequence 6, Appl
C 34	25	1.5	608	17	US-10-437-963-40666	Sequence 40666, A
C 35	25	1.5	824	9	US-09-770-445-715	Sequence 715, App
C 36	25	1.5	850	17	US-10-437-963-31566	Sequence 31566, A
C 37	25	1.5	859	17	US-10-437-963-48530	Sequence 48530, A
C 38	25	1.5	937	17	US-10-437-963-51140	Sequence 51140, Ap
C 39	25	1.5	970	10	US-09-934-455-293	Sequence 293, App
C 40	25	1.5	970	13	US-10-225-066A-691	Sequence 691, App
C 41	25	1.5	970	16	US-10-374-780A-2213	Sequence 2213, Ap
C 42	25	1.5	1475	17	US-10-437-963-18375	Sequence 18375, A
C 43	25	1.5	1607	17	US-10-437-963-9407	Sequence 9407, Ap
C 44	25	1.5	1740	15	US-10-260-046-19	Sequence 19, Appl
C 45	25	1.5	3018	17	US-10-332-406A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-09-755-633-18  
; Sequence 18, Application US/09755633  
; Patent No. US20020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09755633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 1658  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: Intron  
; LOCATION: (171)..(373)  
; NAME/KEY: Intron  
; LOCATION: (407)..(1275)  
; NAME/KEY: Intron  
; LOCATION: (1405)..(1522)  
US-09-755-633-18

Query Match 100.0%; Score 1658; DB 9; Length 1658;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGCAACACTGACATTTAGAGCTATGAGATGCTTCGAAATTTGAGTTTGTCTAGCTC 60  
Qy 61 TTGGGGTGGCTATGTTTCTGCTTCTGCTGTAGAAAATCCCAATGAGTGGTGGCAG 120  
Db 61 TTGGGGTGGCTATGTTTCTGCTTCTGCTGTAGAAAATCCCAATGAGTGGTGGCAG 120  
Qy 121 AGACCTTGACACTGCTCTCACTCATCGAATTTGGCTGATAGCGATGGGTAAATTTCT 180  
Db 121 AGACCTTGACACTGCTCTCACTCATCGAATTTGGCTGATAGCGATGGGTAAATTTCT 180  
Qy 181 TTTTGATTCCTACAGTCTTTAAATGATGGGTAAATTTGGTGGTGGTGGTGGTGGTGGT 240  
Db 181 TTTTGATTCCTACAGTCTTTAAATGATGGGTAAATTTGGTGGTGGTGGTGGTGGTGGT 240  
Qy 241 GATCCATATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 300  
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Qy 301 TCAGAGCAATATATTAAGTTATGAACCTTCAATACATTAATAAATGAATGATGTTTC 360  
Db 301 TCAGAGCAATATATTAAGTTATGAACCTTCAATACATTAATAAATGAATGATGTTTC 360  
Qy 361 CTTTCTTTTTCAGAACCTGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Db 361 CTTTCTTTTTCAGAACCTGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
Qy 421 GATTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
Db 421 GATTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
Qy 481 CAITGGGATGATTAATTTTATCTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 540  
Db 481 CAITGGGATGATTAATTTTATCTATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 540  
Qy 541 TTATGAATATAGGAATGGTGTAGGAATGGTGTAGGAATGGTGTAGGAATGGTGTAGGAAT 600  
Db 541 TTATGAATATAGGAATGGTGTAGGAATGGTGTAGGAATGGTGTAGGAATGGTGTAGGAAT 600  
Qy 601 CAAGTGATCAGGCTCTTTTCTGATGTTGTCAGTCTCTCAATCTCAAGAGCTCTGCTGCA 660  
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Qy 841 ACTTCCACATATTAATGATTTTAACTCTATGGAATCATATACATCTGGAGTATGTC 900  
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Db 1021 CTCGTAAGCATTTATTTTCAATTAATCAATTTTATATCAATTTGTAACACTTCTCAGT 1080  
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Db 1081 AATATATAACATCATTTACTTATAGCTTAATATAGCTTAGTATAGGTGGTGTCCACC 1140  
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Db 1201 AAAGTCTAACTTTTGGACCAAAATTTTATGCTCTGTTTTCATGAATATATTTTAAA 1260  
Qy 1261 ATCTTCTCTATTTAGCACCAACTGTGCATTAAGAAATTTTTCAGGTATAGACATTTG 1320  
Db 1261 ATCTTCTCTATTTAGCACCAACTGTGCATTAAGAAATTTTTCAGGTATAGACATTTG 1320  
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Db 1321 AAGAACCAAACTGCCACGGGAGCTGTGATAAATATTTTCCAAAATTTTCTTTAATA 1380  
Qy 1381 AAGAACCAATAGAGCGCCAAAAGTAAAGTAAAGACATTTGGCAAACTTAAAGTATAT 1440  
Db 1381 AAGAACCAATAGAGCGCCAAAAGTAAAGTAAAGACATTTGGCAAACTTAAAGTATAT 1440  
Qy 1441 TTGCTGACTCTGCTCTGTTTTTTTTTTTTTTTTTTTTTCAAGAAATTCAGAGTTTCTTACAAT 1500  
Db 1441 TTGCTGACTCTGCTCTGTTTTTTTTTTTTTTTTTTTTTCAAGAAATTCAGAGTTTCTTACAAT 1500  
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Db 1501 ATCTCTCTCTGTTCTTTTAAACAGAAAAGTGTGAGGAGAAAGATGGAGAGTGACAAAGTT 1560  
Qy 1561 CTTAGACTCTGCAAGTATTTCTTGTGTAAATAAACACCGAGTGGACACGGAAAGTTG 1620  
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Qy 1621 AGAACCAACCGGCTTTTGTAGTGAAGATTTTGGAGA 1658  
Db 1621 AGAACCAACCGGCTTTTGTAGTGAAGATTTTGGAGA 1658

## RESULT 2

US-09-755-633-19/c  
; Sequence 19, Application US/09755633  
; Patent No. US202020127200A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Shumin  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1-C1  
; CURRENT APPLICATION NUMBER: US/09/755,633  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 1658  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-755-633-19

Query Match 80.5%; Score 1335; DB 9; Length 1658;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1625; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
Qy 32 AATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTGCTGT 91  
Db 1627 AATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCTTTGCTGT 1568  
Qy 92 AGAAATCCCATGAATAGTAGTGGGAGAGACCTTGACACTGCTCTCCACTCATCGAAC 151

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152	Qy	TTGGCTGATAGGCGATGGGCTAAATTTTCTTTTGTATTTCTTACAGTCTTTAAAAATGCAATGG	211
1507	Db	TTGGCTGATAGGCGATGGGCTAAATTTTCTTTTGTATTTCTTACAGTCTTTAAAAATGCAATGG	1448
212	Qy	GTAATTTGGTGGTGGCTAGTTTTTTAAAGATCCATATCAATTAAGTAAGTAATGAGTGT	271
1447	Db	GTAATTTGGTGGTGGCTAGTTTTTTAAAGATCCATATCAATTAAGTAAGTAATGAGTGT	1388
272	Qy	TAAATAATATAT-AATGGGTAAACCATGTTACTCAGAGAATTTATATTTAAAAAGTTATGAACC	330
1387	Db	TAATAATATATTAATTTGGGTAAACCATGTTACTCAGAGAATTTATTTAAAAAGTTATGAACC	1328
331	Qy	TTACAATACATATTAATAATTAATTTGTTTCTTTCTTTTTCAGAACCTGATGATTTCTCTAC	390
1327	Db	TTACAATACATATTAATAATTAATTTGTTTCTTTCTTTTTCAGAACCTGATGATTTCTCTAC	1268
391	Qy	TCCTGAAAAATAAAAACTGAAGTTAAATATATGATTTGATAAAATGATTTACATGAATCAGTT	450
1267	Db	TCCTGAAAAATAAAAACTGAAGTTAAATATATGATTTGATAAAATGATTTACATGAATCAGTT	1208
451	Qy	TCATATTTTAAAGCTATAAAGTATCAGTTAAACATTTGGGATGATTTAAATTTTATCTATTTTG	510
1207	Db	TCATATTTTAAAGCTATAAAGTATCAGTTAAACATTTGGGATGATTTAAATTTTATCTATTTTG	1148
511	Qy	TTTTTTATGCTGCGGATGTAATTTATGCTTATGAATATATAGGAATGGTGTTAGGAATG	570
1147	Db	TTTTTTATGCTGCGGATGTAATTTATGCTTATGAATATATAGGAATGGTGTTAGGAATG	1088
571	Qy	GCCTCAACAATATTAAGTAPAGAAATCCATTAAGCAAGTGGATCAGGCCCTTTTTCATGTTGT	630
1087	Db	GCCTCAACAATATTAAGTAPAGAAATCCATTAAGCAAGTGGATCAGGCCCTTTTTCATGTTGT	1028
631	Qy	CAGTTCTCCATCTCAAAAGAGCGCTGCTGAGGAATCTTTTCCAAAAGAAATCCATATTTGG	690
1027	Db	CAGTTCTCCATCTCAAAAGAGCGCTGCTGAGGAATCTTTTCCAAAAGAAATCCATATTTGG	968
691	Qy	GTACAGAGATATCTCCTAGGCTCCATTCACCTCTGCTGGCTTCTCCTCACCTCAACGTT	750
967	Db	GTACAGAGATATCTCCTAGGCTCCATTCACCTCTGCTGGCTTCTCCTCACCTCAACGTT	908
751	Qy	TTTTCTGAAAAGTACTAGCAACTTGGGTTATATTTTAGAATTATGTCAGTAGACATGAA	810
907	Db	TTTTCTGAAAAGTACTAGCAACTTGGGTTATATTTTAGAATTATGTCAGTAGACATGAA	848
811	Qy	AATATACAGTGAAGTCTCTATATTAATAGTCACCTCCACATATTTAATGATTTTTTAACTC	870
847	Db	AATATACAGTGAAGTCTCTATATTAATAGTCACCTCCACATATTTAATGATTTTTTAACTC	788
871	Qy	TAATGGAATCATATACATCTGGAGTATGTCATGTCATATTTAAAAATGTTGAT	930
787	Db	TAATGGAATCATATACATCTGGAGTATGTCATGTCATATTTAAAAATGTTGAT	728
931	Qy	ATCATTTAGTCTAAATTAGAATAAAATTTACGAGCTAGAACTATACGAGAAATTTCTGAGTG	990
727	Db	ATCATTTAGTCTAAATTAGAATAAAATTTACGAGCTAGAACTATACGAGAAATTTCTGAGTG	668
991	Qy	AGGTAAATTCAGTAAAGGAGTTGTTATTAACCTCGCTAAGCATTTATTTTTTCATTAATCATTT	1050
667	Db	AGGTAAATTCAGTAAAGGAGTTGTTATTAACCTCGCTAAGCATTTATTTTTTCATTAATCATTT	608
1051	Qy	TCATTTATATCATTTTGTAAACACTTCTCAGTAAATTTATATAACATCATTTTACTTTATGTTAA	1110
607	Db	TCATTTATATCATTTTGTAAACACTTCTCAGTAAATTTATATAACATCATTTTACTTTATGTTAA	548
1111	Qy	TTATAGCTTTAGTATATAGTGGTTTCCACCTCGGAAGAGACACAGTAAAAACCTCTTGGG	1170
547	Db	TTATAGCTTTAGTATATAGTGGTTTCCACCTCGGAAGAGACACAGTAAAAACCTCTTGGG	488
1171	Qy	AGAAAGGAAACCTTGCTAAACCCCAAAAAAACAAGCTCTAACTTTTGTGACCAAAATTTTAT	1230

RESULT 3

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US-09-755-633-21
; Sequence 21, Application US/09755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IM-
; FILE REFERENCE: IM-2-CI-CI
; TITLE OF INVENTION: ACID MOLECULES, AND
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 671
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-21

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	Query Match	24.5%;	Score 406;	DB 9;	Length 671;
	Best Local Similarity	100.0%;	Pred. No. 1.1e-183;		
	Matches 406;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	AGGCAACACTGAACATTTGACGCTATGACAATGCITTCGAATTTGAGTTTGCCTAGCTC	60		
Db	1	AGGCAACACTGAACATTTGACGCTATGACAATGCITTCGAATTTGAGTTTGCCTAGCTC	60		
Qy	61	TTGGGGCTGCTATGTTTCTGCCCTTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAG	120		
Db	61	TTGGGGCTGCTATGTTTCTGCCCTTTGCTGTAGAAAAATCCCATGAATAGACTGGTGGCAG	120		
Qy	121	AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGCTGATAGGGCATGGGGTAATTTTCT	180		



Db 63 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 122  
; LENGTH: 610  
; TYPE: DNA  
QY 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGG 170  
; ORGANISM: Canis familiaris  
; FEATURE:  
Db 123 AGACTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGG 172  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-262-439-80

## RESULT 7

US-10-218-654-82/c  
; Sequence 82, Application US/10218654  
; Publication No. US20030099609A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C1  
; CURRENT APPLICATION NUMBER: US/10/218,654  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-82

Query Match 10.3%; Score 170; DB 15; Length 610;  
Best Local Similarity 100.0%; Pred. No. 1.3e-70;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGGCAAACTGACATTTGAGACTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTC 60  
Db 608 AGGCAAACTGACATTTGAGACTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTC 549  
QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 120  
Db 548 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 489  
QY 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGG 170  
Db 488 AGACTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGG 439

## RESULT 8

US-10-262-439-80  
; Sequence 80, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80

; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-10-262-439-80

Query Match 10.3%; Score 170; DB 15; Length 610;  
Best Local Similarity 100.0%; Pred. No. 1.3e-70;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGGCAAACTGACATTTGAGACTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTC 60  
Db 3 AGGCAAACTGACATTTGAGACTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTC 62  
QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 120  
Db 63 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 122  
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## RESULT 9

US-10-262-439-82/c  
; Sequence 82, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; PRIOR FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 09/322,409  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/087,306  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-82

Query Match 10.3%; Score 170; DB 15; Length 610;  
Best Local Similarity 100.0%; Pred. No. 1.3e-70;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGGCAAACTGACATTTGAGACTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTC 60  
Db 608 AGGCAAACTGACATTTGAGACTATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTC 549  
QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 120  
Db 548 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAAATCCATGAATAGACTGGTGGCAG 489  
QY 121 AGACTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGG 170  
Db 488 AGACTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGGCGATGGG 439

## RESULT 10

US-09-755-633-7  
; Sequence 7, Application US/09755633

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Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-7

Query Match      8.7%; Score 144; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCGCTTT 86
DB 1 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCGCTTT 60
QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 120
QY 147 CGAACTTGGCTGATAGGCGATGGG 170
DB 121 CGAACTTGGCTGATAGGCGATGGG 144

RESULT 11
US-09-755-633-8/c
; Sequence 8, Application US/09/755633
; Patent No. US20020127200A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shumin
; APPLICANT: McCall, Catherine A.
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1-C1
; CURRENT APPLICATION NUMBER: US/09/755,633
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-755-633-8

Query Match      8.7%; Score 144; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCGCTTT 86
DB 402 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCGCTTT 343
QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 146
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DB 342 GCTGTAGAAAATCCCATGATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 283
QY 147 CGAACTTGGCTGATAGGCGATGGG 170
DB 282 CGAACTTGGCTGATAGGCGATGGG 259

RESULT 12
US-10-218-654-83
; Sequence 83, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-218-654-83

Query Match      8.7%; Score 144; DB 15; Length 402;
Best Local Similarity 100.0%; Pred. No. 3.6e-58;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCGCTTT 86
DB 1 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGGCTGCTATGTTTCTGCGCTTT 60
QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 146
DB 61 GCTGTAGAAAATCCCATGATAGACTGTGGGAGACCTTGACACTGCTCTCCACTCAT 120
QY 147 CGAACTTGGCTGATAGGCGATGGG 170
DB 121 CGAACTTGGCTGATAGGCGATGGG 144

RESULT 13
US-10-218-654-84/c
; Sequence 84, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 402
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; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-218-654-84

Query Match  
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCGCTATGTTTCTGCCTTT 86  
DB 402 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCGCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146  
DB 342 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170  
DB 282 CGAACTTGGCTGATAGCGGATGGG 259

RESULT 14  
US-10-262-439-83  
; Sequence 83, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IN-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-83

Query Match  
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCGCTATGTTTCTGCCTTT 86  
DB 1 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCGCTATGTTTCTGCCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146  
DB 61 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGG 170  
DB 121 CGAACTTGGCTGATAGCGGATGGG 144

RESULT 15  
US-10-262-439-84/c  
; Sequence 84, Application US/10262439  
; Publication No. US20030143196A1  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin

; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IN-2-C2  
; CURRENT APPLICATION NUMBER: US/10/262,439  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR FILING DATE: US/09/451,527  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-262-439-84

Query Match  
Best Local Similarity 8.7%; Score 144; DB 15; Length 402;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCGCTATGTTTCTGCCTTT 86  
DB 402 ATGAGAAATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCGCTATGTTTCTGCCTTT 343

QY 87 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 146  
DB 342 GCTGTAGAAAATCCCATGATAGACTGTTGGGAGACCTTGACACTGCTCTCCACTCAT 283

QY 147 CGAACTTGGCTGATAGCGGATGGG 170  
DB 282 CGAACTTGGCTGATAGCGGATGGG 259

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-787-382-18

Perfect score: 1658  
Sequence: 1 aggcaaacactgaacatttc.....gragtgaagatttgaga 1658

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
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- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PGTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	10.3	610	4	US-09-322-409-80
C 2	170	10.3	610	4	US-09-322-409-82
3	170	10.3	610	4	US-09-451-527-80
C 4	170	10.3	610	4	US-09-451-527-82
5	144	8.7	402	4	US-09-322-409-83
C 6	144	8.7	402	4	US-09-322-409-84
7	144	8.7	402	4	US-09-451-527-83
C 8	144	8.7	402	4	US-09-451-527-84
9	144	8.7	405	4	US-09-371-615A-1
10	129	7.8	345	4	US-09-322-409-85
C 11	129	7.8	345	4	US-09-322-409-87
12	129	7.8	345	4	US-09-451-527-85
C 13	129	7.8	345	4	US-09-451-527-87
C 14	26	1.6	2235	4	US-09-569-804-20
15	26	1.6	3230	3	US-09-280-799-78
16	26	1.6	3230	6	5324640-1
C 17	25	1.5	29485	4	US-09-785-381-6
18	24	1.4	3182	1	US-08-188-582-12
19	24	1.4	3182	1	US-08-646-715-12
20	23	1.4	40	3	US-09-306-290-11
C 21	23	1.4	442	4	US-09-372-422A-35
C 22	23	1.4	1017	3	US-08-849-751-1
C 23	23	1.4	1017	4	US-09-478-816-1
24	23	1.4	2082	4	US-09-149-476-257
C 25	23	1.4	31571	1	US-08-323-443B-1
C 26	23	1.4	53526	3	US-08-658-136-2
C 27	23	1.4	53577	3	US-08-658-136-1

28	22	1.3	27	1	US-08-434-503-41	Sequence 41, Appl
C 29	22	1.3	32	4	US-09-322-409-138	Sequence 138, App
C 30	22	1.3	32	4	US-09-451-527-138	Sequence 138, App
31	22	1.3	40	3	US-09-306-290-16	Sequence 16, Appl
C 32	22	1.3	47	1	US-08-466-852-2	Sequence 2, Appl
33	22	1.3	127	3	US-09-014-416-59	Sequence 59, Appl
34	22	1.3	176	3	US-09-014-416-63	Sequence 63, Appl
35	22	1.3	183	3	US-09-014-416-60	Sequence 60, Appl
C 36	22	1.3	183	4	US-09-621-976-13606	Sequence 13606, A
37	22	1.3	200	3	US-09-014-416-64	Sequence 64, Appl
38	22	1.3	227	2	US-08-520-678A-28	Sequence 28, Appl
39	22	1.3	227	3	US-08-897-136-28	Sequence 28, Appl
40	22	1.3	253	2	US-08-520-678A-25	Sequence 25, Appl
41	22	1.3	253	3	US-08-897-136-25	Sequence 25, Appl
C 42	22	1.3	255	4	US-09-621-976-9406	Sequence 9406, Ap
C 43	22	1.3	255	4	US-09-621-976-18743	Sequence 18743, A
44	22	1.3	257	2	US-08-520-678A-24	Sequence 24, Appl
45	22	1.3	257	3	US-08-897-126-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-09-322-409-80  
; Sequence 80, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Drelitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-CI  
; CURRENT APPLICATION NUMBER: US/09/322,409  
; CURRENT FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 154  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 80  
; LENGTH: 610  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (29)..(430)  
US-09-322-409-80

Query Match 10.3%; Score 170; DB 4; Length 610;  
Best Local Similarity 100.0%; Pred. No. 3.6e-61;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 60  
Db 3 AGGCAAACTGAACTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 62  
QY 61 TTGGGGCTGCCATATCTTTCTGCTTTGCTAGAAAATCCCATGAAATGAGCTGTGGCAG 120  
Db 63 TTGGGGCTGCCATATCTTTCTGCTTTGCTAGAAAATCCCATGAAATGAGCTGTGGCAG 122  
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATGGCGATGGG 170  
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATGGCGATGGG 172

RESULT 2  
US-09-322-409-82/c  
; Sequence 82, Application US/09322409  
; Patent No. 6471957  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee



US-09-322-409-83

Query Match	8.7%	Score 144;	DB 4;	Length 402;
Best Local Similarity	100.0%;	Pred. No. 2.1e-50;		
Matches 144;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	27	ATGGAAGTCCTTCGAATTTGAGTTTCTAGCTCTTGGGCGTGCCTATGTTCTGCCCTT	86	
Db	1	ATGGAAGTCCTTCGAATTTGAGTTTCTAGCTCTTGGGCGTGCCTATGTTCTGCCCTT	60	
QY	87	GCTGTAGAAAAATCCCATGAATAGACTGGTGGCGAGACCTTGCACACTGCTCCACTCAT	146	
Db	61	GCTGTAGAAATCCCATGAATAGACTGGTGGCGAGACCTTGCACACTGCTCCACTCAT	120	
QY	147	CGAACTTCGCCTGATAGCGATGGG	170	
Db	121	CGAACTTCGCCTGATAGCGATGGG	144	

## RESULT 6

US-09-322-409-84/C  
 / Sequence 84, Application US/09322409  
 / Patent No. 6471957  
 / GENERAL INFORMATION:  
 / APPLICANT: Sim, Gex-Kee  
 / APPLICANT: Yang, Shumin  
 / APPLICANT: Dreitz, Matthew J.  
 / APPLICANT: Wonderling, Ramani S.  
 / TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
 / TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
 / FILE REFERENCE: IM-2-C1  
 / CURRENT APPLICATION NUMBER: US/09/322,409  
 / CURRENT FILING DATE: 1999-05-28  
 / EARLIER APPLICATION NUMBER: 60/067,306  
 / EARLIER FILING DATE: 1998-05-29  
 / NUMBER OF SEQ ID NOS: 154  
 / SOFTWARE: Patentin Ver. 2.0  
 / SEQ ID NO 84  
 / LENGTH: 402  
 / TYPE: DNA  
 / ORGANISM: Caris familiaris  
 / US-09-322-409-84

	Query Match	8.7%	Score 144	DB 4	Length 402	
	Best Local Similarity	100.0%	Pred. NO. 2.1e-50			
	Matches 144	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	27	ATGAGAAATGCTTCGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT	86			
Db	402	ATGAGAAATGCTTCGAATTTGAGTTTGCTAGCTCTTGGGGCTGCCTATGTTTCTGCCCTTT	343			
QY	87	GCTGTAGAAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	146			
Db	342	GCTGTAGAAAAATCCCATGAAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	283			
QY	147	CGAACTTGGCTGATAGCGCATGGG	170			
Db	282	CGAACTTGGCTGATAGCGCATGGG	259			

RESULT 7

US-09-451-527-83  
; Sequence 83, Application US/09451527  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wondersling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527

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, CURRENT FILING DATE: 1999-12-01
, EARLIER APPLICATION NUMBER: 09/322,409
, EARLIER FILING DATE: 1999-05-28
, EARLIER APPLICATION NUMBER: 60/087,306
, EARLIER FILING DATE: 1998-05-29
, NUMBER OF SEQ ID NOS: 174
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 83
, LENGTH: 402
, TYPE: DNA
, ORGANISM: Canis familiaris
US-09-451-527-83

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	Query Match	8.7%;	Score 144;	DB 4;	Length 402;
	Best Local Similarity	100.0%;	Pred. No. 2.1e-50;		
	Matches 144;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	27	ATGAGAATGCTTCTGAAATTTGAGTTTGCTAGCTCTGGGGCTGCTATGTTTCTGCCTTT	86		
Db	1	ATGAGAATGCTTCTGAAATTTGAGTTTGCTAGCTCTGGGGCTGCTATGTTTCTGCCTTT	60		
Qy	87	GCTGTGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACATGCTCTCCACATCAT	145		
Db	61	GCTGTGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACATGCTCTCCACATCAT	120		
Qy	147	CGAACTTGGCTGATAGCGGATGGG	170		
Db	121	CGAACTTGGCTGATAGCGGATGGG	144		

## RESULT 8

US-09-451-527-84/c  
; Sequence 84, Application US/09451527.  
; Patent No. 6482403  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Gek-Kee  
; APPLICANT: Yang, Shumin  
; APPLICANT: Dreitz, Matthew J.  
; APPLICANT: Wonderling, Ramani S.  
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF  
; FILE REFERENCE: IM-2-C2  
; CURRENT APPLICATION NUMBER: US/09/451,527  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 09/322,409  
; EARLIER FILING DATE: 1999-05-28  
; EARLIER APPLICATION NUMBER: 60/087,306  
; EARLIER FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-09-451-527-84

Query Match	8.7%;	Score 144;	DB 4;	Length 402;
Best Local Similarity	100.0%;	Pred. No. 2.1e-50;		
Matches 144;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	27	ATGAGATGCTTCTGAAATTTCAGTTTCTAGCTCTTGGGGCTGCGCTATGTTTCTGCCTT	86	
DB	402	ATGAGATGCTTCTGAAATTTCAGTTTCTAGCTCTTGGGGCTGCGCTATGTTTCTGCCTT	343	
QY	87	GCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	146	
DB	342	GCTGTAGAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT	283	
QY	147	CGAACTTGGCTGATAGCGATGGG	170	
DB	282	CGAACTTGGCTGATAGCGATGGG	259	

```
RESULT 9
US-09-371-615A-1
; Sequence 1, Application US/09371615A
; Patent No. 6537781
; GENERAL INFORMATION:
; APPLICANT: IDEXX LABORATORIES
; TITLE OF INVENTION: METHODS AND COMPOSITIONS CONCERNING
; FILE OF INVENTION: CANINE INTERLEUKIN 5
; FILE REFERENCE: 03604001700US00
; CURRENT APPLICATION NUMBER: US/09/371.615A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-371-615A-1
Query Match      8.7%; Score 144; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2e-50;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 ATGAGATGCTTCGAATTGCTAGCTTGGGCTGCTATGTTCTGCTTT 86
DB 1 ATGAGATGCTTCGAATTGCTAGCTTGGGCTGCTATGTTCTGCTTT 60
QY 87 GCTGTAGAAATCCCATGATAGACTGGTGCAGAGACCTTGACACTGCTCCACTCAT 146
DB 61 GCTGTAGAAATCCCATGATAGACTGGTGCAGAGACCTTGACACTGCTCCACTCAT 120
QY 147 CGAACTTGGCTGATAGCGATGGG 170
DB 121 CGAACTTGGCTGATAGCGATGGG 144
RESULT 10
US-09-322-409-85
; Sequence 85, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322.409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-322-409-85
Query Match      7.8%; Score 129; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1276 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTAAGAACCAACTGCC 1335
DB 121 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTAAGAACCAACTGCC 180
QY 1336 CACGGGAGGCTGGTAAACTTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 1395
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Db 181 CACGGGAGGCTGTGATAAACTATTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 240
QY 1396 CGCCAAAAA 1404
DB 241 CGCCAAAAA 249
RESULT 11
US-09-322-409-87/c
; Sequence 87, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322.409
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-322-409-87
Query Match      7.8%; Score 129; DB 4; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1276 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTAAGAACCAACTGCC 1335
DB 225 CACCACTGTGCATTAAGAAGTTTTTCAGGGTATAGACATTAAGAACCAACTGCC 166
QY 1336 CACGGGAGGCTGTGATAAACTTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 1395
DB 165 CACGGGAGGCTGTGATAAACTTCCAAACTTGCTTTTAAATAAAGAACACATAGAG 106
QY 1396 CGCCAAAAA 1404
DB 105 CGCCAAAAA 97
RESULT 12
US-09-451-527-85
; Sequence 85, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/09/451.527
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322.409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)..(345)
US-09-451-527-85

Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-44; Length 345;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1276 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCACCAACTGCC 1335
DB 121 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCACCAACTGCC 180

QY 1336 CACGGGAGGCTGGTAAACTATTCARAACTGTCTTTAATAAAGAACACATAGAG 1395
DB 191 CACGGGAGGCTGGTAAACTATTCARAACTGTCTTTAATAAAGAACACATAGAG 240

QY 1396 CGCCAAAAA 1404
DB 241 CGCCAAAAA 249

RESULT 13
US-09-451-527-87/c
; Sequence 87, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IN-2-C2
; CURRENT APPLICATION NUMBER: US/09/451,527
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087,306
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-451-527-87

Query Match
Best Local Similarity 100.0%; Pred. No. 3.3e-44; Length 345;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1276 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCACCAACTGCC 1335
DB 225 CACCAACTGTGCATTAAAGAAGTTTTCAGGGTATAGACACATTGAAGAACCACCAACTGCC 166

QY 1336 CACGGGAGGCTGGTAAACTATTCARAACTGTCTTTAATAAAGAACACATAGAG 1395
DB 165 CACGGGAGGCTGGTAAACTATTCARAACTGTCTTTAATAAAGAACACATAGAG 106

QY 1396 CGCCAAAAA 1404
DB 105 CGCCAAAAA 97

RESULT 14
US-09-569-804-20/c
; Sequence 20, Application US/09569804
; Patent No. 6506962
; GENERAL INFORMATION:
; APPLICANT: Bougri, Oleg
; APPLICANT: Rommens, Caius
; APPLICANT: Srivastava, Neelam
; APPLICANT: Swords, Kathleen M
```

```
; TITLE OF INVENTION: Acquired Resistance Genes in Plants
; FILE REFERENCE: 38-21(15415)
; CURRENT APPLICATION NUMBER: US/09/569,804
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/133,965
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Zea mays
US-09-569-804-20

Query Match
Best Local Similarity 100.0%; Pred. No. 0.12; Length 2235;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 TTTTITTTTTTTTTTTTACAGAAT 1483
DB 2196 TTTTITTTTTTTTTTTTACAGAAT 2171

RESULT 15
US-09-280-799-78
; Sequence 78, Application US/09280799
; Patent No. 6136603
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Karras, James G
; APPLICANT: McKay, Robert
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
; FILE REFERENCE: ISPH-0340
; CURRENT APPLICATION NUMBER: US/09/280,799
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 3230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-280-799-78

Query Match
Best Local Similarity 100.0%; Pred. No. 0.11; Length 3230;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 ATAAAAATGTAAGTTAAATTTATGATT 424
DB 930 ATAAAAATGTAAGTTAAATTTATGATT 955

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GenCore version 5.1.6  
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6: Geneseq2002s.\*  
7: Geneseq2003as.\*  
8: Geneseq2003bs.\*  
9: Geneseq2003cs.\*  
10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	170	10.3	610	3 AAZ55546	Aaz55546 Canine in
2	170	10.3	610	3 AAZ55547	Aaz55547 Canine in
3	144	8.7	252	4 AAF74305	Aaf74305 Canine in
4	144	8.7	402	3 AAZ55548	Aaz55548 Canine in
5	144	8.7	402	3 AAZ55549	Aaz55549 Canine in
6	144	8.7	405	4 AAF74300	Aaf74300 Canine in
7	129	7.8	345	3 AAZ55550	Aaz55550 Canine in
8	129	7.8	345	3 AAZ55551	Aaz55551 Canine in
9	129	7.8	393	4 AAF74306	Aaf74306 Canine in
10	43	2.6	399	2 AAT50756	Aat50756 Canine in
11	43	2.6	520	2 AAT50755	Aat50755 Canine in
12	41	2.5	838	3 AAZ44265	Aaz44265 Porcine I
13	26	1.6	357	5 ABV56577	Abv56577 Human pro
14	26	1.6	700	4 AAH92592	Aah92592 Human inf
15	26	1.6	2235	4 AAC84351	Aac84351 Corn clon
16	26	1.6	3230	1 AAN81381	Aan81381 Entire nu
17	26	1.6	3230	2 AAQ74056	Aaq74056 Human int
18	26	1.6	3230	3 AAC73725	Aac73725 Human int
19	26	1.6	3230	7 ABX04379	Abx04379 Human int
20	26	1.6	3241	3 AAA34856	Aaa34856 Human ade
21	26	1.6	3241	3 AAF20978	Aaf20978 Human low
22	26	1.6	3241	7 ABZ96672	Abz96672 Human nuc
23	26	1.6	4057	3 AAA34858	Aaa34858 Human ade

24	26	1.6	4057	3 AAF20980	Aaf20980 Human low
25	26	1.6	4057	7 ABZ96674	Abz96674 Human nuc
26	26	1.6	9738	6 AAS15002	Aas15002 DNA encod
27	25	1.5	274	7 ABZ73094	Abz73094 Rice leaf
28	25	1.5	368	7 ACC55526	Acc55526 Rice endo
29	25	1.5	403	4 AAL14836	Aal14836 Human bre
30	25	1.5	423	4 AAL23698	Aal23698 Human bre
31	25	1.5	512	8 ACC73216	Acc73216 Cat flea
32	25	1.5	596	7 ABX56654	Abx56654 Arabidops
33	25	1.5	700	4 AAH92593	Aah92593 Human inf
34	25	1.5	700	4 AAH92594	Aah92594 Human inf
35	25	1.5	824	6 ABN98947	Abn98947 Arabidops
36	25	1.5	970	9 ADD30659	Add30659 Plant vie
37	25	1.5	1395	1 AAN71243	Aan71243 Sequence
38	25	1.5	1740	7 ACC47166	Acc47166 Z. mays p
39	25	1.5	3018	6 ABK15653	Abk15653 Rice lipo
40	25	1.5	6375	6 ABK15200	Abk15200 Human CDN
41	25	1.5	6410	7 ABZ33706	Abz33706 Human col
42	25	1.5	8443	9 ADC27428	Adc27428 cDNA enco
43	25	1.5	29485	10 ADE86101	Ade86101 BAC clone
44	25	1.5	96599	8 ADA02747	Ada02747 Mouse Iff
45	25	1.5	96599	9 ADB72485	Adb72485 Mouse Iff

## ALIGNMENTS

RESULT 1  
AAZ55546  
ID AAZ55546 standard; cDNA; 610 BP.  
XX  
AC AAZ55546;  
XX  
DT 14-MAR-2000 (first entry)  
XX  
DE Canine interleukin-5 (IL-5) cDNA.  
XX  
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
XX  
OS Canis familiaris.  
XX  
FH Key Location/Qualifiers  
CDS 29..433  
FT /\*tag= a  
FT /product= "Canine IL-5"  
XX  
XX WO961618-A2.  
XX  
XX 02-DEC-1999.  
XX  
XX 28-MAY-1999; 99WO-US011942.  
XX  
XX 29-MAY-1998; 98US-0087306P.  
XX  
XX (HESK-) HESKA CORP.  
XX  
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
XX  
XX WPI; 2000-072623/06.  
XX  
XX P-PSDB; AAY58219.  
XX  
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
XX useful for treating or preventing e.g. tumors or autoimmune disease.  
XX  
XX Claim 1h; Page 223-224; 264pp; English.  
XX  
XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
XX interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
XX feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
XX ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
XX and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
XX nucleotides which encode these immunoregulatory proteins. The proteins,

CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX  
 SQ Sequence 610 BP; 202 A; 114 C; 139 G; 155 T; 0 U; 0 Other;  
 Query Match 10.3%; Score 170; DB 3; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-52;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 60  
 DB 3 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 62  
 QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTGTGAGAAATCCCATGAATAGACTGCTGGCAG 120  
 DB 63 TTGGGGCTGCTATGTTTCTGCTTTGCTGTGAGAAATCCCATGAATAGACTGCTGGCAG 122  
 QY 121 AGACCTTGACACGCTCTCCACTCATCGAATGGCTGATAGCGGATGGG 170  
 DB 123 AGACCTTGACACGCTCTCCACTCATCGAATGGCTGATAGCGGATGGG 172

RESULT 2  
 AAZ55547/c  
 ID AAZ55547 standard; cDNA; 610 BP.  
 AC AAZ55547;  
 XX  
 DT 14-MAR-2000 (first entry)  
 XX  
 DE Canine interleukin-5 (IL-5) cDNA complement.  
 XX  
 KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.  
 XX  
 OS Canis familiaris.

XX Key Location/Qualifiers  
 FH complement(178..582)  
 FT /\*tag= a  
 FT /product= "Canine IL-5"  
 XX  
 PN WO9961618-A2.  
 XX  
 XX 02-DEC-1999.  
 XX  
 XX 28-MAY-1999; 99WO-US011942.  
 XX  
 XX 29-MAY-1998; 98US-0087306P.  
 XX  
 XX (HESK-) HESKA CORP.  
 XX  
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;  
 XX  
 XX WPI; 2000-072623/06.  
 DR P-PSDB; AAY58219.  
 XX  
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 PT useful for treating or preventing e.g. tumors or autoimmune disease.  
 XX  
 XX Claim 1b; Page 224-225; 264pp; English.  
 PS  
 XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine

CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline FLT-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX  
 SQ Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 U; 0 Other;  
 Query Match 10.3%; Score 170; DB 3; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-52;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 60  
 DB 608 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAATTTGAGTTGCTAGCTC 549  
 QY 61 TTGGGGCTGCTATGTTTCTGCTTTGCTGTGAGAAATCCCATGAATAGACTGCTGGCAG 120  
 DB 548 TTGGGGCTGCTATGTTTCTGCTTTGCTGTGAGAAATCCCATGAATAGACTGCTGGCAG 489  
 QY 121 AGACCTTGACACGCTCTCCACTCATCGAATGGCTGATAGCGGATGGG 170  
 DB 488 AGACCTTGACACGCTCTCCACTCATCGAATGGCTGATAGCGGATGGG 439

RESULT 3  
 AAF74305  
 ID AAF74305 standard; DNA; 252 BP.  
 AC AAF74305;  
 XX  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE Canine interleukin-5 coding sequence #2.  
 XX  
 KW Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;  
 KW inflammatory reaction; ds.  
 OS Canis sp.

XX  
 PN WO200111049-A2.  
 XX  
 XX 15-FEB-2001.  
 XX  
 XX 09-AUG-2000; 2000WO-US021651.  
 XX  
 XX 10-AUG-1999; 99US-00371615.  
 XX  
 XX (IDEX-) IDEX LAB INC.  
 XX  
 XX Guo H, Lawton R, Mermer B, Aiyappa AP;  
 XX  
 XX WPI; 2001-191542/19.  
 DR P-PSDB; AAB72616.  
 XX  
 XX Novel canine interleukin 5 polynucleotide and polypeptides are used for  
 PT generating antibodies which are useful in treating allergies in dogs.  
 XX  
 XX Example 1; Fig 1; 48pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences of the



CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
 CC cancer and inflammatory reactions in dogs. The present sequence is one  
 CC version of the IL-5 coding sequence shown in the specification

XX  
 SQ Sequence 252 BP; 69 A; 54 C; 60 G; 69 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 4; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-42;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGGAATTTGAGTTTGGCTAGCTTCTTGGGGCTGCCCTATGTTCTGCTTTT 86  
 Db 1 ATGAGAATGCTTCTGGAATTTGAGTTTGGCTAGCTTCTTGGGGCTGCCCTATGTTCTGCTTTT 60

QY 87 GCTGTGAAAAATCCCATGAATAGACTGGTGGCAGACACCTTGACACTGCTCTCCACTCAT 146  
 Db 61 GCTGTGAAAAATCCCATGAATAGACTGGTGGCAGACACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGG 170  
 Db 121 CGAACTTGGCTGATAGCGGATGGG 144

RESULT 4  
 AAZ55548  
 ID AAZ55548 standard; cDNA; 402 BP.

XX AC AAZ55548;  
 XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5) cDNA coding region.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; AAY58219.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 XX PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX FS Claim 1h; Page 225; 264pp; English.

XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX SQ Sequence 402 BP; 129 A; 79 C; 93 G; 101 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 3; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-42;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGAATGCTTCTGGAATTTGAGTTTGGCTAGCTTCTTGGGGCTGCCCTATGTTCTGCTTTT 86  
 Db 1 ATGAGAATGCTTCTGGAATTTGAGTTTGGCTAGCTTCTTGGGGCTGCCCTATGTTCTGCTTTT 60

QY 87 GCTGTGAAAAATCCCATGAATAGACTGGTGGCAGACACCTTGACACTGCTCTCCACTCAT 146  
 Db 61 GCTGTGAAAAATCCCATGAATAGACTGGTGGCAGACACCTTGACACTGCTCTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGGATGGG 170  
 Db 121 CGAACTTGGCTGATAGCGGATGGG 144

RESULT 5  
 AAZ55549/c  
 ID AAZ55549 standard; cDNA; 402 BP.

XX AC AAZ55549;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-5 (IL-5) cDNA coding region complement.

XX KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011942.

XX PR 29-MAY-1998; 98US-0087306P.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; AAY58219.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 XX PT useful for treating or preventing e.g. tumors or autoimmune disease.

XX FS Claim 1h; Page 226; 264pp; English.

XX Sequences AAZ55546-255551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).

CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

SQ Sequence 402 BP; 101 A; 93 C; 79 G; 129 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 3; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-42;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCTATGTTTCTGCTTT 86  
 DB 402 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCTATGTTTCTGCTTT 343  
 QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146  
 DB 342 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTTCCACTCAT 283  
 QY 147 CGAACTTGGCTGATAGCGATGGG 170  
 DB 282 CGAACTTGGCTGATAGCGATGGG 259

## RESULT 6

AAF74300  
 ID AAF74300 standard; DNA; 405 BP.

AC AAF74300;

DT 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #1.

KW DOG; interleukin-5; IL-5; allergy; cancer; gene therapy;  
 KW inflammatory reaction; ds.

OS Canis sp.

PN WO20011049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-US021651.

XX 10-AUG-1999; 99US-00371615.

XX (INDEX-) IDEXX LAB INC.

PI Guo H, Lawton R, Mermer B, Aiyappa AP;

DR WPI; 2001-191542/19.

DR P-PSDB; AAB72615.

XX Novel canine interleukin 5 polynucleotide and polypeptides are used for  
 XX generating antibodies which are useful in treating allergies in dogs.

PS Claim 31; Page 46; 48pp; English.

XX The present invention provides the protein and coding sequences of the  
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,  
 CC cancer and inflammatory reactions in dogs. The present sequence is one  
 CC version of the IL-5 coding sequence shown in the specification

SQ Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 U; 0 Other;

Query Match 8.7%; Score 144; DB 4; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-42;  
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCTATGTTTCTGCTTT 86  
 DB 402 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTTTGGGGCTGCTATGTTTCTGCTTT 60

QY 87 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTTCCACTCAT 146  
 DB 61 GCTGTAGAAAATCCCATGATAGACTGTGGCAGAGACCTTGACACTGCTTCCACTCAT 120

QY 147 CGAACTTGGCTGATAGCGATGGG 170

DB 121 CGAACTTGGCTGATAGCGATGGG 144

## RESULT 7

AAZ55550

ID AAZ55550 standard; cDNA; 345 BP.

XX AAZ55550;

XX 14-MAR-2000 (first entry)

XX Canine mature interleukin-5 (IL-5) cDNA.

KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;  
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US011942.

XX 29-MAY-1998; 98US-0087306P.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR P-PSDB; AAY58220.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,  
 XX useful for treating or preventing e.g. tumors or autoimmune disease.

PS Claim 1h; Page 226-227; 264pp; English.

XX Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine  
 CC interleukin-5 (IL-5). The invention relates to canine IL-4, canine or  
 CC feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40  
 CC ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)  
 CC and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and  
 CC nucleotides which encode these immunoregulatory proteins. The proteins,  
 CC their associated nucleic acids, specific antibodies and inhibitors may be  
 CC used as vaccines for therapeutic or prophylactic regulation of an immune  
 CC response in animals (particularly cats, dogs, horses and humans). They  
 CC may be used to treat autoimmune or infectious diseases including  
 CC allergies, tumours, inflammation and graft rejection, and to increase the  
 CC response from a co-administered antigen. The nucleotide sequences can  
 CC also be used for the recombinant production of a protein, while  
 CC nucleotide fragments are useful as probes, as amplification primers and  
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).  
 CC The proteins may be used to raise antibodies and to screen for modulators  
 CC of activity, while the antibodies may be used in detection, and in drug  
 CC targeting

XX Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 U; 0 Other;

Query Match 7.8%; Score 129; DB 3; Length 345;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-37;  
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1276 CACCACTGTCATTAAAGAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCC 1335  
 DB 121 CACCACTGTCATTAAAGAGTTTTTCAGGGTATAGACATTTGAAGACCAACTGCC 180

QY	1336	CACGGGGAGGCTGTGGATAAACTATTCCAAACTTGTCTTTAATAAAGAAACACATAGAG	1395
Db	181	CACGGGGAGGCTGTGGATAAACTATTCCAAACTTGTCTTTAATAAAGAAACACATAGAG	240
QY	1396	CGCCAAAAA 1404	
Db	241	CGCCAAAAA 249	
RESULT 8			
AAZ55551/c			
ID	AAZ55551	standard; cDNA; 345 BP.	
XX	AAZ55551;		
XX	14-MAR-2000	(first entry)	
XX	Canine mature interleukin-5 (IL-5) cDNA complement.		
DE	Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;		
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.		
KW	Canis familiaris.		
OS	WO9961618-A2.		
XX	02-DEC-1999.		
XX	28-MAY-1999;	99WO-US011942.	
XX	29-MAY-1998;	98US-0087306P.	
PR	(HESK-) HESKA CORP.		
XX	Sim G, Yang S, Dreitz MJ, Wonderling RS;		
PI	WPI; 2000-072623/06.		
DR	P-PSDB; AAY58220.		
XX	Nucleic acids encoding immunoregulatory proteins from cats or dogs,		
PT	useful for treating or preventing e.g. tumors or autoimmune disease.		
XX	Claim 1h; Page 228; 264pp; English.		
XX	Sequences AAZ55546-Z55551 represent cDNA sequences encoding canine		
CC	interleukin-5 (IL-5). The invention relates to canine IL-4, canine or		
CC	feline FIt-3 ligand, canine or feline CD40, canine or feline CD134 (CD40		
CC	ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha)		
CC	and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and		
CC	nucleotides which encode these immunoregulatory proteins. The proteins,		
CC	their associated nucleic acids, specific antibodies and inhibitors may be		
CC	used as vaccines for therapeutic or prophylactic regulation of an immune		
CC	response in animals (particularly cats, dogs, horses and humans). They		
CC	may be used to treat autoimmune or infectious diseases including		
CC	allergies, tumours, inflammation and graft rejection, and to increase the		
CC	response from a co-administered antigen. The nucleotide sequences can		
CC	also be used for the recombinant production of a protein, while		
CC	nucleotide fragments are useful as probes, as amplification primers and		
CC	as sources of inhibitory therapeutics (e.g., antisense oligonucleotides)		
CC	The proteins may be used to raise antibodies and to screen for modulators		
CC	of activity, while the antibodies may be used in detection, and in drug		
CC	targeting		
XX	Sequence 345 BP; 79 A; 78 C; 68 G; 120 T; 0 U; 0 Other;		
QY	Query Match	7.8%; Score 129; DB 3; Length 345;	
Db	Best Local Similarity	100.0%; Pred. No. 4.6e-37;	
	Matches 129; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1276	CACCAACCTGCATTAAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCRAACTGCC	1335
Db	225	CACCAACCTGCATTAAAGAAGTTTTCAGGGTATAGACATTTGAAGAACCRAACTGCC	166

QY	1336	CACGGGAGGCTGTGGATAAACTATTCAAAACCTTGCTCTTTAATAAAGAACACATAGAG	1395
Db	165	CACGGGAGGCTGTGGATAAACTATTCAAAACCTTGCTCTTTAATAAAGAACACATAGAG	106
QY	1396	CGCCAAAAA 1404	
Db	105	CGCCAAAAA 97	
RESULT 9			
AAAF74306	ID	AAAF74306 standard; DNA; 393 BP.	
XX	AC	AAAF74306;	
XX	DT	04-MAY-2001 (first entry)	
XX	XX	Canine interleukin-5 coding sequence #3.	
DE	DE	Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;	
KW	KW	inflammatory reaction; ds.	
XX	XX	Canis sp.	
OS	OS	WO200111049-A2.	
XX	XX	15-FEB-2001.	
XX	PD	09-AUG-2000; 2000WO-US021651.	
XX	PF	10-AUG-1999; 99US-00371615.	
XX	PR	(INDEX-) IDEXX LAB INC.	
XX	PA	Guo H, Lawton R, Mermer B, Aiyappa AP;	
XX	PI	WPI; 2001-191542/19.	
XX	DR	Novel canine interleukin 5 polynucleotide and polypeptides are used for	
XX	PT	generating antibodies which are useful in treating allergies in dogs.	
XX	PS	Claim 1; Page 35; 48pp; English.	
XX	CC	The present invention provides the protein and coding sequences of the	
CC	CC	canine interleukin-5 (IL-5) protein. This can be used to treat allergies,	
CC	CC	cancer and inflammatory reactions in dogs. The present sequence is one	
CC	CC	version of the IL-5 coding sequence shown in the specification	
XX	XX	Sequence 393 BP; 128 A; 82 C; 86 G; 97 T; 0 U; 0 Other;	
QY	Query Match	7.8%; Score 129; DB 4; Length 393;	
	Best Local Similarity	100.0%; Pred. NO. 4.5e-37;	
	Matches 129; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1276	CACCAACTGTGCATTAAGAAGTGTTCAGGGTATGACACATTGAAGAACCAAACTGCC	1335
Db	76	CACCAACTGTGCATTAAGAAGTGTTCAGGGTATGACACATTGAAGAACCAAACTGCC	135
QY	1336	CACGGGAGGCTGTGGATAAACTATTCAAAACCTTGCTCTTTAATAAAGAACACATAGAG	1395
Db	136	CACGGGAGGCTGTGGATAAACTATTCAAAACCTTGCTCTTTAATAAAGAACACATAGAG	195
QY	1396	CGCCAAAAA 1404	
Db	196	CGCCAAAAA 204	
RESULT 10			
AAT50756	ID	AAT50756 standard; cDNA; 399 BP.	
XX	XX	AAT50756;	
XX	XX		



Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 CCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCAC 142  
 DB 113 CCATGAATAGACTGGTGCAGAGACCTTGACACTGCTCTCCAC 155

## RESULT 12

AZ44265  
 ID AAZ44265 standard; DNA; 838 BP.

XX AC AAZ44265;

XX DT 31-MAR-2000 (first entry)

XX DE Porcine IL-5 DNA.

XX KW Pig; vaccine; cysticercosis, protective antigen; cC1; cC3; cC4;  
 KW tenial cysticercus; gamma interferon; IFN-gamma; interleukin 5; IL-5; ss.

XX OS Sus scrofa.

XX PN CN1231339-A.

XX PD 13-OCT-1999.

XX PF 29-JAN-1999; 99CN-00113447.

XX PR 29-JAN-1999; 99CN-00113447.

XX PA (UYIW-) UNIV NO 2 MILITARY MEDICAL PLA.

XX PI Sun S, Dai J;

XX DR WPI; 2000-087904/08.

XX PT Nucleic acid vaccine for cysticercosis co-contracted by human and pig.

XX PS Claim 3; Page 9; 21pp; Chinese.

XX CC This invention describes a novel nucleic acid vaccine for preventing and  
 CC curing human and pork cysticercosis. The invention involves the formation  
 CC of a eukaryotic expression plasmid from fusion transcript expression unit  
 CC consisting of three protective antigen genes (cC1, cC3 and cC4) of pig  
 CC tenial cysticercus and coexpression unit of related cell factor gamma  
 CC interferon (IFN-gamma) and pork interleukin 5 (IL-5) genes. The  
 CC production and purification process of said nucleic acid vaccine is  
 CC simple and convenient, the physical and chemical properties of the  
 CC vaccine are stable, and the vaccine is easy to store and transport, and  
 CC possesses effective immunological protective function for human and pig  
 CC cysticercosis. This sequence represents the pig IL-5 gene used in the  
 CC method of the invention

XX SQ Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 U; 0 Other;

Query Match 2.5%; Score 41; DB 3; Length 838;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGTTGCTAGCTCTTGGGGCTGCTATGTTCTGCC 83  
 DB 61 ATTGAGTTGCTAGCTCTTGGGGCTGCTATGTTCTGCC 101

## RESULT 13

ABV56577/c

ID ABV56577 standard; cDNA; 357 BP.

XX AC ABV56577;

XX CC ABV56577;

XX DT 17-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 56568.

XX

KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US005171.

XX PR 17-FEB-2000; 2000US-0183319P.

XX PR 16-MAR-2000; 2000US-0189862P.

XX PR 25-MAY-2000; 2000US-0207454P.

XX PR 09-JUN-2000; 2000US-0211314P.

XX PR 18-JUL-2000; 2000US-0219007P.

XX PR 13-DEC-2000; 2000US-0255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI; 2001-662795/76.

XX PS Claim 1; Page 10911; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;

XX CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 357 BP; 104 A; 93 C; 90 G; 69 T; 0 U; 1 Other;

Query Match 1.6%; Score 26; DB 5; Length 357;

Best Local Similarity 100.0%; Pred. No. 7.7; 0; Indels 0; Gaps 0;  
 Matches 26; Conservative 0; Mismatches 0;

QY 1458 TTTTITTTTTTTTTTTTACAGAAT 1483  
 DB 69 TTTTITTTTTTTTTTTTACAGAAT 44

## RESULT 14

AAH92592

ID AAH92592 standard; DNA; 700 BP.

XX AC AAH92592;

XX DT 09-OCT-2001 (first entry)

XX DE Human inflammatory bowel disease related gene fragment IGR1292a.

XX

KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.

XX OS Homo sapiens.

XX PN WO200142511-A2.

XX

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PD XX 14-JUN-2001.
PF XX
PR XX 11-DEC-2000; 2000WO-US033632.
PR XX 10-DEC-1999; 99US-0170257P.
PR XX 10-APR-2000; 2000US-0196046P.
XX XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX XX
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX XX
PS Disclosure; Page 261-262; 463pp; English.
XX XX
CC The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a gene
CC containing a polymorphic site described in the exemplification of the
CC invention
XX XX
SQ Sequence 700 BP; 216 A; 101 C; 125 G; 258 T; 0 U; 0 Other;
Query Match 1.6%; Score 26; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 399 ATAAATGTAAAGTTAAATATGATT 424
DB 183 ATAAATGTAAAGTTAAATATGATT 208

RESULT 15
AAC84351/c
ID AAC84351 standard; DNA; 2235 BP.
XX AC AAC84351;
XX XX
DT 19-MAR-2001 (first entry)
DE Corn clone CPR951 FL cDNA sequence.
XX XX
KW Acquired resistance gene; Nph1; Nph2; rice; Nph2-1; Nph2-2; wheat;
KW plant pathogen; transgenic; disease resistance; corn; Npri; ss.
XX OS Zea mays.
XX XX
FH Key Location/Qualifiers
FT CDS 261..1491
FT /*tag= a
XX XX
FN WO200070069-A1.
XX XX
PD 23-NOV-2000.
XX XX
PF 12-MAY-2000; 2000WO-US013307.
XX XX
PR 13-MAY-1999; 99US-0133965P.
XX XX
PA (MONS ) MONSANTO CO.
XX XX
PI Bougri OV, Rommens CMT, Srivastava N, Swords KM;
XX WPI: 2001-016244/02.
DR P-PSDB; AAB48093.

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SQ

New acquired resistance genes Nph1 from rice, Oryza sativa, and Nph2-1 and Nph2-2 from wheat, Triticum aestivum, useful for producing transgenic plants with increased disease resistance.

Example 1; Page 92; 101pp; English.

The invention relates to acquired resistance genes Nph1 from rice, and Nph2-1 and Nph2-2 from wheat. The Nph1 and Nph2 polypeptides can be expressed by standard recombinant methodology. The Nph1 and Nph2 polynucleotides or polypeptides can be used to enhance acquired resistance in plants (e.g. wheat or rice) to control plant pathogens e.g. the genes can be introduced to make transgenic plants with increased disease resistance. The polynucleotides are also useful to produce probes and primers useful to detect the polynucleotides (to identify transgenic plants containing an acquired resistance gene) and to isolate similar sequences e.g. from other species. The polypeptides can be used to make antibodies useful to monitor protein production e.g. in transgenic plants. The present sequence represents a corn clone CPR951 FL cDNA sequence, used in the identification of acquired resistance genes from rice and wheat

Sequence 2235 BP; 630 A; 466 C; 566 G; 573 T; 0 U; 0 Other;  
Query Match 1.6%; Score 26; DB 4; Length 2235;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1458 TTTTITTTTTTTTTTTTACAGAAAT 1483  
DB 2196 TTTTITTTTTTTTTTTTACAGAAAT 2171

Search completed: August 31, 2004, 14:34:30  
Job time : 676 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 15:56:41 ; Search time 790.781 Seconds  
(without alignments)  
8907.036 Million cell updates/sec

Title: US-10-787-382-18  
Perfect score: 1658  
Sequence: 1 agcaaacactgaacatttc.....gtagtgaagatttggaga 1658

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseqn\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	634.6	38.3	3241	3 AAA34856	Aaa34856 Human ade
2	634.6	38.3	3241	3 AAF20978	Aaf20978 Human low
3	634.6	38.3	3241	7 ABZ96672	Abz96672 Human nuc
4	634.6	38.3	4057	3 AAA34858	Aaa34858 Human ade
5	634.6	38.3	4057	3 AAF20980	Aaf20980 Human low
6	634.6	38.3	4057	7 ABZ96674	Abz96674 Human nuc
7	634.6	38.3	9738	6 AAS15002	Aas15002 DNA encod
8	600.6	36.2	3230	1 AAN81381	Aan81381 Entire nu
9	600.6	36.2	3230	2 AAQ74056	Aaq74056 Human int
10	600.6	36.2	3230	3 AAC73725	Aac73725 Human IL-
11	600.6	36.2	3230	7 ABX04379	Abx04379 Human int
12	272.6	16.4	700	4 AAH92592	Aah92592 Human inf
13	221.6	13.4	700	4 AAH92594	Aah92594 Human inf
14	216	13.0	700	4 AAH92591	Aah92591 Human inf
15	215.4	13.0	700	4 AAH92593	Aah92593 Human inf
16	205.2	12.4	1395	1 AAN71243	Aan71243 Sequence
17	171.8	10.4	610	3 AAZ55546	Aaz55546 Canine in
18	171.8	10.4	610	3 AAZ55547	Aaz55547 Canine in
19	150.8	9.1	5397	6 ABL33044	AbL33044 Human imm
20	149.4	9.0	838	3 AAZ44265	Aaz44265 Porcine I
21	145.8	8.8	252	4 AAF74305	Aaf74305 Canine in
22	145.8	8.8	402	3 AAZ55548	Aaz55548 Canine in
23	145.8	8.8	402	3 AAZ55549	Aaz55549 Canine in

24	145.8	8.8	405	4 AAF74300	Aaf74300 Canine in
25	138.2	8.3	520	3 AAT50755	Aat50755 Ovine IL-
c 26	134.6	8.1	5397	6 ABL33045	AbL33045 Human imm
27	131.6	7.9	345	3 AAZ55550	Aaz55550 Canine ma
c 28	131.6	7.9	345	3 AAZ55551	Aaz55551 Canine ma
29	131.6	7.9	393	4 AAF74306	Aaf74306 Canine in
30	117.4	7.1	385	3 AAA43842	Aaa43842 Human sec
31	117.4	7.1	816	3 AAA34857	Aaa34857 Human ade
32	117.4	7.1	816	3 AAA13338	Aaa13338 Human int
33	117.4	7.1	816	3 AAF20979	Aaf20979 Human low
34	117.4	7.1	816	7 ABZ96673	Abz96673 Human nuc
35	117.4	7.1	816	7 ACF63368	AcF63368 Human int
36	112.6	6.8	399	2 AAT50756	Aat50756 Ovine IL-
37	108	6.5	6727	2 AAT88014	Aat88014 Murine IL
38	108	6.5	6727	3 AC73648	Ac73648 Murine IL
39	108	6.5	6727	7 ABX04302	Abx04302 Mouse int
40	99.4	6.0	402	1 AAN81380	Aan81380 A human B
41	97.2	5.9	444	3 AAC68875	Aac68875 Modified
42	96.2	5.8	858	8 AAL61293	Aal61293 hIL5-P2-P
43	96.2	5.8	858	8 AAL61294	Aal61294 hIL5-P30-
44	89.4	5.4	381	3 AAC68867	Aac68867 Modified
45	89	5.4	864	8 AAL61296	Aal61296 hIL5.37 v

## ALIGNMENTS

RESULT 1  
AAA34856  
ID AAA34856 standard; DNA; 3241 BP.  
XX  
AC AAA34856;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2545.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
PS Disclosure; Page 715-716; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,





Db 2209 TAGAAGTTGAGACTAAACTGGTTTGTTCGACCAAGATTTGGAG 2255

## RESULT 2

AAE20978

ID AAF20978 standard; DNA; 3241 BP.

XX AC AAF20978;

XX DT 14-MAR-2001 (first entry)

XX Human low adenosine antisenase oligonucleotide related sequence #2545.

XX Low adenosine antisenase oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cyrostatic;  
XX respiratory obstruction; pulmonary obstruction; impeded respiration;  
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
XX cancer; ss.

XX Homo sapiens.

XX WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J.W.

XX Nyce JW;

XX WPI; 2000-679535/66.

XX Low adenosine (A) content antisenase oligonucleotides which do not trigger  
XX adenosine receptors during metabolism, useful e.g. for treating cancers  
XX and respiratory obstructions.

XX Disclosure; Page 787-788; 1592pp; English.

XX The present invention describes low adenosine (A) content antisenase  
XX oligonucleotides and compositions (I) comprising them. In the antisenase  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antiasthmatic, hypotensive and cyrostatic activities.  
XX The antisenase oligonucleotides and (I) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with  
XX lung/respiratory disorders and malignancies, such as stimulating and  
XX activating peptide factors and transmitters, transcription factors,  
XX immunoglobulins and antibodies, antibody receptors, cytokines and  
XX chemokines, endogenously produced specific and non-specific enzymes,  
XX binding proteins, adhesion molecules and their receptors, cytokine and  
XX chemokine receptors, adenosine receptors, bradykinin receptors, central  
XX nervous system (CNS) and peripheral nervous and non-nervous system  
XX receptors, CNS and peripheral nervous and non-nervous system peptide  
XX transmitters, defensins, growth factors, vasoactive peptides and  
XX receptors, binding proteins and malignancy associated proteins. The  
XX antisenase oligonucleotides may be used in this way to treat disorders  
XX including respiratory obstruction (especially pulmonary obstruction  
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
XX surfactant hypoproduction which are associated with a disease or  
XX condition selected from pulmonary vasoconstriction, inflammation,  
XX allergies, asthma, impeded respiration, respiratory distress syndrome  
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisenase oligonucleotides used in the exemplification of  
CC the present invention

XX Sequence 3241 BP; 1026 A; 546 C; 632 G; 1037 T; 0 U; 0 Other;

Query Match 38.3%; Score 634.6; DB 3; Length 3241;

Best Local Similarity 68.6%; Pred. No. 1e-115;

Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;

SQ 1 AGGCAACACCTGAACATTCAGAGCTATGAGAACTCTTCTGAATTTGAGTTTGTAGCTC 60  
536 AGGCAACACGCAAGCTTCAGAGCCATGAGAGTCTTCTCAITTTGAGTTTGTAGCTC 585

Qy 61 TTGGGCTGCTATGTTTCTGCTTGTAGAAATCCCATGAATAGACTGGTGGAG 120

Db 586 TTGGAGCTGCTATGCTGATGCCATCCACAGAAATTCACAGAGTGCAATGGTGAAG 645

Qy 121 AGACCTTGACACTGCTCTCCACTCATGAACTTGCTGATAGGCGATGGGTAATTTCT 180

Db 646 AGACCTTGGCACTGCTTCTACTCATCGAATCTGCTGATAGCAATGAGTAATTTCT 705

Qy 181 TTTGATTTCTACAGTCTTTTAAATGCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 234

Db 706 TTTGATTTCTACAGTCTTTTAAATGCAATGCAATGCTGCTGCTGCTGCTGCTGCTGCT 765

Qy 235 -TTTAAAGATCCATTTATCAATAAGTAAATGAGTGTAAATATATATATATGCTAAC 293

Db 766 ATATAGAGATCTGTTATTAATAATAAGATTTCTGAG-CACATTAGTACATGGTGATACT 824

Qy 294 ATGTTACTCAGAAGAATTTATTTAAAGTTATGAACCTTACAAATACATTAATAAATGAATG 353

Db 825 ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGCTGCTGCTGCTGCTGCTGCTG 884

Qy 354 TTGTTTCTCTTTTTCAGAACCTGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 413

Db 885 -TATTTCT 943

Qy 414 AAATATGATTTGATAAAATGATTTACATGAATCAGT-----TTCATATTTTAAAGCTATAAA 469

Db 944 AAATATGATTTGATAAAATGATTTACATGAATGATTAATTTCTGTTTAAAGCTATAAA 1003

Qy 470 GTATCAGTTAATTTGGGATGATTTTATTTTCTATTTCTATTTCTATTTCTATTTCTATTT 529

Db 1004 TCATTTAGTTATTCATTTGGAATTTTAAATTTCTATTTCTATTTCTATTTCTATTTCTATTT 1063

Qy 530 AAAT-TATGTCCTTATGAATTTAGGAATGCTGTTAGGAATGCTCTACAAATATTAAGTA 588

Db 1064 GAATGCTGCTATTAATAATGAGGATGACTTT-----TTATCAAGTA 1108

Qy 589 GAATCCATTAAGCAAGTGGATCAGGCCCTTTTGAATGTTGTCAGTTCTCCTCATCTCAAG 648

Db 1109 GAATCCTTTAAACAAAGTGGATTTAGGCTCTTTGGTGATGTTGTTAGTT-TGCTCCCAAG 1167

Qy 649 AGCTTCGTCAGGATTTCTTCCAAAGAAATTCATATGCGTCAGAGACTTCCCTAG 708

Db 1168 AGCATCGTTCAGGATTTCTTCCAGAGGATTTCCACTGAGTGAGGTCGTCGCTAG 1227

Qy 709 GCTCCATTCACCTCTGCTGGCTTTCCCTCACCTCAACGTTTTTCTGAAAGTACTAGCA 768

Db 1228 TCTCCGTCAGTCTTGAC----TCTTCTCACTCAACGTTTCTGAAAGTATTAGCA 1282

Qy 769 ACTTGGGTTATTTTGAATTTATGCTCAGTAGACATGAATATACAGTGAAGTCT 828

Db 1283 ACTCAGAATTTATTTTATAGAACCTATCATCAGTACATTAATAATATATAACAATGCC- 1341

Qy 829 ATATTAATAGTCACCTCCACATATTTAAATGATTTTAACTCTAATGAATCATATACAT 888

Db 1342 -CTATTTAATAATTTCTGCATCTTAAATATATGATCTATGATGCTGTTGATGCA 1400

Qy 889 CTGAGTAGTCATGCTCATATTAATAATGTTTAAATAATGATATCATTTAGTCTTAATAGA 948

Db 1401 TTTGAATATGCTCCTGCTCATATTAATAATGTTTAAATATATATAGTTTATTAGTCTAAATAGA 1460





CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA3392) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;  
Query Match 38.3%; Score 634.6; DB 3; Length 4057;  
Best Local Similarity 68.6%; Pred. No. 1e-115;  
Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;  
QY 1 AGGCAACACCTGAACTTCAGAGCTATGAGATGCTTCGAAATTTGAGTTTCTAGCTC 60  
DB 526 AGGCAACGAGACGTTTCAGAGCCATGAGGATGCTTCGATTGAGTTTCTAGCTC 585  
QY 61 TTGGGGTGGCTATGTTTCTGCTTTCGCTGTAGAAATCCATGATAGACTGGTGGCAG 120  
DB 586 TTGGAGCTGGCTACGTGTATGCCATCCCCAGAAATTCACAGTGCATTGGTGAAG 645  
QY 121 AGACCTTGACACTGCTCCACTCATCGAATCTGGCTGATAGGCGATGGGTAATTTCT 180  
DB 646 AGACCTTGGCACTGCTTCTACTCATCGAATCTGGCTGATAGGCGAATGAGTAAATTTCT 705  
QY 181 TTTTGAATCTTACAGTCTTTAAATGCAATGGTAAATTTGGTGGTGGCTAGTT----- 234  
DB 706 TTATGATCTTACAGTCTGTAAAGTGCATAGGTAATCATTTGTGATGGTTCTTACTAT 765  
QY 235 -TTTAAAGATCCATATCAATGAATGAGTATGATGTTTAAATATATATATATGATGTAACC 293  
DB 766 ATATAGAGATCTGTTTAAATGAATGAATTCGAG-CACATTAGTACATGGGTGATAACT 824  
QY 294 ATGTTTACTCAGAAGAAATTTATTTAAAGTTATGAACCTTACAATPACATTTAAAAATGAATG 353  
DB 825 ACATCACCAGCAACATCTGTAAAGTTATGAATGCTGGTGTGCTGTAATAATGATTTG 884  
QY 354 TTGTTTCTTCTTTTTCAGAACCTGATGATCTCTCTGAAATATAAATGATAGTT 413  
DB 885 -TAATTTCTTCTCTCAGACTCTGAGGATTCCTGTTTCTGTTTACATAAATGTAAGTT 943  
QY 414 AAATATGATTTGATAAAATGATTTACATGAATCAGT-----TTTCAATTTTAAAGTATAAA 469  
DB 944 AAATATGATTTAGTAAATGATGCAATGAATGAATGAATTTCTGTTTAAAGCTGATAA 1003  
QY 470 GTATCAGTTTAACTGGGATGATTTTATCTATTTTATTTTATGTTGGGATGT 529  
DB 1004 TCAATAGTTTATCATTTGGAATTTTAAATTTTCTATATTTTCTATTTTCTATGTTGGGCTGT 1063  
QY 530 AAAT-TATGTTGCTTATGATATAGGAATGCTGTTAGGAATGGCTCTACATATTTAAGTA 588  
DB 1064 GAATGCTGTACTTTAAATATGAGGATGACTTT-----TTATCAAGTA 1108  
QY 589 GAATCCATTAAGCAAGTGAATCAGGCCCTTTTGTGATGTTGCTCATCTCAAG 648  
DB 1109 GAATCCTTTAAACAAGTGATGAGTCTTCTTGGTATGTTTGTAGTT-TGCCTCCCAAG 1167

QY 649 AGCTCGTGTGAGCATTCTTCCAAAGAAATCCATATTGGGTGAGAGATATCTTCTAG 708  
DB 1168 AGCATCGTGTGAGGATTTCTTCCAGAAAGATTTCCACATGAGTGAGAGGTGGTGTAG 1227  
QY 709 GCTCCATTACCTCTGCTGTTGGCTTTCTCACCCTCAACGTTTTTCTGAAAGTACTAGCA 768  
DB 1228 TCTCGGTGAGTCTGAC-----TCTTCTCCTCTTAACTGTTTCTGAAAGTACTAGCA 1282  
QY 769 ACTTGGGGTATATTTTAGAATTTATGGTCAGTAGACATGAATATACAGTGAAGTCTCT 828  
DB 1283 ACTCAGAATTTATTTTATAGAACCATGATCAGTAGACATTAATAATATATACAAATGCC- 1341  
QY 829 ATATTAATAGTCACTTCCACATATTTAAATGAATTTTAACTCTAATGAATCATATACAT 888  
DB 1342 -CTATATTAATATTTCTGACATCTTAAATAATTTATGACTATATGATGGTGTGTATGCA 1400  
QY 889 CTGAGTAGTATGTCATGTCATATTAATAATGTTAAATAATGATATCATATGATCTTAATA 948  
DB 1401 TTTGAATATGTCCTGGTCATATTAATAATGTTAAATAATATATAGTTTATAGTCTAAATAGA 1460  
QY 949 ATAAATTTACCAGCTAGAACCTATACGAGGAATTTCTGAGGTGAGGTAAATCAGTAAGCA 1008  
DB 1461 ATAAATCTACCAGCTAGAACCTGAGAACACAT--TGNATATGATTTTAAATGATAA--- 1514  
QY 1009 GTTGTATTTATACCTCGTAAGCATTTATTTTCAATTAATCATTTTCAATTTATCATTTGTA 1068  
DB 1515 --TGCATTACACTTCCAAACATTTTTTCCAGTTTACATTAATTAAGTTATATCTCTTTATA 1572  
QY 1069 ACATTTCTCAGTAATTTATTAACATCATTTTAC--TTATGGTAAATTTAGCTTACTATTAAG 1127  
DB 1573 AAATCTCTCGTAAATCATATAGCTTCTATCTCTTTTGGAAATTTTATCTTAATATGTG 1632  
QY 1128 GTGGTTTCCCACCTCGAAAGACACAACTTCTGGGAGAGGGAACCTTTGTGTA 1187  
DB 1633 GTGGTTTGTGCTTAGAA---ACAAACAAATAAATCTTTGGAGAGGGAACCTCATGTA 1688  
QY 1188 AACCCCAAAACAAAGTCTAATCTT----- 1213  
DB 1689 AATACCAAAACAAAGCTTAATCTTTGGACCAAAATTTGTTTAAATTAATTTATTTTAA 1748  
QY 1214 ----- 1213  
DB 1749 TTGATGAATTAAGATATATATTTATTTGTGTACATAATGATGTTTGAAGTATGAT 1808  
QY 1214 -----TTGGACCAAAATTTTATGCTTGTGTTTGAATGAAATATATTTT 1256  
DB 1809 ACATTTGAGATGGAACAATGAGCAAAATTTTATACCTTGTCTTGAATTTTGA-TTTT 1867  
QY 1257 TAAATCTTCTCATTTTACGACCAACTGTGCATTTAAAGAAAGTTTTCAGGGTATAGACAC 1316  
DB 1868 AAAATTTTCTCTCATTTTACGACCAACTGTGCATGAAGAAATCTTTCAGGGAATAGGCAC 1927  
QY 1317 ATTGAAGAACCAACTGCCCCAGGGAGCTGTGTGATTAACATTTTCCAAAACCTGCTTT 1376  
DB 1928 ACTGGAGAGTCAACTGTGCAAGGGGTAAGTTTAAAGACATTTTCAAAAACCTGCTTT 1987  
QY 1377 AATAAAGAACATAGCGCCCAAAAGTAAGTTTAAAGACATTTGGCAAAACCTTAAGT 1436  
DB 1988 AATAAAGAAATACATTTGAGCCCAAAAGTAAGTTTACACATTT-----CAATGGAAGCT 2042  
QY 1437 ATATTTGTCTGACTGCTGCTGTTTTTTTTTTTTTTTCAAGAAATTTGACAGTTTCTTA 1496  
DB 2043 ATATTTGTCTGCTGCTGCTTATTTCTAT-----GGAAATTTGACAGTTTCTGCTG 2088  
QY 1497 CAATATCT-----CCTCTGTTCTTTTACAGAAAGGTGTGAGAGAAAGATGGAGAG 1550  
DB 2089 TAATACCTATTGTCATTTTCTTTTTCACAGAAAGGTGAGAGAAAGATGGAGAG 2148  
QY 1551 TGACAAAGTCTCAGACTACCTGCAAGTATTTCTTTGGTGTATTAATAACCCGAGTGGACAC 1610  
DB 2149 TAAACCAATTTCTAGACTACCTGCAAGGATTTCTTTGGTGTATTAATAACCCGAGTGGATAA 2208  
QY 1611 CGAAAGTTGAGAACAAACCCGCTTATTTGTAGTGAAGATTTTGGAG 1657

Db 2209 TAGAAGTTGAGACTAACTGTTGTTGCGACCAAGATTTGGAG 2255  
|||||

## RESULT 5

AAF20980  
ID AAF20980 standard; DNA; 4057 BP.

XX AAF20980;  
XX

DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2547.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.

XX Homo sapiens.

XX WO2000062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
XX adenosine receptors during metabolism, useful e.g. for treating cancers  
XX and respiratory obstructions.

XX Disclosure; Page 788-789; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
XX oligonucleotides and compositions (i) comprising them. In the antisense  
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.  
XX (i) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
XX The antisense oligonucleotides and (i) can be used to down-regulate the  
XX expression and or activity of target polypeptides associated with  
XX lung/respiratory disorders and malignancies, such as stimulating and  
XX activating peptide factors and transmitters, transcription factors,  
XX immunoglobulins and antibodies, antibody receptors, cytokines and  
XX chemokines, endogenously produced specific and non-specific enzymes,  
XX binding proteins, adhesion molecules and their receptors, cytokine and  
XX chemokine receptors, adenosine receptors, bradykinin receptors, central  
XX nervous system (CNS) and peripheral nervous and non-nervous system  
XX receptors, CNS and peripheral nervous and non-nervous system peptide  
XX transmitters, defensins, growth factors, vasoactive peptides and  
XX receptors, binding proteins and malignancy associated proteins. The  
XX antisense oligonucleotides may be used in this way to treat disorders  
XX including respiratory obstruction (especially pulmonary obstruction  
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
XX surfactant hypoproduction which are associated with a disease or  
XX condition selected from pulmonary vasoconstriction, inflammation,  
XX allergies, asthma, impeded respiration, respiratory distress syndrome  
XX (RDS), pain, cystic fibrosis (Cf), allergic rhinitis (AR), pulmonary  
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),

CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention

XX SQ Sequence 4057 BP; 1303 A; 683 C; 796 G; 1275 T; 0 U; 0 Other;

Query Match 38.3%; Score 634.6; DB 3; Length 4057;  
Best Local Similarity 68.8%; Pred. No. 1e-115;  
Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;

QY	1	AGGCAACACTGAACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTTCTGCTAGCTC	60
Db	526	AGGCAACAGCAGAACGTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTCTGCTAGCTC	585
QY	61	TTGGGCTGCTATGTTTCTGCTTTGCTGTAGAAAATCCCATGAATAGACTGGTGGCAG	120
Db	586	TTGGAGCTGCTACGCTGATGCCATCCCAAGAAATTTCCCAAGTGCATTTGGTGAAG	645
QY	121	AGACCTTGACACCTGCTCTCCACTCATCGAATCTGGCTGATAGCGATGGGGTAATTTCT	180
Db	646	AGACCTTGGACCTGCTTCTACTCATCGAATCTGCTGATAGCCATGAGGTAAATTTCT	705
QY	181	TTTGTATTCCTACAGTCTTTTAAATCCATGGGTAATTTGGTGGTGGCTAGTT-----	234
Db	706	TTATGATTCCTACAGTCTCTAAAGTCATAGTAAATCAATTTGTGATGTTCTCTTACTAT	765
QY	235	-TTTAAAGATCCATTAATGAAGTAAGTGAAGTGAATTAATAATATAATGGGTAACC	293
Db	766	ATATAGAGATCTGTTAATAATAATAGATTTCTGAG-CACATTAGTACATGGGTGATACT	824
QY	294	ATGTTACTCAGAAGAAATATATTTAAAGTTATGAACCTTTACAATACATTAATAAATGAATG	353
Db	825	ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGGTGTGCTGTAATAATGATTG	884
QY	354	TTGTTTCCTTCTTTTTCAGAACCTGATGATTCCTACTCTCTGAAATAATAAATGTAAGTT	413
Db	885	-TATTTCTTCTCTCTCCAGATCTGAGGATTCCTGTTCTCTGTACATATAAATAATGTAAGTT	943
QY	414	AAATATGATTTGATAAAATGATTACATGAATCAGT-----TTCATATTTTAAAGCTATAAA	469
Db	944	AAATATGATTTGATAAAATGATTGATGAATGAATTAATTTCTGTTTAAAGCTGATAA	1003
QY	470	GTAATGATTAACATTTGGGATGATTAATTTATCTATTTTGTATTTTATGTTGGCGATGT	529
Db	1004	TCAATAGTTATCATTTGGAATTTTAAATTTCTATATTTTGTATTTTTCATATGGTGGCTGT	1063
QY	530	AAAT-TATGCTGCTTATGAATATTAGGAATGGTGTAGGAATGGCTCTACATATTAAGTA	588
Db	1064	GAATGCTGCTTATTAATAATAGGAATGACTTT-----TTATCAAGTA 1108	
QY	589	GAATCATTAAGCAAGTGGATCAGCCCTTTTGTATGTTGTCAGTTTCTCCATCTCAAAG	648
Db	1109	GAATCCTTTAAACAAAGTGGATTAGGCTCTTTGGTGTATGTTGTTAGTT-TGCCTCCCAAAG	1167
QY	649	AGCCTCGTGTAGGATCTTTTCCAAAGAAATTCATATTTGGTTCAGAGATCTTCTTAG	708
Db	1169	AGCATCGTGTAGGATCTTTTCCAGAGGATTTCCACACTGAGTGGAGGTCGTCGTAG	1227
QY	709	GTCATCATCACTCTGCTGGTGGCTTCTCTCACCTCAACGTTTCTCTGAAAGTACTAGCA	768
Db	1228	TCTCCGTGCAAGTCTGAC-----TCTTCTCACTCAACGTTTCTGAAAGTATTAGCA	1282
QY	769	ACTTGGGTTATATTTTATAGATTAATGTCAGTAGACATGAATAATATACAGTGAAGTCT	828
Db	1283	ACTCAGAATTAATTTTATAGAACCATGATCATGACATTAATAATATAACAATGCTC- 1341	
QY	829	ATATTAATAGTCACTTCCACATATTTAATGATTTTAACTTAATGAATCATATACAT	888
Db	1342	-CTATTAATAATTTCTGACATCTTAATAATATGACTATATGATGCTGTTGTATGCA	1400
QY	889	CTGGAGTATGTCATGCTCATATTAATGTTAAATAATGATATATCATTTAGTCTAAATAGA	948



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QY 294 ATGTTACTCAGAGAAATATATATAAAGTTATGAACCTTACAATACATTAATAAATGATG 353
Db 825 ACATCACCAGCAAAATCTCTGTTAAAAGTTATGAATCGTGGTGTGTTAAAATGATG 884
QY 354 TTGTTTCTCTTTCTTTTTCAGAACCTGATGATTCCTCTCTGAAATAAATAAATGTAAGTT 413
Db 885 -TATTTCTTCTCTCTCAGACTCTGAGGATTCCTGTTCTGTACATAAATAATGTAAGTT 943
QY 414 AAATATGATGTTGATAAATGATTAATGATGATGATGATGATGATGATGATGATGATGATG 469
Db 944 AAATATGATGTTGATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1003
QY 470 GTATCAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
Db 1004 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063
QY 530 AAAT-TATGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 588
Db 1064 GAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1108
QY 589 GAATCCATTAAGCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 648
Db 1109 GAATCCATTAAGCAAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1167
QY 649 AGCTCTGTCAGGCAATCTTTTCCAAAGAAATCCATATGTTGGTTCAGAGATGATGATGATG 708
Db 1168 AGCATCGTGCAGGCAATCTTTTCCAAAGAAATCCATATGTTGGTTCAGAGATGATGATGATG 1227
QY 709 GTCCTATTCACCTCTGCTGTTGGCTTTTCCATCAGCTCAAGTTTCTTGAAGTACTAGCA 768
Db 1228 TCTCCGTCAGGCTCTGAC-----TCTTCTCCTCTCTAAAGTGTCTTCTGAAAGTATTAGCA 1282
QY 769 ACTTGGGGTTATATTTTAGAATATGCTCAGTAGACATGAAATATATACAGTCAAGTCTCT 828
Db 1283 ACTCAGAATATATTTTAGAATATGCTCAGTAGACATGAAATATATACAGTCAAGTCTCT 1341
QY 829 ATATTAATGCTACTTCCACATATTTAAATGATTTTAACTCTAAATGGAATCATATACAT 888
Db 1342 -CTATATTAATAATTTCTGCATATCTTAAATATATATGACTATATGATGTTGTTGATGCA 1400
QY 889 CTGAGTATCTCATGGTCATATTAATAATGTTAAATATGATATCATATCATATCATATCAT 948
Db 1401 TTGGAATATGCTGTCATATTAATAATGTTAAATATATATGATTTTATTTAGTCTAAATAGA 1460
QY 949 ATAAATACCACTAGAACTATACAGGAAATCTGAGTGAGGTAAATCATAGTAGGCA 1008
Db 1461 ATAAATACCACTAGAACTATAGAAACACAT--TGATATGAGTTTAAATGATATA-- 1514
QY 1009 GTTGTATTAACCTCGTAGCATTTATTTTCAATTAATCATTTTCAATTAATCATTTGTA 1068
Db 1515 --TGCAATTCACCTCCAAACATTTTTTCCAGTTACATAATTAAGTTATATCCCTTATA 1572
QY 1069 ACATCTCTCAGTAATATATAAATCATCATTTAC--TTATGTTAATATAGCTTAGTATAAG 1127
Db 1573 AAATCTCTCAGTAATATATAAATCATCATTTTCAATTAATCATTTTCAATTAATCATTTG 1632
QY 1128 GTGGTTTCCCACTCGGAAAGACACAGTAATAAATCTTTGGAGAGGAACTGTTGTA 1187
Db 1633 GTGGTTTGTGCTGAGAAA-----ACAAACAAAAAACTCTTTGGAGAGGAACTCATGTA 1688
QY 1188 AACCCCAAAAAACAAAGTCTAACTTT----- 1213
Db 1689 AATACCAAAAAACAAAGCTTAATTTTGTGGACCAAAATGTTTAAATATATTTTAA 1748
QY 1214 ----- 1213
Db 1749 TTGATGAATTAATAAAGTATATATATTTATGTTGATACATATGATGTTTGAAGATGTA 1808
QY 1214 -----TTGGACCAAAATTTTATGCTGTTGTTTGAATGATTAATTTT 1256
Db 1809 ACATTCAGATGGAATGAGCAATGGACCAAAATTTTATACCTTGTCTGATTAATTTGCA-TTT 1867
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QY 1257 TAAATCTTCTCTCATTTAGCACCAACTGTGCAATTAAGAAGTTTTTTCAGGGTATAGACAC 1316
Db 1868 AAAAAATTTTCTCTCATTTAGCACCAACTGTGCAATTAAGAAGTTTTTTCAGGGTATAGGAC 1927
QY 1317 ATTGAAGAACCAAACTGCCCGGGAGGCTGTGTGATAAACTATTTCCTCAAACTTCTCTTT 1376
Db 1928 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAAAGACTATTTCAAAACTTGTCTTT 1987
QY 1377 AATAAAGAACACATAGAGCGCCAAAAAGTAAGTTTAAAGACATTTGGCAAAACTTAAAGT 1436
Db 1988 AATAAAGAAATACATATGACGGCCAAAAAGTAAGTTTACACATTT-----CAATGCAAGCT 2042
QY 1437 ATATTGCTGCTACTGCTGCTGTTTTTTTTTTTTTTTTTACAGAAATTCAGAGTTTCTTA 1496
Db 2043 ATATTGCTGCTGCTGCTGTTTTCTAT-----GGAAATGACAGTTTCTGTG 2088
QY 1497 CAATATCT-----CCTCTGTTCTTTTAAACAGAAAAAGGTGTCAGGAGAAAGATGGAGAG 1550
Db 2089 TAATACCTATTGTCATTTTCTTTTTCACAGAAAAAGGTGTCAGGAGAAAGATGGAGAG 2148
QY 1551 TGACAAAGTTCTAGACTACCTGCAAGTATTCTTGTGTGTAATAAACACCGAGTGGACAC 1610
Db 2149 TAAACCAATTCCTAGACTACCTGCAAGAGTTTCTTGTGTGTAATAAACACCGAGTGGATA 2208
QY 1611 CGGAAAGTTGAGAACAAACCGGCTTATTGTAGTGAAGATTTTGGAG 1657
Db 2209 TAGAAGTTGAGACTTAATCTGTTGTTGTCAGCCAAAGATTTTGGAG 2255

RESULT 7
AAS15002
ID AAS15002 standard; DNA; 9738 BP.
XX
AC AAS15002;
XX
DT 14-FEB-2002 (first entry)
XX
DE DNA encoding interleukin 5 (IL5).
KW Human; interleukin 5; IL5; antiinflammatory; antiasthmatic; asthma;
KW haplotyping; inflammatory disorder; single nucleotide polymorphism; SNP;
XX ds.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(3325,C)
FT /*tag= b
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace(3430,G)
FT /*tag= c
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace(3453,A)
FT /*tag= d
FT /*standard_name= "Single nucleotide polymorphism"
FT variation replace(3825,A)
FT /*tag= e
FT /*standard_name= "Single nucleotide polymorphism"
FT CDS 4071..5738
FT /*tag= a
FT /*product= "Interleukin 5"
FT /*note= "The CDS is specifically claimed in claim 24"
FT exon 4071..4214
FT /*tag= f
FT intron 4215..4422
FT /*tag= g
FT /*number= 1
FT variation replace(4359,G)
FT /*tag= h
FT /*standard_name= "Single nucleotide polymorphism"
FT exon 4423..4455
FT /*tag= i
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FT intron /number= 2  
 FT 4456..5405  
 FT /\*tag= j  
 FT /number= 2  
 FT variation replace(5389,T)  
 FT /\*tag= k  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT 5406..5534  
 FT /\*tag= 1  
 FT /number= 3  
 FT variation replace(5507,C)  
 FT /\*tag= n  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT intron 5535..5639  
 FT /\*tag= m  
 FT /number= 3  
 FT 5640..5738  
 FT /\*tag= o  
 FT /number= 4  
 FT variation replace(5717,A)  
 FT /\*tag= p  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT MO200177132-A2.  
 PN 18-OCT-2001.  
 XX 11-APR-2001; 2001WO-US012011.  
 XX 11-APR-2000; 2000US-0196250P.  
 PR (GENA-) GENAISSANCE PHARM INC.  
 XX Bentivegna SC, Chew A, Choi JY, Denton RR, Kazemi A;  
 PI Nandabalan K, Parks KE;  
 PI WPI; 2002-041289/05.  
 DR P-PSDB; AAU10353.  
 XX New haplotypes of the human interleukin 5 gene, useful to diagnose and  
 PT treat diseases associated with the gene including inflammatory disorders  
 PT such as asthma.  
 XX Claim 19; Fig 1; 65pp; English.  
 PS The invention relates to haplotyping the human interleukin 5 (IL5) gene  
 CC of an individual, comprising determining if the individual has one of the  
 CC IL5 haplotypes or haplotype pairs fully defined in the specification.  
 CC Haplotyping the IL5 gene of an individual, comprises determining the  
 CC identity of the nucleotide at two or more polymorphic sites in one copy  
 CC of the gene. The method also involves identifying an association between  
 CC a trait and a haplotype or haplotype pair of the IL5 gene, comprising  
 CC comparing the frequency of the haplotype/pair in a population exhibiting  
 CC the trait with that of a reference population. A higher frequency in the  
 CC trait population indicates the trait is associated with the haplotype.  
 CC The polymorphisms and screened compounds are useful to develop  
 CC treatment for diseases associated with IL-5 activity including  
 CC inflammatory disorders such as asthma. The present sequence represents  
 CC the coding sequence of interleukin 5 (IL5) as described in the method of  
 CC the invention  
 XX Sequence 9738 BP; 2808 A; 2015 C; 1982 G; 2933 T; 0 U; 0 Other;  
 SQ Query March 38.3%; Score 634.6; DB 6; Length 9738;  
 Best Local Similarity 68.6%; Pred No. 1.2e-115;  
 Matches 1226; Conservative 0; Mismatches 374; Indels 187; Gaps 18;  
 QY 1 AGGCAACACATGAACTTCAGAGCTATGAGATGCTTCCTGAAATTGAGTTGCTAGCTC 60  
 DB 4045 AGGCAACGCGAGACGTTTCAGAGCCATGAGGATGCTTCGCAATTTGAGTTGCTAGCTC 4104  
 QY 61 TTGGGCTGCTATGTTCTGCTTCTGCTAGAAATCCCATCAATAGACTGCTGGCAG 120

Db 4105 TTGGAGCTGCTACGTGTATGCCATCCCCACAGAAATCCCAAGTGCATTCGGTGAAG 4164  
 QY 121 AGACCTTGACACGTCTCTCCACTCATCGAACTTGGCTGATAGCGATGGGGTAATTTTCT 180  
 Db 4165 AGACCTTGGCACTGCTTTCTACTCATCGAACTCTGCTGATAGCAATGAGTAAATTTCT 4224  
 QY 181 TTTTGAATTCCTACAGTCTTTTAAATGATGGGTAATTTGGTGGTGGTGGTGGTGGTGGT 234  
 Db 4225 TTATGAATTCCTACAGTCTGTAAGTGCATAGTAATCATTTGTGATGGTTTCTTTACTAT 4284  
 QY 235 -TTTAAAGATCCATTATCAATATGAGTGTATTAATATATATATATATATATATATATAT 293  
 Db 4285 ATATAGAGATCTGTTTATAAATAATAGATTTCTGAG-CACATTTAGTACATGGGTGATACT 4343  
 QY 294 ATGTTACTCAGAGAATTTATTTAAAGTTATGAACCTTACAATACATTTAAAAATGAATG 353  
 Db 4344 ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGCTGTTAAATGATTCG 4403  
 QY 354 TTGTTTCTTTCTTTTTCAGAACTGATGATTTCTACTCTCTGAAATATAAATATGATGTT 413  
 Db 4404 -TATTTCTTTCTCTCCAGACTCTGAGGATTTCTGTTCTCTGTACATAAAATGTAAGTT 4462  
 QY 414 AAATTTATGATTTGATTTAAATGATTTACATGAATCAGT-----TTCATATTTTAAAGCTATAA 469  
 Db 4463 AAATTTATGATTTCACTAAATGATGGCATGAATGAATTAATTTCTGTTTAAAGCTATAA 4522  
 QY 470 GTATCAGTTAACTGGGATGATTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 529  
 Db 4523 TCATTAGTTATCATTTGAATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 4582  
 QY 530 AAAT-TATGTGCTTATGAATTTAGGAATGCTGTAGGAATGGCTTCACAAATATTAAGTA 588  
 Db 4583 GAATGTCGTACTTATAAATATGAGGAATGACTTT-----TTATCAAGTA 4627  
 QY 589 GAATCCATTTAAAGCAAGTGGATCAGGCCCTTTTATTTTATTTTATTTTATTTTATTTTATTT 648  
 Db 4628 GAATCCCTTTAAACCAAGTGGATAGGCTCTTTGGTGTATGTTTGTAGTT-TGCCTCCCAAG 4686  
 QY 649 AGCTCGTGTGAGGATTTTCCAAAGAAATTCATATTTGGGTGAGAGATCTTCTCTAG 708  
 Db 4687 AGCATCGTGTGAGGATTTTCCAGAAAGATTTCCACATGATGAGAGGTTGCTGTAG 4746  
 QY 709 GCTCATTTCACTCTGTGCTGTGGCTTTCTCACTCACTCAACGTTTTCGAAAGTACTAGCA 769  
 Db 4747 TCTCGTGCAGTTCTGAC-----TCTTTCTCACTCTAAAGTGTTCGAAATATTAGCA 4801  
 QY 769 ACTTGGGGTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 828  
 Db 4802 ACTCAGAAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 4860  
 QY 829 ATATTATAGTCACTTCCACATATTTAAATGATTTTAACTCTAATGGAATCATATACAT 888  
 Db 4861 -CTATTTTAAATTTCTGACATCTTAAATATTTATGACATATATATGATGTTGTTGATGCA 4919  
 QY 889 CTGAGTATGTCATGCTCATATTTAAATGTTTAAATGTTGATATCATAGTCTTAAATAGA 948  
 Db 4920 TTTGAATATGTCCTGCTCATATTTAAATGTTTAAATGTTTATTTTATTTTATTTTATTTTAT 4979  
 QY 949 ATAAATTTACCAGCTAGAACTATACGAGGAATTTCTGAGGTGAGGTAATCAGTAAGGCA 1008  
 Db 4980 ATAAATTTACCAGCTAGAACTATACGAGGAATTTCTGAGGTGAGGTAATCAGTAAGGCA 5033  
 QY 1009 GTTGTATTATACCTGTAAGCAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1068  
 Db 5034 --TGCATTACACTTCCAAACATTTTTCAGTTTACATAATTAAGTTATATTCCTTTTATA 5091  
 QY 1069 ACATCTTCTCAGTAATTTATTAACATCATTTTAC--TTATGTTAAATTTATAGCTTTAGTATAAG 1127  
 Db 5092 AAATCTCTCAGTAATTTATTAAGCTTCATCTCTTTTGAATTTTATCTTTATTTATTTATTT 5151  
 QY 1128 GTGGTTTCCACCTCGGAAAGACACAAGTAAAAACCTCTTGGGAGAGGGAACTTTGTGTA 1187  
 Db 5152 GTGGTTTCTGCTAGAAA-----ACAAACAAAAAACTCTTTGGAGAGGGAACTCATGTA 5207



QY 1188 AACCCACAAAACAAAGTCTAATCTTT----- 1213  
Db 5208 AATACCACAAAACAAAGCCTAACTTTTGGACAAAATTTGTTTAAATAATTTTAA 5267  
QY 1214 ----- 1213  
Db 5268 TTGATGAATTAAGAGTATATATATTTATTTGTGTACAATATGATGTTTGAAGTATAT 5327  
QY 1214 -----TTGGACAAATTTTATGCTTGTGTTTGAAGTATATATTTT 1256  
Db 5328 ACATTGAGAAATGACAAATGACAAATTTTATACCTTGTCTGTATTTTGA-TTTT 5386  
QY 1257 TAAATCTTCTCATTTAGCACCAACTGTGTCATTTAAAGAGTTTTCAGGGTATAGACAC 1316  
Db 5387 AAAAAATTTTCTCATTTAGCACCAACTGTGTCATTTAAAGAGTTTTCAGGGTATAGCAC 5446  
QY 1317 ATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACCTGCTTT 1376  
Db 5447 ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGTATTCAAAAACCTGCTTT 5506  
QY 1377 AATAAAGACACATAGAGCGCCAAAAGTAAGTTAAAGACATTTGGCAAAACTTAAGT 1436  
Db 5507 AATAAAGAAATACATTGACGGCCAAAAGTAAGTTAAAGACATTT-----CAATGGAAGT 5561  
QY 1437 ATATTGCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTACAAAGAAATGACAGTTTCCCTA 1496  
Db 5562 ATATTGCTGCTGCTGCTATTCTAT-----GGAATTGACAGTTTCTCT 5607  
QY 1497 CAATATCT-----CCTCTGCTTTTAAAGAAAAGGTGTGAGGAGAAAGTGGAG 1550  
Db 5608 TAATACCTATTGCTATTTCTTTTTCACAGAAAAGTGTGAGAAAGACGGAGAG 5667  
QY 1551 TGCAAAAGTTCCTAGACTACCTGCAAGTATTTCTTGTGTGTAATAAACACCGAGTGGACAC 1610  
Db 5668 TAAACCAATTCCTAGACTACCTGCAAGTATTTCTTGTGTGTAATAAACACCGAGTGGATTA 5727  
QY 1611 CGGAAAGTTGAGAACAAACCGGCTTATTTAGTGGAGATTTGGAG 1657  
Db 5728 TAGAAAGTTGAGACTAACTGGTTGTTGTCAGCCAAAAGATTTGGAG 5774

RESULT 8  
ID AN81381  
XX AN81381 standard; DNA; 3230 BP.  
AC AN81381;  
XX  
DT 25-MAR-2003 (revised)  
DT 04-DEC-1990 (first entry)  
XX  
DE Entire nucleotide sequence of the human B-cell differentiation factor  
XX chromosomal gene (3.2kb BamHI fragment).  
XX Immunodeficiency disease; cancer therapy; interleukin; lymphocyte; ss.  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key  
FT exon  
FT  
FT Location/Qualifiers  
553..696  
/tag= a  
/note= "Exon 1"  
905..937  
/tag= b  
/note= "Exon 2"  
1883..2011  
/tag= c  
/note= "Exon 3"  
2118..2216  
/tag= d  
/note= "Exon 4"

FN EP261625-A.

XX 30-MAR-1988.  
PD  
XX 21-SEP-1987; 87EP-00113774.  
XX  
XX 20-SEP-1986; 86JP-00223284.  
PR 21-SEP-1987; 87JP-00236842.  
XX  
XX (HONJ/) HONJO T.  
XX  
XX Honjo T, Takatu K, Severinson B;  
PI  
XX WPI; 1988-085927/13.  
XX P-PSDB; AAP81056.  
DR  
XX Recombinant human B-cell differentiation factor - used for diagnosis or  
PT treatment of immuno-deficiency diseases, various infections and cancers.  
FI Example; Fig 5(1)-5(4); 5pp; English.  
XX Nucleotide sequence of the exon portions of the human BCDF chromosomal  
CC gene completely coincided with the nucleotide sequence of human BCDF cDNA  
CC (AAN81380). The BCDF is useful in the diagnosis or treatment of e.g.  
CC immunodeficiency diseases occurring due to the deficiency of this factor  
CC in a living body and also in the treatment of various infections and  
CC cancers. (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;  
Query Match 36.2%; Score 600.6; DB 1; Length 3230;  
Best Local Similarity 67.8%; Pred. No. 5.1e-109; Indels 191; Gaps 19;  
Matches 1212; Conservative 0; Mismatches 384;  
QY 1 AGGCAAAACACTGAAACATTTTCAGAGCTATGAGATGCTTCTGAATTTAGTTGCTAGCTC 60  
Db 527 AGGCAAAACGAGAACGTTTTCAGAGCCATGAGAGTCTTCTGATTTGCTAGCTC 586  
QY 61 TTGGGGCTGCTATGTTTCTGCTTCTGCTAGAAAATCCCATGATAGACTGGTGGCAG 120  
Db 587 TTGGAGCTGCTATGCTATGCCATCCCAAGTATTTCCCAAGTGCATTTGGTGAAG 646  
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGGGGATGGGTAAATTTCT 180  
Db 647 AGACCTTGGCACTGCTTCTACTCATCGAACTTGCTGATAGCCAAATGAGTAAATTTCT 706  
QY 181 TTTGATTCCTACAGTCTTTAAATGCAATGCGGTAAATTTGCTGCTGCTAGTT----- 234  
Db 707 TTATGATTCCTACAGTCTGTAAGTGCATAGGTAAATTTGCTGATGCTTCTTTACTAT 766  
QY 235 -TTTAAAGATCCATATCAATAATCAAGTAAATGATGTTTAAATATATATATGGTAACC 293  
Db 767 ATATAGATCTGTTATATAATTAATTAAGATTTCTGAG-CACATTTGATGCTGCTGATACT 825  
QY 294 ATGTTTACTCAGAAAGTATATATAAAGTTATGAACTTACCACTTACATACATTAATAATGATG 353  
Db 826 ACATCACCAGCAACATTTCTGTTAAAGTTATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 885  
QY 354 TTGTTTCTTTCTTTTTCAGAACCTGATGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413  
Db 886 -TATTTCTTTCTCTCTCCAGACTCTGAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944  
QY 414 AAATTATGATTTGATAAAATGATTACATCAATCAG-----TTTTCATATTTTAACTATATAA 469  
Db 945 AAATTATGATTTGATAAAATGATTACATCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1004  
QY 470 GTATCAGTTAACTTTGGGATGATTTTAAATTTTATCTATTTTGTGTTTGTGCTGCTGCTGCTGCTG 529  
Db 1005 TCATTAGTTATCATTGGAAGTATTTTAAATTTTCTATATTTTGTGTTTGTGCTGCTGCTGCTGCTGCTG 1064  
QY 530 AAAT-TATGCTGCTTATGATATTTAGGAATGGTGGTGGAGAAATGGCTCTACATATTAAGTA 588  
Db 1065 GAATGCTGCTTATTAATAATGAGAAATGACTTT-----TTATCAAGTA 1109

QY 589 GAATCCATTAAAGTGGATCAGGCCCTTTTGTGTTGTCAGTTCTCCATCTCAAAG 648  
Db 1110 GAATCCCTTAAACAGTGGATAGGCTCTTTGGTGTGTTGTTAGTTTGGCTTCCCAAAG 1169  
QY 649 AGCTCGTGTGAGGATCTTTTCCAAAGAAATCCATATTGGGTGAGAGATCTTCTAG 708  
Db 1170 AGCATCGTGTGAGG-ATTCCTTCCAGAAAGATCCACATGAGTGAGAGTGGTGTAG 1228  
QY 709 GCTCCATTCACCTCTGCTGGTGGCTTTCCTCACCTCAACGTTTTTCTGAAAGTACTAGCA 768  
Db 1229 TCTCCGTGCGATCTGAC-----TCTTCTCACCTCAACGTTTTTCTGAAAGTATTAGCA 1283  
QY 769 ACTTGGGGTATATTTTAGAATTTATGTCAGTAGACATGAAATATACAGTGAAGTCT 828  
Db 1284 ACTCAGAATTATATTTTAGAACCATGATCAGTAGACATTAATAATATATACAAATGCC- 1342  
QY 829 ATATTAATAGTCACCTCCACATTTTAAATGATTTTAACTCTAATGGAATCATATACAT 888  
Db 1343 --CTATATTAATAATCTGCATACCTTAAATTAATATGACATATATGATGTTGTATGCAT 1400  
QY 889 CTGGAGTATGTCATGTCATATAATAATGTTAAATGTGATATCATTTAGTCTAAATAGA 948  
Db 1401 TGAATATG--CTTGGTATATTAATGTTAAATGTTAAATATATATATATAGTTT-ATTAGTCTAAATAGA 1456  
QY 949 ATAAATTTACAGCTAGACATATACAGAGAAATTTCTGAGGTGAGGTAAATCAGTAAGGCA 1008  
Db 1457 ATAAATCTACAGCTAGACATATACAGAGAAATTTCTGAGGTGAGGTAAATCAGTAAGGCA 1008  
QY 1009 GTTGTATTAATACCTGTAAGCATTTTTCATTAATCATTTTCAATTTATATCATTTGTA 1068  
Db 1514 -----ATTACACTTCCAAACATTTTTCAGTTTCAATTAATTAATTTATTTTATA 1568  
QY 1069 ACATTTCTAGTAAATATAAATCATATTTAC--TTATGTTAATTTATAGCTTAGTATAAG 1127  
Db 1569 AAATCTCTAGTAAATATAAATCATATTTTCTATTTTGAATTTTATCTTAATATGTTG 1628  
QY 1128 GTGGTTTCCACCTGGAAGACACAGTAAATCTTCTGGAGAGGGAAGTCTGTGTA 1187  
Db 1629 GTGGTTTGTGCTTGAAGAA-----ACAAACAAATCTTCTGGAGAGGGAAGTCTGTGTA 1684  
QY 1188 AACCCCAACAAACAAAGTCTAACTTTT----- 1214  
Db 1685 AATACCAACAAACAAAGCTTAACTTTGTGGACCAAAATTTGTTTAAATTTATTTTAA 1744  
QY 1215 ----- 1214  
Db 1745 TTGATGAATTAAGATPATATATATTTTGTGTACAAATATGATTTTGAAGTATGTAT 1804  
QY 1215 -----TGGACCAATTTTATGCTTGTGTTTGTGATGAATATATTTT 1256  
Db 1805 ACATTGAGAAATGACAAATGGAATTTTATACCTTGTCTGATTTTGAATTTGCA-TTTT 1863  
QY 1257 TAAATCTTCTCATTTAGCACCAACTGTGATTAAGAAAGTTTTCAGGGTATAGACAC 1316  
Db 1864 AAAAAATTTCTCATTTAGCACCAACTGTGATTAAGAAAGTTTTCAGGGTATAGACAC 1923  
QY 1317 ATTGAAGAACCAAACTGCCACGGGAGGCTGGATTAATCTTCCAAATCTGCTTT 1376  
Db 1924 ACTGGAGAGTCAAACTGTGCAAGGGGACTGTGGAAGACTTATCAAAATCTGTCTTT 1983  
QY 1377 AATAAAGAACACATAGAGCGCCAAAGTAAGTTAAAGACATTTGGCAAAATTAAGT 1436  
Db 1984 AATAAAGAAATACATTTGACGGCCAAAGTAAGTTTACACATTTCAATGGAAGCTATATT 2043  
QY 1437 ATATTGTCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTTA 1496  
Db 2044 TGTCTTGGCTG-----TGCCTATTTCTATGGAATGACAGTTTCTCTG 2085  
QY 1497 CAATATCT-----CCTCTGTTTTTAAACAGAAAAAGGTGTGAGAGAAAGATGGAGAG 1550  
Db 2086 TAATACCTATTGTCACTTTTCTTTTTCACAGAAAGGTGTGAGAGAAAGATGGAGAG 2145  
QY 1551 TGACAAAGTCTTAGACTACCTGCAAGTATTTCTTGGTGTATTAACACCCGAGTGGACAC 1610

Db 2146 TAAACCAATTCCTAGACTACCTGCAAGAGTTTCTTGGTGTATTAACACCCGAGTGGATAA 2205  
QY 1611 CGAAAGTTGAGAACAAACCGCTTTATTGTAGTGAAGATTTTGGAG 1657  
Db 2206 TAGAAAGTTGAGACTAAACTGTTTGTTCAGCCAAAGATTTTGGAG 2252  
RESULT 9  
AAQ74056  
ID AAQ74056 standard; DNA; 3230 BP.  
XX AAQ74056;  
XX AC AAQ74056;  
XX DT 29-JAN-1996 (first entry)  
XX Human interleukin-5.  
XX Interleukin-5; primer; mRNA; specificity; pharmaceutical; ss.  
XX OS Homo sapiens.  
XX PN JP07123984-A.  
XX PD 16-MAY-1995.  
XX PF 05-NOV-1993; 93JP-00275852.  
XX PR 05-NOV-1993; 93JP-00275852.  
XX PA (HITB) HITACHI CHEM CO LTD.  
XX WPI; 1995-211627/28.  
XX A primer for the detection and the determin. of a specific messenger RNA -  
XX can detect and determine specific mRNA(s) with high reliability.  
XX Example 22; Page 22-24; 35pp; Japanese.  
XX AAQ74056 is the human interleukin-5 gene. This gene is amplified by the  
XX primers AAQ74031-Q74032. The primers are used specifically for the  
XX detection and isolation of this sequence. They have the advantage of high  
XX sensitivity and reliability and are useful in the pharmaceutical industry  
XX  
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;  
Query Match 36.2%; Score 600.6; DB 2; Length 3230;  
Best Local Similarity 67.8%; Pred. No. 5.1e-109;  
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;  
QY 1 AGGCAAAACACTGAACATTTGAGAGCTATGAGAAATCTTCTGAATTTGAGTTTCTAGCTC 60  
Db 527 AGGCAAAACGAGAAACGTTTTCAGAGCCATGAGGATGCTTCTGCAATTTGAGTTTCTAGCTC 586  
QY 61 TTGGGCTGCTATGTTTCTGCTTCTGCTAGAAATCCCATGAAATAGACTGTTGGCAG 120  
Db 587 TTGAGCTGCTAGCTGATGCTATGCCATCCCAAGAAATCCCAAGTGCATTTGTTGAAAG 646  
QY 121 AGACCTTGACATGCTCTCCACTCATGAACTTGGCTGATAGGCGATGGGGTAAATTTCT 180  
Db 647 AGACCTTGGCACTGCTTTTCTACTCATCGAACTCTGCTGATAGCCAAATGAGGTAAATTTCT 706  
QY 181 TTTTGTCTCTACAGCTCTTAAATGATGAGTAAATTTGGTGGTGGCTAGTT----- 234  
Db 707 TTATGATTTCTACAGTCTGTAAGTGCATAGGTAATCAITTTGATGTTTCTTTACTAT 766  
QY 235 -TTTAAAGATCCATTAATCAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 293  
Db 767 ATATAGAGATCTGTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 825  
QY 294 ATGTTACTCAGAGAAATTAATAAAGTATGAACCTTACAATACATTAATAAATGAATG 353  
Db 826 ACATCACCAGCAACATCTCTGTTAAAGTTATGAATGCTGTTGTTGTTGTTGTTGTTGTTGTTG 885

QY 354 TTGTTTCCTTCTCTTTTTCAGAACCTGATGATTCCTTCTTCTGAAATATATAAATGATTAAGTT 413  
Db -TATTTCTCTCTCTCTCAGACTCTGAGGATTCCTGTTCTCTGTACATAAATAATGATTAAGTT 944  
QY 414 AAATTAATGATTTGATTAATAATGATTAACATGATCAG- - -TTTTCATATTTTAAGCTATAAA 469  
Db AAATTAATGATTTGATTAATAATGATTAAGTAAATTTCTGTTTAAAGCTGTA 1004  
QY 470 GTATCAGTTAATCATGGGATGATTAATTTTATCTATTTTCTTTTATGTTGCGGATGT 529  
Db TCATTAAGTATCATTTGGAATATTAATTTTCTATATTTTCTTATATTTTCTATATGCGTGT 1064  
QY 530 AAAT-TATGTCCTTATGATTAATGATTAAGTATGTTAGGAATGGCTCTACATATTAAGTA 588  
Db GAATGCTGTACTTAATAATATGAGGAATGACTTT- - -TTATCAAGTA 1109  
QY 589 GAATCCATTAAGCAAGTGGATCAGCCCTTTTGTGATTTGTCAGTTCTCTCATCTCAAG 648  
Db GAATCCCTTTAAACAAGTGGATTAGGCTCTTTGGTGTGTTGTTAGTTGCTTCCCAAG 1169  
QY 649 AGCTCTGTGTCAGGATCTTTTCAAAAGAAATTCATATTTGGGTCAGAGATATCTCTAG 708  
Db AGCATCGTGTGAGG-ATTCCTTCCAGAGAGATTCACACTGAGTGAGAGTGCGTGTAG 1228  
QY 709 GCTCATTCACCTCTGTCGTTGGCTTCTCCTCACTCAAGCTTTTCTGAAAGTACTAGCA 768  
Db TCTCGTGCACTTCTGAC- - -TCTTCTCCTCTACGTTTCTGAAAGTATTAAGCA 1283  
QY 769 ACTTGGGGTTATATTTTAGAATTAATGTCAGTACAGATGAAATATACAGTGAAGPCT 828  
Db ACTCAGAAATTAATTTTAGAACCATGATCAGTAGACATTAATAATAATAACAAATGCC- 1342  
QY 829 ATATTAATAGTCACTTCACATATTTAAATGATTTTAACTCTAATGGAATCATATACAT 888  
Db --CTATTAATAATTCGCAATCTTAATAATTAATGACTATATGATGGTGTGATGCAT 1400  
QY 889 CTGGAGTATGTCAGTCAATTAATAATGTTAAATGTCATATCATATGCTAAATAGA 948  
Db TGAATATG- - -CCTGGTCAATTAATAATGTAATAATATAGTTT-ATTAGTCTAAATAGA 1456  
QY 949 ATAAATATCAGCTAGTACACTATACAGGAGAAATTCAGGTGAGGTAATCAGTAGGCA 1008  
Db ATAAATATCAGCTAGTACACTATACAGGAGAAATTCAGGTGAGGTAATCAGTAGGCA 1053  
QY 1009 GTTGATTAATACCTCTGAAGCAATTTATTTTCAATATCATTTTCAATATATCATTTGTA 1068  
Db -1514 - - -ATTACATCTCCAAACATTTTTCAGTTACATTAATTAAGTTATATCTTTATA 1568  
QY 1069 ACATCTCTCAGTAATTAATAACATCATTTAC- -TTATGTAATTAATGATTTAGTATAG 1127  
Db AAATCTCTCAGTAATTAATAAGCTTCATCTACTTTTGAATAATTTTATCTTAATATGTG 1628  
QY 1128 GTGGTTTCCCACTGGAAAGACACAACTGTAACCTCTTGGGAGAGGGAATCTGTGTA 1187  
Db GTGGTTTGTGCTTAGAAA- - -ACAAACAAATAACTCTTTGGAGAGGGAATCTGTA 1684  
QY 1188 AACCCCAAAACAAAGCTTAATCTTTT- - - - -1214  
Db AATACCAAAACAAAGCTTAATCTTTGAGCAAAATTTGTTAATAATTAATTTTAA 1744  
QY 1215 - - - - -1214  
Db TTGATGAATTAATAAGTATATATTAATTTGTTGATCAATTAATGATTTTGAAGTATAT 1804  
QY 1215 - - - - -1256  
Db ACATTGAGAAATGAGCAATGAGCAATTTTATACCTCTCTGATTTATTTGCA- -TTT 1863  
QY 1257 TAAATCTTCTCTATTTAGCACCAACTGTGCAATTAAGAGATTTTTCAGGATATAGACAC 1316  
Db AAAAAATTTCTCTATTTAGCACCAACTGTGCAATTTTTCAGGAAATAGGCAC 1923

QY 1317 ATTGAAGAACCAAACTGCCACGGGAGGCTGTGGATAAACTATTCCAAAACTTGTCTTT 1376  
Db ACTGGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAAGACTATTCAAAAACCTTGTCTTT 1983  
QY 1377 AATAAAGACACATAGAGCGGCCAATAAGTAAGTTAAAGACATTTGGCAAAACTTAAGT 1436  
Db AATAAAGAAATACATTGACGGGCCAAAAGTAAGTTACACACATTTCAATGGAAGCTATAT 2043  
QY 1437 ATATTTGTCTGACTCTGCTGTTTTTTTTTTTTTTTTTTTTTTTACAGAAATTCACAGTTTCCTTA 1496  
Db TGCTCTGGCTG- - - - -TGCTATTTCTATGGAATTCACAGTTTCCTG 2085  
QY 1497 CAATATCT- - - - -CCTCTGTTCTTTTAACAGAAAGGTGTGAGGAGAAAGATGGAGAG 1550  
Db TAATACCTATTTGCAFTTTTCTTTTTCACAGAAAGGTGTGAGGAGAAAGATGGAGAG 2145  
QY 1551 TGACAAAGTTCCTAGACTACCTGCAAGTATTTCTTGGTATAATAACACCGAGTGGACAC 1610  
Db TAAACCAATTCCTAGACTACCTGCAAGTATTTCTTGGTATAATAACACCGAGTGGATAA 2205  
QY 1611 CGGAAGTGTGAGAACAAACCGCTTATTTAGTGTGAAGATTTTGAG 1657  
Db TAGAAAGTTGAGACTAAACTGTTTGTTCAGCCAAAGATTTTGAG 2252

## RESULT 10

AACT3725  
ID AAC73725 standard; DNA; 3230 BP.

XX AAC73725;

XX AC AC  
XX 02-FEB-2001 (first entry)

XX Human IL-5 nucleotide sequence.

XX Human; interleukin-5; IL-5; signal transduction;

KW antisense oligonucleotide; antisthmatic; immunosuppressive; cytostatic;

KW IL-5 receptor-alpha; asthma; eosinophilic syndrome; infection;

KW inflammation; cancer; ds.

XX Homo sapiens.

XX WO200058512-A1.

XX 05-OCT-2000.

XX 17-MAR-2000; 2000WO-US007318.

XX 26-MAR-1999; 99US-00280799.

XX (ISIS-) ISIS PHARM INC.

PI Dean NM, Karras JG, McKay R;

DR WPI; 2000-594648/56.

XX Antisense oligonucleotide compound used to treat asthma and eosinophilic syndrome in humans modulates interleukin-5 signal transduction.

XX Example 22; Page 127-128; 156pp; English.

CC The present sequence was used to design oligonucleotides for antisense modulation of interleukin-5 (IL-5) signal transduction. Oligonucleotides were designed to target nucleic acids encoding IL-5 and IL-5 receptor-alpha. The antisense oligonucleotides may be used for the treatment of diseases associated with IL-5 signal transduction, IL-5 expression or IL-5 receptor-alpha expression. Such diseases include asthma and eosinophilic syndrome. The oligonucleotides are also useful for research uses and to prevent or delay infection, inflammation or tumour formation

XX Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;

XX Query Match 36.2%; Score 600.6; DB 3; Length 3230;

Best Local Similarity 67.8%; Pred. No. 5.le-109; Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;	
QY 1 AGGCAACACATGACATTCAGAGCTATGAGATGCTTCGAATTTGAGTTGCTAGCTC 60	
Db 527 AGGCAACACGCAAGCTTTAGAGCCATGAGGATGCTTCGCAATTTGAGTTGCTAGCTC 586	
QY 61 TTGGGGTGGCTATGTTTCTGCTTGTCTAGAAAATCCCATGAATAGACCTGGTGGCAG 120	
Db 587 TTGAGCTGCTACTGCTATGCGCATCCCCACAGAAATCCCAAGTGCAATGGTGAAG 646	
QY 121 AGACTTGACACTGCTCTCCACTCATCGAATCTGGCTGATAGGGATGGGTAATTTTCT 180	
Db 647 AGACTTTGGCACTGCTTTCTACTCATCGAACTGCTGATAGCCAATGAGGTAATTTCT 706	
QY 181 TTTTGATTCCTACAGTCTTTTAAATGATGGTAATTTGGTGGTGGCTAGTT----- 234	
Db 707 TTATGATTCCTACAGTCTGTAAGTGATGATGTAATCATTTGATGGTTCCTTTACTAT 766	
QY 235 -TTTAAAGATCCATTAATCAATPAATGAAGTAAATGATGTTTAAATATATATGATGGTAAC 293	
Db 767 ATATAGAGATCTGTTATAAATAATAAGATTCAG-CACATTTAGTACATGGGTGATAACT 825	
QY 294 ATGTTACTCAGAAGATTAATTAAGATTTAGAACCTTACAATACATTAATAAATGAATG 353	
Db 826 ACATCAGCAGAAACATTCGTTAAAGTTTAAGATTCGCTGGTGTGCTGTAATAATGATG 885	
QY 354 TTGTTTCTCTTTTTCAGAACCTGATGATTCCTACTCCTGAAATPAAAAATGTAAGTT 413	
Db 886 -TAITTCCTTCTCCAGACTCTGAGGATTCCTGTTCTGTACATAAAAAATGTAAGTT 944	
QY 414 AAATATGATTTGATTAATAATGATTAAGATCAG-----TTTCATATTTTAAGCTATAA 469	
Db 945 AAATATGATTCAGTAAATGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1004	
QY 470 GTATCAGTTAACTGGGATGATTAATTTTATCTATTTTATTTGTTTATGTCGGGATGT 529	
Db 1005 TCAATGATTCATGAGAACTATTTAATTTTCTATATTTTGTGTTTTCATATGGTGGCTGT 1064	
QY 530 AAAT-TATGCTGTTATGAATATTAAGATGTTAGGAATGGCTCTACAAATTAAGTA 588	
Db 1065 GAATGCTGCTTATAAATATGAGGAATGACTTT-----TTATCAAGTA 1109	
QY 589 GAATCCATTAAGCAAGTGGATCAGCCCTTTTGTGATGTTGTCAGTTCTCCATCTCAAG 648	
Db 1110 GAATCCTTTAAACAGTGGATGAGCTCTTTGGTGTGTTGTTAGTTGCTTCCCAAAG 1169	
QY 649 AGCCTCGTGTGAGGCATTTTCCAAAGAAATCCATATTTGGGTGAGATATCTCTAG 708	
Db 1170 AGCATGCTGTGAGG-ATTCCTTCCAGAGGATTCACACTGAGTGAGAGGTGGCTGTAG 1228	
QY 709 GCTCAATTCACCTCTGCTGGTGGCTTCTCCACTCAAGCTTTTCTGGAAGTACTAGCA 768	
Db 1229 TCTCGTGGCTGTGAC-----TCTTCTCCTCACTCAAGCTTCTGGAAGTACTAGCA 1283	
QY 769 ACTTGGGGTATATTTTATGAATTTATGCTCAGTACATGAAATATAACATGAGTGCCT 828	
Db 1284 ACTCAGATTTATTTTATGAAACCATGATCAGTACATTAATAATATAACAAATGCC- 1342	
QY 829 ATATTAATAGTCACTTCCACATTTTAAATGATTTTAACTCTAATGAATCATATACAT 888	
Db 1343 --CTATATTAATATCTGCTACTTAAATTAATATGATCATATGATGGTGTGATGCAT 1400	
QY 889 CTGGAGTATGTCATGCTATTAATAATGTTTAAATAATGATATCATTTAGTCTAAATAGA 948	
Db 1401 TGAATATG---CCTGGTCAATTAATAATGTAATAATATAGTTT-ATTAGTCTAAATAGA 1456	
QY 949 ATAAATATCCAGCTAGAACTATACGAGGAATTTCTGAGGTGAGGTAAATCAGTAAAGCA 1008	
Db 1457 ATAAATATCCAGCTAGAACTATGAAACACAT--TGATATGAGTTTAAATGATATAGTC- 1513	
QY 1009 GTTGTATTTATCTCGTAGCAATTTATTTTTCATTAATCAATTCATTTATATCATTTGTA 1068	
RESULT 11	
ABX04379	
ID	ABX04379 standard; cDNA; 3230 BP.
XX	ABX04379;
AC	ABX04379;
XX	
DT	13-JAN-2003 (first entry)
XX	
XX	Human Interleukin 5 cDNA.
DE	
XX	
KW	Human; ss; antisense; gene; interleukin 5; IL-5; IL-5 receptor;
KW	antiasthmatic; immunosuppressant; eosinophilic syndrome; asthma.
OS	Homo sapiens.
OS	
XX	US2002128216-A1.
PN	
XX	
PD	12-SEP-2002.
XX	
PF	07-MAR-2001; 2001US-00800629.
XX	
XX	26-MAR-1999; 99US-00280799.
PR	
Db 1514 -----ATTACACTTCCAAAACATTTTTTTCAGTTACATTAATTAAGTTATATCCTTTATA 1568	
QY 1069 ACACCTTCTCAGTAATTTATATAAAACATCATTTTAC-TTATGTTAATTTAGCTTAGTATAAG 1127	
Db 1569 AAATCTCTCAGTAATCATATAAGCTTTCATCTACITTTTTTGAATTTTATCTTAATATGTG 1628	
QY 1128 GTGGTTTCCCACCTGGGAAAAGACACAACTGTAATAAAACCTCTTGGGAGAGGGAACCTTGTA 1187	
Db 1629 GTGGTTTCTTCCCTAGAAA-----ACAAACAAAACCTCTTGGGAGAGGGAACCTCATGTA 1684	
QY 1188 AACCCCAACAAAACAAAGTCTAACTTTT----- 1214	
Db 1685 AATACACAAAACAAAGCTTAACITTTTGGGACCAAAATTTGTTTAATAATTTATTTTAA 1744	
QY 1215 ----- 1214	
Db 1745 TTGATGAATTAATAAGTATATATATTTATTTGTGTAATATGATGTTTTGAAGTATGAT 1804	
QY 1215 -----TGACCAAAATTTTTATGCCCTTTGTTTGTGATGAATTAATTTT 1256	
Db 1805 ACATTCGAGATGGAATGGAATGGAATTTTATACCTTGTCTTGATTTATGCA-TTTT 1863	
QY 1257 TAAATCTTCTCATTTTAGCACCAACTGTGCAATTAAGAAAGTTTTTCAGGGTATAGACAC 1316	
Db 1864 AAAAAATTTCTCATTTTAGCACCAACTGTGCACTGAAGAAATCTTTCAGGGAATAGGCAC 1923	
QY 1317 ATTGAAGAACCAACTGCCACGGGAGCTGTGATATAAATCTATTTCCAAAACTTGTCTTT 1376	
Db 1924 ACTGGAGATCAAACTGTGCAAGGGGTACTGTGGAAGACTTTCAAAACTTGTCTT 1983	
QY 1377 AATAAAGAACACATAGAGCGCCAAAAGTAAGTTAAAGACATTTGGCAAAAACCTTAAGT 1436	
Db 1984 AATAAAGAAATACATTTGACGGCCAAAAGTAAGTTACACATTTCAATGGAAGCTATATT 2043	
QY 1437 ATATTGTCTGACTGCTGCTGTTTTTTTTTTTTTTTTTTTCAAGAAATGACAGTTTCTTA 1496	
Db 2044 TGTCTGCTGCTG-----TGCTATTTCTATGGAATGACAGTTTCTG 2085	
QY 1497 CAATATCT-----CCTCTGTTCTTTTAAAGAAAAGGTGTCAGGAGAAAAGATGGAG 1550	
Db 2086 TAATACCTATTGTCATTTTCTTTTTCACAGAAAAGTGTGGAGAGAAAAGACGGAGAG 2145	
QY 1551 TGACAAAAGTCTAGACTACCTGCAAGTATTTCTTTGTTGTTAATAAACHCCGAGTGGACAC 1610	
Db 2146 TAAACCAATTCCTAGACTACCTGCAAGATTTCTTGTGTAAATGAACACCGAGTGGATA 2205	
QY 1611 CGGAAAGTTGAGAACAAACCGCTTTATTTAGTGGAGAAATTTGGAG 1657	
Db 2206 TAGAAAGTTGAGACTAAACTGGTTTGTGGAGCCAAAGATTTTGGAG 2252	

PR 17-MAR-2000; 2000WO-US007318.  
XX (DEAN/) DEAN N M.  
PA (KARR/) KARRAS J G.  
PA (MCKA/) MCKAY R.  
XX (MANO/) MANOHARAN M.  
PI Dean NM, Karras JG, McKay R, Manoharan M;  
XX WPI; 2003-039602/03.  
DR  
XX Novel antisense compound for treating disease/condition e.g. eosinophilic  
PT syndrome or asthma associated with interleukin-5 or IL-5 receptor  
PT expression or IL-5 signal transduction, modulates IL-5 signal  
XX transduction.  
XX  
PS Example 20; Page 48-49; 77pp; English.  
XX  
CC The invention relates to an antisense compound of 8-30 nucleobases in  
CC length, which modulates interleukin (IL)-5 signal transduction. Also  
CC include are a pharmaceutical composition comprising the antisense  
CC oligonucleotide and a pharmaceutically acceptable carrier or diluent, and  
CC a diagnostic kit for detecting the expression level of the membrane form  
CC versus soluble form of IL-5 receptor a. The antisense compound is useful  
CC for modulating IL-5 signal transduction, modulating expression of  
CC mammalian IL-5 or modulating the expression of mammalian IL-5 receptor a,  
CC in cells or tissues, for altering the ratio of the isoforms of mammalian  
CC IL-5 receptor a in mammalian cells or tissues, treating a mammalian  
CC having a disease or condition associated with IL-5 signal transduction,  
CC IL-5 expression or IL-5 receptor a expression, where the disease or  
CC condition include eosinophilic syndrome or asthma. An antisense compound  
CC which alters splicing of an RNA encoding IL-5 receptor a is also useful  
CC for treating a mammal having a disease or condition. The present sequence  
CC is a cDNA encoding Human IL5, a target of the antisense compounds of the  
XX invention  
XX  
SQ Sequence 3230 BP; 1027 A; 545 C; 622 G; 1036 T; 0 U; 0 Other;  
  
Query Match 36.2%; Score 600.6; DB 7; Length 3230;  
Best Local Similarity 67.8%; Pred. No. 5.1e-109;  
Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;  
  
QY 1 AGGCCAACACTGACATTTTCAGAGCTATGAGATGCTTCGAAATTTGAGTTTCTCTAGCTC 60  
DB 527 AGGCCAACCGAGAACGTTTCAGAGCCATGAGGATGCTTCGCAATTTGAGTTTCTCTAGCTC 586  
  
QY 61 TTGGGGTGCCTATGTTTCTGCTCTGTAGAAAATCCCATGAATAGACTGGTGGCAG 120  
DB 587 TTGGAGCTGCTACGTGTATGCCATCCACAGAAAATCCCAAGTGCATTGGTGAAG 646  
  
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGGGTAATTTCT 180  
DB 647 AGACCTTGGCACTGCTTCTACTCATCGAATCTGCTGATAGCAATGAGGTAATTTCT 706  
  
QY 181 TTTTGATTCCTACAGCTCTTAAATGATGGGTAATTTGGTGGTGGCTAGTT----- 234  
DB 707 TTATGATTCCTACAGCTCTGTAAGTGCATAGGTAATCATTTTGTGATGTTCTTTACTAT 766  
  
QY 235 -TTTAAAGATCCATTATCAATATGAAGTAATGAGTGTAAATATATATATGCGTAACC 293  
DB 767 ATATAGAGATCTGTATATAATAATAAGATTTCTGAG-CACATTAGTACATGGGTGATACT 825  
  
QY 294 ATGTTACTCAGAAGAAATATATATAAAGTTATGAACCTTACAATACATTAATAAATGAATG 353  
DB 826 ACATCACCAGCAACATCTGTTAAAGTTATGATGCTGGTGTGTTAAATATGATTG 885  
  
QY 354 TTGTTTCTTTCTTTTTCAGAACCTGATGATTTCTACTCTCTGAAAATAAATAATGTAAGTT 413  
DB 886 -TATTTCTTCTCTCCAGACTCTGAGGATTCCTGTTCTCTGTACATAAATAATGTAAGTT 944  
  
QY 414 AATATTATGATTTGTAATAAATGATTTACATGATCAG-----TTTCATATTTTAACTATAA 469  
DB 945 AATATTATGATTTACGTAATAAATGATGGCAATGAATAGTAAATTTCTGTTTAACTGTAAA 1004

QY 470 GTATCAGTTAAACATTTGGGATGATTTAAATTTTATCTATTTTCTTTTATATGTTGGGATGT 529  
DB 1005 TCATTAGTTATCATTTGGAACTATTTAATTTTCTATATTTTCTTTTCAATATGGTGGCTGT 1064  
  
QY 530 AAAT-TATGTCTTATGAATATAGGAATGGTGTAGGAATGGCTCTACAATATTAAGTA 588  
DB 1065 GAATGTCTGTACTTATAAATATGAGGAATGACTTT-----TTATCAAGTA 1109  
  
QY 589 GAATCCATTAAAGCAAGTGGATCAGCCCTTTTGTAGTGTCTCAGTTCTCCATCTCAAG 648  
DB 1110 GAATCCCTTTAAACAAGTGGATTAGCTCTTTGGTGAATGTTTGTAGTTTGGCTTCCCAAAG 1169  
  
QY 649 AGCTCGTGTCAAGCAATCTTTTCCAAAAGAAATCCATATTCGGTCAGAGATCTCTAG 708  
DB 1170 AGCATCGTGTGAGG-ATTTCTTTCCAGAAGGATCCACACTGAGTGAGAGGTGGTGTAG 1228  
  
QY 709 GCTCCATTCACTCTGTCTGGCTTTCTCCTCACTCAACGTTTTTCTGAAAGTACTAGCA 768  
DB 1229 TCTCCGTGCAGTTCTGAC-----TCTTTCTCACTCTAACGTTTCTGAAAGTATTAGCA 1283  
  
QY 769 ACTTGGGCTTATATTTTATAGAAATATGTCAGTAGACATGAAATATACAGTGAAGTCT 828  
DB 1284 ACTCAGAATTTATTTTATAGAACCATGATCAGTAGACATTAATAATATAACAATGCC- 1342  
  
QY 829 ATATTAAATAGTCACTCCACATTTTAAATGAATTTTAACTCTAATGGAATCATATACAT 888  
DB 1343 --CTATATTAATAATTTCTGCATCTTAAATTAATATGACTATATCATGCTGTGTATGCAT 1400  
  
QY 889 CTGGAGTATGTCATGGTCTATATTAAGTGTAAAGTGTATATCATTCATTAGTCTAAATAGA 948  
DB 1401 TGAATATG---CCTGCTCATATTAAGTGTAAATATATATAGTTT-ATTAGTCTAAATAGA 1456  
  
QY 949 ATAAATTTACCAGCTAGAACTATACGAGGAAATTTCTGAGGTGAGGTAATCAGTAAGCA 1008  
DB 1457 ATAAACTACCAGCTAGAACTGTAGAAACACAT--TGATATGAGTTTAAATGTATAATGC- 1513  
  
QY 1009 GTTGTATTATACCTCGTAAGCATTTATTTTTCATTAATCATTTCTATATATATTTCTA 1068  
DB 1514 -----ATTACACTTCCAAAACATTTTTCAGTTTACATAATTAAGTTATATCTTTATA 1568  
  
QY 1069 ACACCTCTCAGTAATATATAAACATCATTTTAC-TTATGSGTAATTTATAGCTTAGTATAAG 1127  
DB 1569 AAACCTCTCAGTAATCATATAAGCTTCTATCTTTTGAATAATTTTATCTTAATATGTG 1628  
  
QY 1128 GTGTTTCTCCACTGGGAAAAGACAGTAAAAACCTCTCGGAGAGAGGAACTGTGTGTA 1187  
DB 1629 GTGTTTCTGCTAGAAA-----ACAAACAAAAAACTCTTTGGAGAGGGAACATCATGTA 1684  
  
QY 1188 AACCCCAACAAACAAAGCTTAACCTTT----- 1214  
DB 1685 AATACCAACAAACAAAGCTTAACCTTTGGGACCAAAATGTTTAAATAATTTATTTTAA 1744  
  
QY 1215 ----- 1214  
DB 1745 TTGATGAATTAATAAGTATATATATTTATGTGTACAATATGATGTTTGAAGTATGTAT 1804  
  
QY 1215 -----TGGACCAAAATTTTATGCTTGTGCTTTTATGATGAATTTATTTT 1256  
DB 1805 ACATTGCAAGATGGAATGGACCAATTTTATACCTTGTCTTGTATTATTGCA-TTTT 1863  
  
QY 1257 TAAATCTTCTCTCAATTTAGCACCACCTGTGCAATTAAGAAGTTTTCAGGGGTATAGACAC 1316  
DB 1864 AAAAATTTTCTCAATTTAGCACCACCTGTGCAATTAAGAAGTTTTCAGGGAAATAGGCAC 1923  
  
QY 1317 ATTGAAGAACCAAACTGCCAGGGGAGCTGTGGATAAACTATTTCCAAAACCTGTCTTT 1376  
DB 1924 ACTGAGAGTCAAACTGTGCAAGGGGTACTGTGGAAGAGCTATTTCAAAAAACTTTGCTT 1983  
  
QY 1377 AATAAAGAACACATAGAGCGCCAAAAGTAAGTTAAAGACATTTGGCAAAAACCTTAAGT 1436  
DB 1984 AATAAAGAAATACATTTGACGCCCAAAAAGTAAGTTACACATTCATCGGAGGCTATATT 2043



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XX PI Daly, M, Hudson TJ, Lander ES, Rioux J, Siminovich K;
XX XX
XX PN WPI; 2001-367874/38.
XX XX
XX PD Testing for the presence of polymorphisms associated with inflammatory
XX PT bowel disease, using a hybridization assay.
XX PF Disclosure; Page 262; 463pp; English.
XX PS
XX CC The present invention describes a method for detecting the presence of
XX CC polymorphisms associated with inflammatory bowel diseases such as
XX CC ulcerative colitis and Crohn's disease. The methods can be used to detect
XX CC the presence of genetic polymorphisms associated with inflammatory bowel
XX CC disease and correlating their occurrence with disease states. They may be
XX CC used in this way for phenotypic correlations, forensics, paternity
XX CC testing, medicine and genetic analysis. The present sequence is a gene
XX CC containing a polymorphic site described in the exemplification of the
XX CC invention
XX SQ Sequence 700 BP; 242 A; 101 C; 137 G; 218 T; 0 U; 2 Other;

Query Match      13.4%; Score 221.6; DB 4; Length 700;
Best Local Similarity 75.3%; Pred. No. 2.4e-34;
Matches 338; Conservative 0; Mismatches 85; Indels 26; Gaps 4;

QY 1215 TGGACCAAAATTTTATGCTTGTGTTGATGAATATATATTTTAAATCTTCTCTATTGA 1274
DB 83 TGGACCAAAATTTTATGCTTGTGTTGATGAATATATATTTTAAATCTTCTCTATTGA 141
QY 1275 GCACCACTGTCATTAAGAAGTTTTCAGGTATAGACACATTAAGAACCAACTGC 1334
DB 142 GCACCACTGTCATTAAGAAGTTTTCAGGTATAGACACATTAAGAACCAACTGC 201
QY 1335 CCACGGGGAGCTGTGTGATTAATATTCCTCAAACTTGTCTTTAATAAAGAACACATAGA 1394
DB 202 GCAAGGGGTACTGTGGAAGACTATTTNAAACTTGTCTCTTAATAAGAAATACATTGA 261
QY 1395 GCGCCAAAAGTAAGTTAAAGACATTTGGCAAAACTTAAGTATATTTGCTGACTCTGC 1454
DB 262 GCGCCAAAAGTAAGTTAAAGACATTTGGCAAAACTTAAGTATATTTGCTGACTCTGC 316
QY 1455 CTGTTTTTTTTTTTTTTTTTACAGAAATGACAGTTTCTTCAATATCT- - - - -CCTC 1508
DB 317 CTATTTCTAT- - - - -GGAAATGACAGTTTCTTCTGTAATACCTATTTGTCATTT 362
QY 1509 TGTCTTTTAAACAGAAAAGGTGTGCGAGGAAAGATGGAGAGTGACAAAAGTTCTTAGACT 1568
DB 363 TTCTTTTTCACAGAAAAGGTGTGGAAGAAAGACGGAGAGTAAACCAATTCCTAGACT 422
QY 1569 ACCTGCAAGTATTTCTTGGTGTATTAACACACCGAGTGGACACCGGAAAGTTGAGAACAA 1628
DB 423 ACCTGCAAGAGTTTCTTGGTGTATTAACACACCGAGTGGATTAATAGAAAGTTGAGACTAA 482
QY 1629 CCGGCTTATTGTAGTGAAGATTTTGGAG 1657
DB 483 CTGGTTTGTGACGCCAAGATTTGGAG 511

RESULT 14
AAH92591
ID AAH92591 standard; DNA; 700 BP.
XX
XX AC AAH92591;
XX XX
XX DT 09-OCT-2001 (first entry)
XX XX
XX DE Human inflammatory bowel disease related gene fragment IGR1291a.
XX KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX XX

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OS Homo sapiens.
XX XX
XX PN WO200142511-A2.
XX XX
XX PD 14-JUN-2001.
XX XX
XX PF 11-DEC-2000; 2000WO-US033632.
XX XX
XX PR 10-DEC-1999; 98US-0170257P.
XX PR 10-APR-2000; 2000US-0196046P.
XX XX
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX XX
XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovich K;
XX XX
XX WPI; 2001-367874/38.
XX XX
XX PT Testing for the presence of polymorphisms associated with inflammatory
XX PT bowel disease, using a hybridization assay.
XX PS Disclosure; Page 261; 463pp; English.
XX XX
XX CC The present invention describes a method for detecting the presence of
XX CC polymorphisms associated with inflammatory bowel diseases such as
XX CC ulcerative colitis and Crohn's disease. The methods can be used to detect
XX CC the presence of genetic polymorphisms associated with inflammatory bowel
XX CC disease and correlating their occurrence with disease states. They may be
XX CC used in this way for phenotypic correlations, forensics, paternity
XX CC testing, medicine and genetic analysis. The present sequence is a gene
XX CC containing a polymorphic site described in the exemplification of the
XX CC invention
XX SQ Sequence 700 BP; 216 A; 117 C; 133 G; 234 T; 0 U; 0 Other;

Query Match      13.0%; Score 216; DB 4; Length 700;
Best Local Similarity 74.3%; Pred. No. 3e-33;
Matches 315; Conservative 0; Mismatches 100; Indels 9; Gaps 3;

QY 1 AGGCAAAACATGAAACATTCAGAGCTATGAGATGCTTCTGAAATTCAGTTTGTAGTCTC 60
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QY 61 TTGGGGCTGCTATGTTTCTGCTTGTGTAGAAATCCCATGATAGAGTGGTGGCAG 120
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QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGCTGATAGCGGATGGGTAATTTTCT 180
DB 399 AGACCTTTGGCACTGCTTCTACTCATCGAACTTCTGCTGATAGCAATGAGGTAATTTCT 458
QY 181 TTTTCATTCCTACAGTCTTTTAAATGCGATGGGTAATTTGGTGGTGGCTAGTT- - - - - 234
DB 459 TTATCATTCCTACAGTCTGTAAGTGCATAGGTATCATTTGTGATGGTTCCTTTACTAT 518
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DB 578 ACATCACCAGCAACATTCCTGTTAAAGTTATGAATGCTGGTGTCTGCTGTAATAATGATTG 637
QY 354 TTGTTTCTCTTTCTTTTTCAGAACCTGATGATTCCTACTCTCTGAAATAATAAATGTAAGTT 413
DB 638 -TATTTCCTTCTCTCTCCAGACTCTGAGGATTCCTGTTTCTCTGTACATAAAATGTAAGTT 696
QY 414 AAAT 417
DB 697 AAAT 700

RESULT 15

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AAH92593  
ID AH92593 standard; DNA; 700 BP.  
XX AC  
XX AAH92593;  
XX AC  
XX DT 09-OCT-2001 (first entry)  
XX DB  
XX DE Human inflammatory bowel disease related gene fragment IGR1293a.  
XX KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
XX KM single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
XX KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX OS Homo sapiens.  
XX PN WO200142511-A2.  
XX PD 14-JUN-2001.  
XX PF 11-DEC-2000; 2000WO-US033632.  
XX PR 10-DEC-1999; 99US-0170257P.  
XX PR 10-APR-2000; 2000US-0196046P.  
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX WPI; 2001-367874/38.  
XX DR  
XX PT Testing for the presence of polymorphisms associated with inflammatory  
XX PT bowel disease, using a hybridization assay.  
XX PS Disclosure; Page 262; 463pp; English.  
XX CC The present invention describes a method for detecting the presence of  
XX CC polymorphisms associated with inflammatory bowel diseases such as  
XX CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
XX CC the presence of genetic polymorphisms associated with inflammatory bowel  
XX CC disease and correlating their occurrence with disease states. They may be  
XX CC used in this way for phenotypic correlations, forensics, paternity  
XX CC testing, medicine and genetic analysis. The present sequence is a gene  
XX CC containing a polymorphic site described in the exemplification of the  
XX CC invention  
XX SQ Sequence 700 BP; 253 A; 98 C; 95 G; 254 T; 0 U; 0 Other;  
Query Match 13.0%; Score 215.4; DB 4; Length 700;  
Best Local Similarity 69.6%; Pred. No. 3.9e-33;  
Matches 368; Conservative 0; Mismatches 146; Indels 15; Gaps 5;  
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Db 3 TTTCTCACTCTAAGCTTTCTGAAAGTATTAGCAACTGAGAATTTATTTTAGAACCA 62  
Qy 794 TGGTCAGTACATGAATAATACAGTGAAGTCTATATTAATAGTCACTCCACATATT 853  
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Db 121 TAAATAATTATGACTATATCATGTGTGTGATGCAATTTGAATATGCTGGTCATATTAA 180  
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Db 181 AATGTTAAATATATAGTTTTTATTAGTCTAATAATAGATAAATAATACCAGCTAGAACTG 240  
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Qy 1153 AAGTAAAAACCTCTTGGGAGAAGGAACTTGTGTAAAAACCCCAACAAACAAAGTCAACTT 1212  
Db 409 AAACAAAAAAGTCTTTGGAGAGGGAAGTCTATGTAAATACCAACAAACAAAGCTAACTT 468  
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Db 469 TGTGGACCAAAATTTGTTTAAATAATTTTAAATTTTAAATTTGAATATAAAA 517

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Job time : 800.781 secs



GenCore version 5.1.6  
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41: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	170	10.3	610	4	AF331919	Canis fam
3	170	10.3	610	6	AR241536	Sequence
C	170	10.3	610	6	AR241537	Sequence
5	170	10.3	610	6	AR254492	Sequence
C	170	10.3	610	6	AR254493	Sequence
7	170	10.3	610	6	BD211558	Canine an
C	170	10.3	610	6	BD211559	Canine an
9	144	8.7	402	6	AR241538	Sequence
C	144	8.7	402	6	AR241539	Sequence
11	144	8.7	402	6	AR254494	Sequence
C	144	8.7	402	6	AR254495	Sequence
13	144	8.7	402	6	BD211560	Canine an
C	144	8.7	402	6	BD211561	Canine an
15	144	8.7	405	6	AR300436	Sequence
16	144	8.7	405	6	AX083939	Sequence
17	129	7.8	343	6	AX083948	Sequence
18	129	7.8	345	6	AR241540	Sequence
C	129	7.8	345	6	AR241541	Sequence
20	129	7.8	345	6	AR254496	Sequence
C	129	7.8	345	6	AR254497	Sequence
22	129	7.8	345	6	BD211562	Canine an
C	129	7.8	345	6	BD211563	Canine an
24	129	7.8	356	4	AF091133	Canis fam
25	43	2.6	520	4	OA035038	U35038 Ovis aries
26	43	2.6	1140	4	OALV1	U17052 Ovis aries
27	42	2.5	405	4	SSC010088	AJ010088 Sus scrof
28	42	2.5	529	4	SSC133452	AJ133452 Sus scrof
29	41	2.5	405	4	AF068770	Felis cat
30	41	2.5	405	4	BTNTLEUS	Z67872 B.taurus mr
31	41	2.5	838	4	AF025436	Felis cat
32	39	2.4	405	4	ECU91947	AF025436 Felis cat
33	30	1.8	354	4	AF051372	Equus cabal
34	30	1.8	144571	9	BX664726	Felis cat
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C	29	1.7	159990	9	AL954139	Human DNA
C	29	1.7	163795	9	AX005192	Human DNA
C	29	1.7	174366	9	AL590491	Human DNA
C	29	1.7	209112	2	AC084146	Human DNA
40	28	1.7	405	9	AF294756	Homo sapi
41	28	1.7	564	10	CPU34588	AF294756 Saimiri s
C	28	1.7	162083	9	AC005962	U34588 Cavia porce
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44	27	1.6	186373	9	AC006229	BX323828 Danilo fer
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## ALIGNMENTS

RESULT 1  
AF331920  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

AF331920  
Canis familiaris interleukin-5 gene, complete cds.  
AF331920  
AF331920.1 GI:15919182

Canis familiaris (dog)  
Canis familiaris

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 1658)

Yang, S., Sellins, K.S., Weber, E. and McCall, C.

Canine interleukin-5: molecular characterization of the gene and  
expression of biologically active recombinant protein

1658 bp DNA linear  
MAM 04-OCT-2001

J. Interferon Cytokine Res. 21 (6), 361-367 (2001)  
21334408  
MEDLINE  
11440633  
PUBMED  
REFERENCE  
2 (bases 1 to 1658)  
AUTHORS  
Yang, S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (22-DEC-2000) Immunology, Heeka Corporation, 1613  
Prospect Parkway, Ft Collins, CO 80525, USA  
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LOCUS AF331919 610 bp mRNA linear MAY 04-OCT-2001
DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION AF331919
VERSION AF331919.1 GI:15919180
KEYWORDS Canis familiaris (dog)
SOURCE Canis familiaris
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 610)
AUTHORS Bukayyozu, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
JOURNAL Yang, S., Sellins, K.S., Weber, E. and McCall, C.
MEDLINE Canine interleukin-5: molecular characterization of the gene and
PUBMED expression of biologically active recombinant protein
REFERENCE 2 (bases 1 to 610)
AUTHORS J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
TITLE 21334408
JOURNAL
MEDLINE
PUBMED
REFERENCE 2 (bases 1 to 610)
AUTHORS Yang, S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Immunology, Heska Corporation, 1613
JOURNAL Prospect Parkway, Ft Collins, CO 80525, USA
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DEFINITION Sequence 80 from patent US 6471957.
ACCESSION AR241536
VERSION AR241536.1 GI:27287245
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 80 29-OCT-2002;
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ACCESSION AR254492
VERSION AR254492.1 GI:27303380
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 80 19-NOV-2002;
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QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGG 170
DB 123 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGG 172
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LOCUS AR241537/c 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 82 from patent US 6471957.
ACCESSION AR241537
VERSION AR241537.1 GI:27287246
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 82 29-OCT-2002;
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QY 61 TTGGGGCTGCCTATGTTTCTGCTTGTGCTGAGAAATCCCATGAATAGACTGGTGGCAG 120
DB 548 TTGGGGCTGCCTATGTTTCTGCTTGTGCTGAGAAATCCCATGAATAGACTGGTGGCAG 489
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGG 170
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LOCUS AR254492 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 80 from patent US 6482403.
ACCESSION AR254492
VERSION AR254492.1 GI:27303380
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim, G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 80 19-NOV-2002;
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Location/Qualifiers
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Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 62
QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
Db 63 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 122
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGG 170
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGG 172

RESULT 6
AR254493/c
LOCUS AR254493 610 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 82 from patent US 6482403.
ACCESSION AR254493
VERSION AR254493.1 GI:27303381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-13 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6482403-A 82 19-NOV-2002;
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Query Match      10.3%; Score 170; DB 6; Length 610;
Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 60
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QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
Db 548 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 489
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGG 170
Db 488 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGG 439

RESULT 7
BD211558
LOCUS BD211558 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211558
VERSION BD211558.1 GI:33021328
KEYWORDS JP 2002516104-A/64.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.

RESULT 8
BD211559/c
LOCUS BD211559 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211559
VERSION BD211559.1 GI:33021329
KEYWORDS JP 2002516104-A/65.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
JOURNAL Patent: JP 2002516104-A 65 04-JUN-2002;
COMMENT
    OS Canis familiaris (dog)
    PN JP 2002516104-A/65
    PD 04-JUN-2002
    PF 28-MAY-1999 JP 2000551002
    PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAWANI S WONDERLING PC
    C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
    PC A61K39/395,
    PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
    PC C07K14/54,
    PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10,PC
    G01N33/15,
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    molecules and
    CC method of using the same
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Best Local Similarity 100.0%; Pred. No. 3e-74;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 60
Db 3 AGGCAACACTGACATTTTCAGAGCTATGAGATGCTTCTGAAATTTGAGTTGCTAGCTC 62
QY 61 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 120
Db 63 TTGGGGCTGCTATGTTTCTGCTTTCCTGCTAGAAAATCCCATGAATAGACTGGTGGCAG 122
QY 121 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGG 170
Db 123 AGACCTTGACACTGCTCTCCACTCATCGAATTTGGCTGATAGCGGATGG 172

RESULT 8
BD211559/c
LOCUS BD211559 610 bp DNA linear PAT 17-JUL-2003
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211559
VERSION BD211559.1 GI:33021329
KEYWORDS JP 2002516104-A/65.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 610)
AUTHORS Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
JOURNAL Patent: JP 2002516104-A 65 04-JUN-2002;
COMMENT
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    PN JP 2002516104-A/65
    PD 04-JUN-2002
    PF 28-MAY-1999 JP 2000551002
    PI GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAWANI S WONDERLING PC
    C12N15/09,A61K31/7088,A61K38/00,A61K39/00,A61K39/395,
    PC A61K39/395,
    PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
    PC C07K14/54,
    PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10,PC
    G01N33/15,
    PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
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    molecules and
    CC method of using the same
    FH Key Location/Qualifiers
    FT CDS (29)..(430).

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PC C07K14/54,  
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G01N33/15,  
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and feline immunoregulatory proteins, nucleic acid CC  
molecules and  
CC method of using the same  
FH Key Location/Qualifiers  
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FT /organism="Canis familiaris (dog)"  
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1..610  
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## ORIGIN

Query Match 10.3%; Score 170; DB 6; Length 610;  
Best Local Similarity 100.0%; Pred. No. 38-74; 0; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCAACACTGAACATTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCTC 60  
DB 608 AGCAACACTGAACATTCAGAGCTATGAGAAATGCTTCTGAATTTGAGTTGCTAGCTC 549  
QY 61 TTGGGCTGCTATGTTCTGCTTCTGCTAGAGAAATCCATGAATAGACTGTGGCAG 120  
DB 548 TTGGGCTGCTATGTTCTGCTTCTGCTAGAGAAATCCATGAATAGACTGTGGCAG 489  
QY 121 AGACCTTGACATGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGG 170  
DB 488 AGACCTTGACATGCTCTCCACTCATCGAACTTGGCTGATAGCGATGGG 439

## RESULT 9

AR241538  
LOCUS AR241538 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6471957.  
ACCESSION AR241538  
VERSION AR241538.1 GI:27287247  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 83 29-OCT-2002;  
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Query Match 8.7%; Score 144; DB 6; Length 402;  
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Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 86  
DB 1 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 60  
QY 87 GCTGTAGAAATCCCATGAATAGACTGGTGCGAGACCTTGACACTGCTCTCCACTCAT 146  
DB 61 GCTGTAGAAATCCCATGAATAGACTGGTGCGAGACCTTGACACTGCTCTCCACTCAT 120  
QY 147 CGAACTTGGCTGATAGCGATGGG 170  
DB 121 CGAACTTGGCTGATAGCGATGGG 144

## RESULT 10

AR241539/c

LOCUS AR241539 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 84 from patent US 6471957.  
ACCESSION AR241539  
VERSION AR241539.1 GI:27287248  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-4 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6471957-A 84 29-OCT-2002;  
FEATURES Location/Qualifiers  
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## ORIGIN

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Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 86  
DB 402 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 343  
QY 87 GCTGTAGAAATCCCATGAATAGACTGGTGCGAGACCTTGACACTGCTCTCCACTCAT 146  
DB 342 GCTGTAGAAATCCCATGAATAGACTGGTGCGAGACCTTGACACTGCTCTCCACTCAT 283  
QY 147 CGAACTTGGCTGATAGCGATGGG 170  
DB 282 CGAACTTGGCTGATAGCGATGGG 259

## RESULT 11

AR254494  
LOCUS AR254494 402 bp DNA linear PAT 20-DEC-2002  
DEFINITION Sequence 83 from patent US 6482403.  
ACCESSION AR254494  
VERSION AR254494.1 GI:27303382  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 402)  
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.  
TITLE Canine IL-13 immunoregulatory proteins and uses thereof  
JOURNAL Patent: US 6482403-A 83 19-NOV-2002;  
FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 8.7%; Score 144; DB 6; Length 402;  
Best Local Similarity 100.0%; Pred. No. 4.2e-61;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 27 ATGAGATGCTTCTGAATTTGAGTTTGTAGCTCTTGGGCTGCCTATGTTTCTGCCTTT 86  
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QY 87 GCTGTAGAAATCCCATGAATAGACTGGTGCGAGACCTTGACACTGCTCTCCACTCAT 146  
DB 61 GCTGTAGAAATCCCATGAATAGACTGGTGCGAGACCTTGACACTGCTCTCCACTCAT 120  
QY 147 CGAACTTGGCTGATAGCGATGGG 170  
DB 121 CGAACTTGGCTGATAGCGATGGG 144

## RESULT 12

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AR254495/c
LOCUS AR254495 402 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 84 from patent US 6482403.
ACCESSION AR254495
VERSION AR254495.1 GI:27303383
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 402)
  S.M.G.-K., Yang, S., Dreitz, M.J. and Wonderling, R.S.
  Caniney IL-13 immunoregulatory proteins and uses thereof
  Patent: US 6482403-A 84 19-NOV-2002;
JOURNAL
  Location/Qualifiers
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Query Match 8.7%; Score 144; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.2e-61;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTTCTGCTTT 86
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Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTTCCACTCAT 146
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Qy 147 CGAACTTGGCTGATAGCGGATGG 170
Db 282 CGAACTTGGCTGATAGCGGATGG 259

RESULT 13
BD211560 402 bp DNA linear PAT 17-JUL-2003
LOCUS BD211560
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211560.1 GI:33021330
VERSION BD211560.1
KEYWORDS JP 2002516104-A/66.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 402)
Sim, G., Yang, S., Dreitz, M.J. and Wonderling, R.S.
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 66 04-JUN-2002;
HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/21, A61K39/00, A61K39/395,
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PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
PC C07K14/54,
PC C07K14/56, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
G01N33/15,
HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/66
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/21, A61K39/00, A61K39/395,
PC A61K39/395,
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
PC C07K14/54,
PC C07K14/56, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
G01N33/15,
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
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/organism="Canis familiaris (dog)".

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Query Match 8.7%; Score 144; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.2e-61;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTTCTGCTTT 86
Db 1 ATGAGAATGCTTCTGAATTTGAGTTTCTAGCTCTTGGGGCTGCCCTATGTTTCTGCTTT 60
Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGGAGACCTTGACACTGCTTCCACTCAT 120
Qy 147 CGAACTTGGCTGATAGCGGATGG 170
Db 121 CGAACTTGGCTGATAGCGGATGG 144

RESULT 14
BD211561/c 402 bp DNA linear PAT 17-JUL-2003
LOCUS BD211561
DEFINITION Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION BD211561.1 GI:33021331
VERSION BD211561.1
KEYWORDS JP 2002516104-A/67.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 402)
Sim, G., Yang, S., Dreitz, M.J. and Wonderling, R.S.
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 67 04-JUN-2002;
HESKA CORP
OS Canis familiaris (dog)
PN JP 2002516104-A/67
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PI GEKKEE SIM, SHUMIN YANG, MATTHEW J DREITZ, RAMANI S WONDERLING PC
C12N15/09, A61K31/7088, A61K38/21, A61K39/00, A61K39/395,
PC A61K39/395,
PC A61K45/00, A61K48/00, A61P37/02, A61P37/04, C07K14/475, C07K14/535,
PC C07K14/54,
PC C07K14/56, C07K16/24, C07K16/28, C12N1/21, C12N5/10, PC
G01N33/15,
PC G01N33/50, C12N15/00, A61K37/02, A61K37/66, C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.2e-61;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 342 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 283
Qy 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 282 CGAACTTGGCTGATAGCGGATGGG 259
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RESULT 15
AR300436
LOCUS AR300436 405 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6537781.
ACCESSION AR300436
VERSION AR300436.1 GI:31687875
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 405)
AUTHORS Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.
TITLE Methods and compositions concerning canine interleukin 5
JOURNAL Patent: US 6537781-A 1 25-MAR-2003;
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source Location/Qualifiers
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ORIGIN

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Query Match 8.7%; Score 144; DB 6; Length 405;
Best Local Similarity 100.0%; Pred.No. 4.2e-61;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAAATGCTTCGAATTTGAGTTTCTAGCTCTTGGGGCTGCCTATGTTTCTGCCTTT 60
Qy 87 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 146
Db 61 GCTGTAGAAAATCCCATGAATAGACTGGTGGCAGAGACCTTGACACTGCTCTCCACTCAT 120
Qy 147 CGAACTTGGCTGATAGCGGATGGG 170
Db 121 CGAACTTGGCTGATAGCGGATGGG 144
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